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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:35:40 ; Search time :57.2 Seconds

(Without alignments)
11.880 Million cell updates/sec

Title: US-08-934-367-32

Perfect score: 102
Sequence: 1 GELFQEVGFPSSQAQVTVH 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_14:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	29.4	20	6 Q9TR70	Q9TR70 ursus arcto
2	29	28.4	16	13 P82388	P82388 litorea ran
3	29	28.4	16	13 P82392	P82392 litorea ran
4	27	26.5	19	5 Q9TRK8	Q9TRK8 trypanosoma
5	27	26.5	19	12 Q84274	Q84274 human papil
6	27	26.5	20	5 Q9TWW8	Q9TWW8 dermatophag
7	26	25.5	19	10 Q04817	Q04817 sporobolus
8	26	25.5	20	2 Q9R424	Q9R424 proteus mir
9	26	25.5	20	4 Q9UC43	Q9UC43 proteus mir
10	25.5	25.0	20	10 Q9S8T0	Q9S8T0 artocarpus
11	25	24.5	18	5 Q9TWL4	Q9TWL4 lucilia cup
12	25	24.5	19	2 Q06140	Q06140 melissaria m
13	25	24.5	19	2 Q9R511	Q9R511 brevilbacter
14	24	23.5	18	5 Q9UR87	Q9UR87 drosophila
15	24	23.5	19	11 Q62637	Q62637 rattus norv
16	23	22.5	15	5 Q9TWP5	Q9TWP5 artemia (br
17	23	22.5	16	13 P82389	P82389 litorea aur
18	23	22.5	16	13 P82390	P82390 litorea aur
19	23	22.5	17	4 Q9UC13	Q9UC13 homo sapien

20	23	22.5	17	11 Q9QWC2	Q9QWC2 rattus sp.
21	23	22.5	18	6 Q9TR30	Q9TR30 saginus la
22	23	22.5	18	10 Q9S892	Q9S892 glycine max
23	23	22.5	19	13 P82095	P82095 uperolela m
24	23	22.5	20	4 Q9UD25	Q9UD25 homo sapien
25	22	21.6	14	11 Q10734	Q10734 mus musculu
26	22	21.6	15	12 Q88954	Q88954 vaccinia vl
27	22	21.6	16	2 Q9R514	Q9R514 porphyromon
28	22	21.6	17	6 Q9TRD5	Q9TRD5 oryctolagus
29	22	21.6	18	4 Q14042	Q14042 homo sapien
30	22	21.6	19	2 Q9R5A9	Q9R5A9 artirobacte
31	22	21.6	19	4 Q9UCG2	Q9UCG2 rattus sp.
32	22	21.6	20	11 Q9QU77	Q9QU77 rattus sp.
33	22	21.6	20	13 Q9PRR8	Q9PRR8 gadus morhu
34	22	21.6	20	13 Q9PRR3	Q9PRR3 scyllorhinu
35	21.5	21.1	18	6 Q9TRB6	Q9TRB6 sus scrofa
36	21.5	21.1	20	4 Q9UCM1	Q9UCM1 homo sapien
37	21	20.6	9	11 Q9QW70	Q9QW70 mus musculu
38	21	20.6	9	12 Q88953	Q88953 vaccinia vl
39	21	20.6	10	12 Q85462	Q85462 avian sarco
40	21	20.6	13	2 Q50038	Q50038 mycobacteri
41	21	20.6	15	11 Q9Q0Z5	Q9Q0Z5 mus sp. 38-
42	21	20.6	16	4 Q9UC48	Q9UC48 homo sapien
43	21	20.6	16	13 P82391	P82391 litorea aur
44	21	20.6	20	4 Q9UMU3	Q9UMU3 homo sapien
45	21	20.6	20	6 Q9TRH6	Q9TRH6 canis famli

ALIGNMENTS

RESULT 1
Q9TR70 PRELIMINARY: PRT: 20 AA.
AC Q9TR70:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE HAPTOGLOBIN BETA CHAIN (FRAGMENT).
OS Ursus arctos (Brown bear) (Grizzly bear).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
RN [1]
RP SEQUENCE.
RX MEDLINE: 95268704.
RA Mononuki K., Nakagawa-Tosa N., Morimatsu M., Syuto B., Saito M.;
RT "Haptoglobin in Carnivora: a unique molecular structure in bear, cat
and dog haptoglobins.";
RL Comp. Biochem. Physiol. Biochem. Mol. Biol. 110:785-789(1995).
SQ SEQUENCE 20 AA: 2020 MW: F605BCC82667DC3F CRC64;

Query Match 29.4%; Score 30; DB 6; Length 20;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 GGFPSQAQV 17
Db 10 GSFPXQAKM 18
RESULT 2
P82388 PRELIMINARY: PRT: 16 AA.
AC P82388:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE AUREIN 2.1/2.1.1.
OS Litorea raniformis, and Litorea aurea (Australian frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litorea.

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RN [1]
RA SEQUENCE.
RP Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer aurein peptides from the Australian
RT bell frogs Litoria aurea and Litoria raniformis.";
RC Eur. J. Biochem. 0:0-0(2000).
CL -1- FUNCTION: AUREIN 2.1 HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
KW Amidation; Antibiotic.
FT PEPTIDE 3
FT MOD_RES 16
SQ SEQUENCE 16 AA; 1616 MW; 1D9A5DADB4D40F9 CRC64;

Query Match
Best Local Similarity 28.4%; Score 29; DB 13; Length 16;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 EIFQEVVGFPSS 13
   :|:|:|:|:|
DB 4 DIVKVVGAFGS 15

RESULT 3
P82392 PRELIMINARY; PRT; 16 AA.
AC P82392;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE AUREIN 2.5.
OS Litoria raniformis, and Litoria aurea (Australian frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
RN [1]
RP SEQUENCE.
RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer aurein peptides from the Australian
RT bell frogs Litoria aurea and Litoria raniformis.";
RC Eur. J. Biochem. 0:0-0(2000).
CL -1- FUNCTION: HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
KW Amidation; Antibiotic.
FT MOD_RES 16
SQ SEQUENCE 16 AA; 1650 MW; 1D9A5DADB4DAE2F9 CRC64;

Query Match
Best Local Similarity 28.4%; Score 29; DB 13; Length 16;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 EIFQEVVGFPSS 13
   :|:|:|:|:|
DB 4 DIVKVVGAFGS 15

RESULT 4
O9TWK8 PRELIMINARY; PRT; 19 AA.
AC O9TWK8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE HAPOGLOBIN-RELATED PROTEIN BETA SUBUNIT (FRAGMENT).
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
RN [1]
RP SEQUENCE.
RX MEDLINE; 95232503.
RA Smith A.B., Esko J.D., Hajduk S.L.;
RT "Killing of trypanosomes by the human haptogloblin-related protein.";
RL Science 268:264-266(1995).
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SQ SEQUENCE 19 AA; 2055 MW; 65BD135667C94056 CRC64;

Query Match
Best Local Similarity 26.5%; Score 27; DB 5; Length 19;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 GGFPSQAOV 17
   | | | | |
DB 10 GGFPSQAKM 18

RESULT 5
O84274 PRELIMINARY; PRT; 19 AA.
ID O84274;
AC O84274;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE E6 PROTEIN (FRAGMENT).
OS Human papillomavirus type 25.
OC Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88089511.
RA Krubke J., Kraus J., Delius H., Chow L., Broker T.R., Iftner T.,
RA Pfister H.;
RT "Genetic relationship among human papillomaviruses associated with
RT benign and malignant tumours of patients with epidermodysplasia
RT verruciformis.";
RL J. Gen. Virol. 68:3091-3103(1987).
DR EMBL; D00205; BAA00145.1; -.
FT NON_TER 19
SQ SEQUENCE 19 AA; 1955 MW; 5C820487F69A5ED1 CRC64;

Query Match
Best Local Similarity 26.5%; Score 27; DB 12; Length 19;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GGFPSQAOV 17
   | | | | |
DB 11 GGFPSQAOV 18

RESULT 6
O9TWV8 PRELIMINARY; PRT; 20 AA.
ID O9TWV8;
AC O9TWV8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE TRYPSIN-LIKE PROTEASE (DER F III ALLERGEN HOMOLOG) (FRAGMENT).
OS Dermatophagoides farinae (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptiformes; Astigmata; Analgoidea; Pyroglyphidae;
OC Dermatophagoides.
RN [1]
RP SEQUENCE.
RX MEDLINE; 93074427.
RA Ando T., Homma R., Ito G., Miyahara A., Yamakawa H., Iwaki M.,
RA Okumura Y., Suko M., Haida M.;
RT "Is a trypsin-like protease of mites a Der f III allergen?";
RL Jpn. J. Allergy 41:704-707(1992).
SQ SEQUENCE 20 AA; 2087 MW; 961537685DB396A2 CRC64;
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Query Match
Best Local Similarity 26.5%; Score 27; DB 5; Length 20;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 VVGGFPSQA 15
   :|:|:|:|:|
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DT 01-MAR-1992 (Rel. 21, last sequence update)
 DT 15-JUL-1998 (Rel. 36, last annotation update)
 DE FERREDOXIN-NAD(+) REDUCTASE (EC 1.18.1.3) (FRAGMENT).
 OS Streptomyces griseus.
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 RN [1]
 RP SEQUENCE.
 RA MEDLINE: 92041607.
 RX Ramachandra M., Seetharam R., Emplage M.H., Sarlasani F.S.;
 RT "Purification and characterization of a soybean flour-inducible
 ferredoxin reductase of Streptomyces griseus.";
 RL J. Bacteriol. 173:7106-7112(1991).
 CC -1- FUNCTION: COUPLE ELECTRON TRANSFER FROM NADH TO CYTOCHROME
 P450(SOY) IN THE PRESENCE OF FERREDOXIN.
 CC -1- CATALYTIC ACTIVITY: REDUCED FERREDOXIN + NAD(+) = OXIDIZED
 FERREDOXIN + NADH.
 CC -1- COFACTOR: FAD; REQUIRES MAGNESIUM.
 CC HSSP: P09063; 11VL.
 KW Oxidoreductase; Flavoprotein; NAD; FAD; Magnesium.
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1485 MW; 27D11A7C37AC0510 CRC64;

Query Match 21.6%; Score 22; DB 1; Length 16;
 Best Local Similarity 50.0%; Pred. No. 9.5e+02;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 VVGFP 12
 Db 5 IICGP 10

RESULT 14
 ID FIXA_RHILE STANDARD; PRT; 18 AA.
 AC P14313;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE FIXA PROTEIN (FRAGMENT).
 GN FIXA.
 OS Rhizobium leguminosarum.
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Rhizobiaceae; Rhizobium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90066358.
 RA Hontelez J.G.J., Lankhorst R.K., Katinakis P., van den Bos R.C.,
 RA van Kammen A.;
 RT "Characterization and nucleotide sequence of a novel gene fixw
 upstream of the fixABC operon in Rhizobium leguminosarum.";
 RL Mol. Genet. 218:536-544(1989).
 CC -1- FUNCTION: MAY PLAY A ROLE IN A REDOX PROCESS INVOLVED IN NITROGEN
 FIXATION.
 CC -1- SUBUNIT: FIXA AND FIXB FORM A HETERODIMER (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE ETF BETA-SUBUNIT / FIXA FAMILY.
 CC -----
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 CC -----
 CC EMBL: X16521; CAA34527.1; -.
 DR PIR: P00022; P00022.
 DR INTERPRO: IPR000049; -.
 DR PROSITE: PS01065; ETF_BETA; PARTIAL.
 KW Electron transport; Nitrogen fixation.
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 2036 MW; 74973C8BA2087663 CRC64;

Query Match 21.6%; Score 22; DB 1; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 PSQAQTV 19
 Db 11 PSQAQIRV 18

RESULT 15
 ID TCBI_TRILO STANDARD; PRT; 19 AA.
 AC P80070;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE TRICHOLOLONGIN BI AND BII.
 OS Trichoderma longibrachiatum.
 CC Eukaryota; Fungi; Ascomycota; anamorphic Ascomycota; Trichoderma.
 RN [1]
 RP SEQUENCE, AND STRUCTURE BY NMR.
 RX MEDLINE: 92037622.
 RA Rebuffat S., Prigent Y., Auvin-Guette C., Bodo B.;
 RT "Tricholongs BI and BII, 19-residue peptides from Trichoderma
 longibrachiatum. Solution structure from two-dimensional NMR
 spectroscopy.";
 RL Eur. J. Biochem. 201:661-674(1991).
 CC -1- FUNCTION: TRICHOLOLONGINS ARE PEPTIDES WHICH DISPLAY ANTIFUNGAL
 CC AND ANTIBACTERIAL ACTIVITY. PROBABLY INTERACT WITH BIOLOGICAL
 CC MEMBRANES AND PROBABLY PRODUCES HOLES LEADING TO LEAKAGE.
 CC -1- PTM: AIB IS ALPHA-AMINO ISOBUTYRIC ACID.
 CC -1- PTM: IVA IS ISOVALINE.
 KW Antibiotic; Fungicide; Methylation; Acetylation; Hydroxylation;
 KW Membrane.
 FT MOD_RES 1 1 ACETYLATION. (TO FORM AIB).
 FT MOD_RES 1 1 METHYLATION (TO FORM AIB).
 FT MOD_RES 4 4 METHYLATION (TO FORM AIB).
 FT MOD_RES 5 5 METHYLATION (TO FORM AIB).
 FT MOD_RES 7 7 METHYLATION (TO FORM AIB).
 FT MOD_RES 8 8 METHYLATION (TO FORM AIB).
 FT MOD_RES 9 9 METHYLATION (TO FORM AIB).
 FT MOD_RES 12 12 METHYLATION (TO FORM AIB).
 FT MOD_RES 15 15 METHYLATION (TO FORM AIB).
 FT MOD_RES 16 16 METHYLATION (TO FORM AIB).
 FT MOD_RES 16 16 METHYLATION (TO FORM AIB).
 FT MOD_RES 19 19 ETHYLATION (TO FORM IVA; IN BII).
 FT MOD_RES 19 19 HYDROXYLATION.
 SQ SEQUENCE 19 AA; 1756 MW; B908C2DFF83D238 CRC64;

Query Match 21.6%; Score 22; DB 1; Length 19;
 Best Local Similarity 40.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFPSQAQTV 19
 Db 2 GFPAQMAASL 11

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 Job time: 442 sec

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 OC Urodelele.
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RA TISSUE-SKIN SECRETION;
 RC Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "New antibiotic uperin peptides from the dorsal glands of the
 Australian toadlet *Urodelele mobergii*.";
 RL Aust. J. Chem. 49:1325-1331(1996).
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MM=1948; METHOD=FAE.
 KM Amphibian skin.
 SQ SEQUENCE 19 AA; 1949 MW; 24E4F83A6BA35F21 CRC64;

Query Match 22.5%; Score 23; DB 1; Length 19;
 Best Local Similarity 44.4%; Pred. No. 7.8e+02;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 EFOEVVGG 10
 Db 4 DIKKLVGG 12

RESULT 10
 TRYL-STREX STANDARD; PRT; 20 AA.
 AC P80420;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE TRYPSIN-LIKE PROTEASE (EC 3.4.21.-) (FRAGMENT).
 OS Streptomyces exfoliatus (Streptomyces hydroganans).
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-SMF13;
 RX MEDLINE: 95291424.
 RA Kim I.S., Lee K.J.;
 RT "Physiological roles of leupeptin and extracellular proteases in
 mycelium development of Streptomyces exfoliatus SMF13.";
 RL Microbiology 141:1017-1025(1995).
 CC -1- FUNCTION: INVOLVED IN MYCELIAL DIFFERENTIATION.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2A; ALSO KNOWN AS THE
 CC ALPHA-LYTIC PROTEASE FAMILY.
 DR HSSP: P00775; 1SGT.
 DR INTERPRO: IPR001254;
 DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
 DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
 KM Hydrolyase; Serine protease.
 FT NON_TER 20
 FT SEQUENCE 20 AA; 2129 MW; 4568F56D0E7393AF CRC64;

Query Match 22.5%; Score 23; DB 1; Length 20;
 Best Local Similarity 36.4%; Pred. No. 8.2e+02;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 9 GGFPSQAQVTV 19
 Db 10 GNFPFOOXISM 20

RESULT 11
 SAMP_MUSCA STANDARD; PRT; 9 AA.
 AC P19095;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SERUM AMYLOID P-COMPONENT (SAP) (FRAGMENT).
 OS Mustelus canis (Smooth dogfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphi; Galeidae; Carcharhiniformes; Triakidae;
 OC Mustelus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 83160932.
 RA Robey F.A., Tanaka T., Liu T.-Y.;
 RT "Isolation and characterization of two major serum proteins from the
 RT dogfish, *Mustelus canis*, C-reactive protein and amyloid P
 component.";
 RL J. Biol. Chem. 258:3889-3894(1983).
 CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
 CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
 CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
 DR INTERPRO: IPR001759;
 DR PROSITE: PS00289; PENTAXIN; PARTIAL.
 KM Amyloid; Glycoprotein; Plasma; Pentaxin.
 FT DOMAIN 1
 FT NON_TER 9
 FT SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match 21.6%; Score 22; DB 1; Length 9;
 Best Local Similarity 37.5%; Pred. No. 8.8e+04;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 10 GGFPSQAQV 17
 Db 1 GFPSKSLI 8

RESULT 12
 UN46_CLOPA STANDARD; PRT; 14 AA.
 ID UN46_CLOPA
 AC P81362;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE UNKNOWN PROTEIN CP 46 FROM 2D-PAGE (FRAGMENT).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=M5;
 RX MEDLINE: 98291870.
 RA Flensburg R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5.";
 RL Electrophoresis 19:802-806(1998).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.4, ITS MW IS: 38.2 KDA.
 FT NON_TER 14
 FT SEQUENCE 14 AA; 1550 MW; 198078F4C0367170 CRC64;

Query Match 21.6%; Score 22; DB 1; Length 14;
 Best Local Similarity 42.9%; Pred. No. 8.3e+02;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 IFQEVVG 9
 Db 2 IFNDLIG 8

RESULT 13
 FENR_STRGR STANDARD; PRT; 16 AA.
 ID FENR_STRGR
 AC P24134;
 DT 01-MAR-1992 (Rel. 21, Created)

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 EIFQEVWG 10
: : : : :
Db 4 DLAKVVG 12

RESULT 6
UP23_UPEIN STANDARD: PRT: 19 AA.
AC P82029;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE UPERIN 2.3.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Uperoleia.
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
RA Adams G.W., Severini C.;
RT "Novel upeirin peptides from the dorsal glands of the Australian
RT floodplain toadlet Uperoleia inundata.";
RL Aust. J. Chem. 49:475-484(1996).
CC -1- FUNCTION: SHOWS A MEDIUM ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS,
CC L. MESENTERIDES AND S.UBERIS.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=1974; METHOD=FA-B.
KW Amphibian skin; Antibiotic.
SQ SEQUENCE 19 AA; 1975 MW; 2F34EF07BA35B70 CRC64;

Query Match 23.5%; Score 24; DB 1; Length 19;
Best Local Similarity 44.4%; Pred. No. 5.2e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 EIFQEVWG 10
: : : : :
Db 4 DLAKVVG 12

RESULT 7
COG1_CHIOP STANDARD: PRT: 20 AA.
AC P84153;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE COLLAGENOLYTIC PROTEASE 25 KDA II/III (EC 3.4.21.32) (FRAGMENT).
OS Chionoecetes opilio (Crab-beetle).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Majoidae; Majidae; Chionoecetes.
RN [1]
RP SEQUENCE.
RC TISSUE=HEPATOPANCREAS;
RX MEDLINE; 92120073.
RA Klimova O.A., Vedishcheva Y.V., Strongin A.Y.;
RT "Isolation and characteristics of collagenolytic enzymes from the
RT hepatopancreas of the crab Chionoecetes opilio.";
RL Dokl. Akad. Nauk SSSR 317:482-484(1991).
CC -1- FUNCTION: THIS ENZYME IS A SERINE PROTEASE CAPABLE OF DEGRADING
CC THE NATIVE TRIPLE HELIX OF COLLAGEN.
CC -1- CATALYTIC ACTIVITY: BROAD SPECIFICITY; DEGRADATES NATIVE COLLAGEN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR HSSP: P00771; 1A2Z.
DR INTERPRO: IPR001254; -
DR PROSITE: PS00134; TRYPSIN_HIS. PARTIAL.
DR PROSITE: PS00135; TRYPSIN_SER. PARTIAL.

KW Hydrolase; Serine protease; Collagen degradation.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2204 MW; CE0D7B996E7281A7 CRC64;

Query Match 23.5%; Score 24; DB 1; Length 20;
Best Local Similarity 35.7%; Pred. No. 5.5e+02;
Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 7 VVGFPQAQVTVH 20
: : : : :
Db 1 IVGQEARPHPTWVH 14

RESULT 8
CPAX_BOVIN STANDARD: PRT: 18 AA.
AC P22779;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450 2A (OLEF2) (OLEFACTIVE) (P52) (EC 1.14.14.1) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovioidea;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RX MEDLINE; 91027757.
RA Lazard D., Tal N., Rubinstein M., Khen M., Lancet D., Zupko K.;
RT "Identification and biochemical analysis of novel olfactory-specific
RT cytochrome P-450IIA and UDP-glucuronosyl transferase.";
RL Biochemistry 29:7433-7440(1990).

CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC ACIDS, AND XENOBIOTICS.

CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

DR PIR: A35704; A35704.
DR INTERPRO: IPR001128; -
DR PROSITE: PS00086; CYTOCHROME_P450; PARTIAL.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum; Olfaction.
FT NON_TER 1 6 G -> D.
FT VARIANT 11 11 A -> E.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2058 MW; F80746F76CDD77FF CRC64;

Query Match 22.5%; Score 23; DB 1; Length 18;
Best Local Similarity 44.4%; Pred. No. 7.3e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 OEIFQEVWG 9
: : : : :
Db 9 OQAFKELOG 17

RESULT 9
UP27_UPEMJ STANDARD: PRT: 19 AA.
AC P82039;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE UPERIN 2.7.
OS Uperoleia mjobergii (Australian toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RESULT 2

COCO_LIMPO STANDARD: PRT: 14 AA.
 AC P35586;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE COCONASE (EC 3.4.21.-) (FRAGMENT)
 OS Limulus polyphemus (Atlantic horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 Limulidae; Limulus.
 CC [1]
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 78037243.
 RA Law J.H., Dunn P.E., Kramer K.J.;
 RT Insect proteases and peptidases.
 CC Adv. Enzymol. Relat. Areas Mol. Biol. 45:389-425(1977).
 CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC HSSP: P00760; 4TP1.
 DR INTERPRO: IPR001254;
 DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
 DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
 KM Hydrolase; Serine protease.
 FT NON_TER 14
 SQ SEQUENCE 14 AA; 1452 MW; 1615FB1D73747570 CRC64;

Query Match 24.5%; Score 25; DB 1; Length 14;
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 VVGGF 11
 :|||
 Db 1 IVGGF 5

RESULT 3

TRYP_FELCA STANDARD: PRT: 16 AA.
 ID TRYP_FELCA
 AC P81071;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TRYPSIN PRECURSOR (EC 3.4.21.4) (FRAGMENT).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 CC [1]
 RN [1]
 RP SEQUENCE.
 RX TISSUE-PANCREAS;
 RX MEDLINE: 97235546.
 RA Steiner J.M., Medinger T.L., Williams D.A.;
 RT Purification and partial characterization of feline trypsin.
 CC Comp. Biochem. Physiol. 116B:87-93(1997).
 CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC INTERPRO: IPR001254;
 DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
 DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
 KM Hydrolase; Serine protease; Digestion; Pancreas; Zymogen.
 FT PROPEP 1
 FT CHAIN 9 >16
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1825 MW; A6D751B58760A86 CRC64;

Query Match 23.5%; Score 24; DB 1; Length 16;
 Best Local Similarity 33.3%; Pred. No. 4.4e+02;
 Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 6 EYVGCFPSQ 14
 :|||:
 Db 8 KIVGGYTNR 16

RESULT 4

ALL7_OLEU STANDARD: PRT: 19 AA.
 ID ALL7_OLEU
 AC P81430;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE POLLEN ALLERGEN OLE E 7 (OLE E VII) (FRAGMENT).
 OS Olea europaea (Common olive).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Lamiales; Oleaceae; Olea.
 CC [1]
 RN [1]
 RP SEQUENCE.
 RC TISSUE-POLLEN;
 RA Tejera M.L., Villalba M., Rodriguez R.;
 RT Isolation and characterization of Ole e 7, a new allergen from olive
 RT tree pollen.
 RL Submitted (JUL-1998) to the SWISS-PROT data bank.
 KM Allergen.
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 1986 MW; 999A5008C41A67E CRC64;

Query Match 23.5%; Score 24; DB 1; Length 19;
 Best Local Similarity 71.4%; Pred. No. 5.2e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 12 PSQAQVT 18
 ||| |
 Db 2 PSQGTVT 8

RESULT 5

UP22_UPEIN STANDARD: PRT: 19 AA.
 ID UP22_UPEIN
 AC P82028;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE UPERIN 2.2.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 OC Uperoleia.
 CC [1]
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-SKIN SECRETION;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini G.;
 RT Novel uperin peptides from the dorsal glands of the Australian
 RT floodplain toadlet Uperoleia inundata.
 CC Aust. J. Chem. 49:475-484(1996).
 CC -1- FUNCTION: SHOWS A WEAK ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS,
 CC E.COLI, L.MESENTERIOIDES, L.INNOCUA, M.LUTEUS, P.HAEMOLYTICA,
 CC S.AUREUS AND S.UBERTIS
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=1926; METHOD=FAV.
 KM Amphibian skin; Antibiotic.
 SQ SEQUENCE 19 AA; 1927 MW; 3283EF077BA35B70 CRC64;

Query Match 23.5%; Score 24; DB 1; Length 19;
 Best Local Similarity 44.4%; Pred. No. 5.2e+02;

Db 3 VSGGFAS 9

RESULT 14

PA0026

protein QA300027 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997

C:Accession: PA0026

R:Ramo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional

A:Reference number: PA0001

A:Accession: PA0026

A:Molecule type: protein

A:Residues: 1-15 <KAM>

A:Experimental source: leaf

Query Match

22.5%; Score 23; DB 2; Length 15;

Best Local Similarity 45.5%; Pred. No. 1,le+03;

Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 8 VGGFPSQAQVT 18

1 1 1 1 1

Db 4 VVGXPFAXQIT 14

RESULT 15

A35704

cytochrome P450 olf2 - bovine (fragment)

N:Contains: oxidoreductase (EC 1.-.-.-)

C:Species: Bos primigenius taurus (cattle)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 12-Mar-1999

C:Accession: A35704

R:Lazard, D.; Tal, N.; Rubinstein, M.; Khen, M.; Lancet, D.; Zupko, K.

Biochemistry 29, 7433-7440, 1990

A:Title: Identification and biochemical analysis of novel olfactory-specific cytochrome

A:Reference number: A35704; MUID:91027757

A:Accession: A35704

A:Molecule type: protein

A:Residues: 1-18 <LAZ>

C:Gene: CYP2A

C:Genetics:

C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C:Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane protei

Query Match

22.5%; Score 23; DB 2; Length 18;

Best Local Similarity 44.4%; Pred. No. 1,4e+03;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 OEIPEVVG 9

1 1 1 1 1

Db 9 QQAFFKELDG 17

Search completed: December 21, 2000, 08:30:07
Job time: 271 sec

A:Experimental source: cytolytic T-lymphocyte
 C:Superfamily: Immunoglobulin homology
 C:Keywords: receptor; T-cell

Query Match 24.5%: Score 25; DB 2; Length 15;
 Best Local Similarity 83.3%: Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 VGGFPS 13
 |||||
 Db 5 VGGFAS 10

RESULT 9

A20190
 hypodermin B - early cattle grub (fragment)
 C:Species: Hypoderma lineatum (early cattle grub)
 C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Jun-1993
 C:Accession: A20190
 R:Leclercq, A.; Tong, N.T.; Kell, B.
 Eur. J. Biochem. 134, 261-267, 1983
 A:Title: Hypodermin B, a trypsin-related enzyme from the insect Hypoderma lineatum.
 A:Reference number: A20190; MUID:83261874
 A:Accession: A20190
 A:Molecule type: Protein
 A:Residues: 1-16 <LECC>

Query Match 24.5%: Score 25; DB 2; Length 16;
 Best Local Similarity 80.0%: Pred. No. 5.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVGGF 11
 :|||
 Db 1 IVGGF 5

RESULT 10

A45806
 T-cell receptor beta chain C region type 1 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Jul-1999
 C:Accession: A45806
 R:Dent, A.L.; Fink, P.J.; Hedrick, S.M.
 J. Immunol. 143, 322-328, 1989
 A:Title: Characterization of an alternative exon of the murine T cell receptor beta chain
 A:Reference number: A45806; MUID:89278666
 A:Accession: A45806
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-20 <DEN>
 A:Cross-references: GB:M27225; NID:q339373; PIDN:AAA61099.1; PID:g553781
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: T-cell receptor

Query Match 24.0%: Score 24.5; DB 2; Length 20;
 Best Local Similarity 35.3%: Pred. No. 8.6e+02;
 Matches 6; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 2 EIVGVGGF-PSQAQV 17
 :|||
 Db 4 KVFPPEVAVFEPSEAEI 20

RESULT 11

I52698
 hypothetical THRA1/BTR mutant fusion protein, cell line BT474 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
 C:Accession: I52698
 R:Putreal, P.A.; Cochran, C.; Marks, J.R.; Iglehart, J.D.; Zimmerman, W.; Barrett, J.C.;

Cancer Res. 54, 1791-1794, 1994
 A:Title: Mutation analysis of the THRA1 gene in breast cancer: deletion/fusion of the
 A:Reference number: I52698; MUID:94185019
 A:Accession: I52698

A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-15 <FUT>
 A:Cross-references: GB:S71020; NID:q546111; PIDN:AAB30341.1; PID:g546112
 C:Comment: This sequence is the chimeric product of a deletion or translocation mutat
 C:Genetics:
 A:Gene: THRA1/BTR
 A:Map position: 17q11.2
 C:Keywords: fusion protein

Query Match 23.5%: Score 24; DB 4; Length 15;
 Best Local Similarity 50.0%: Pred. No. 7.5e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 11 PPSQAQVTVH 20
 | | : | | |
 Db 3 PSEQFRVOVH 12

RESULT 12

PC2241
 heat shock protein 42A - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 17-Mar-1999
 C:Accession: PC2241
 R:Hataiyama, T.; Yasuda, K.; Nishiyama, E.
 Biochem. Biophys. Res. Commun. 204, 357-365, 1994
 A:Title: Characterization of high-molecular-mass heat shock proteins and 42oc-specific
 A:Reference number: PC2238; MUID:95032120
 A:Accession: PC2241
 A:Molecule type: protein
 A:Residues: 1-17 <HAT>
 C:Keywords: heat shock; stress-induced protein

Query Match 23.5%: Score 24; DB 2; Length 17;
 Best Local Similarity 80.0%: Pred. No. 8.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 EVVGG 10
 | : |||
 Db 8 EIVGG 12

RESULT 13

PH1448
 T-cell receptor alpha chain (clone A24/PEG2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C:Accession: PH1448
 R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.;
 J. Exp. Med. 177, 811-820, 1993
 A:Title: T cell receptor selection by and recognition of two class I major histocompa
 A:Reference number: PH1430; MUID:93171821
 A:Accession: PH1448
 A:Molecule type: mRNA
 A:Residues: 1-14 <CAS>
 A:Experimental source: cytolytic T-lymphocyte
 C:Superfamily: immunoglobulin homology
 C:Keywords: receptor; T-cell

Query Match 22.5%: Score 23; DB 2; Length 14;
 Best Local Similarity 71.4%: Pred. No. 1e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 VVGGFPS 13
 | ||| |

RESULT 3
S56122
Type I DNA methyltransferase M.Ecor124 I chain HsdM - Escherichia coli (fragments)
C:Species: Escherichia coli
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
C:Accession: S56122
R:Webb, M.; Taylor, I.A.; Firman, K.; Kneale, G.G.
J. Mol. Biol. 250, 181-190, 1995
A:Title: Probing the domain structure of the type IC DNA methyltransferase M.Ecor124I by
A:Reference number: S56121; MUID:95333175
A:Accession: S56122
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <WEB>

Query Match 25.5%; Score 26; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 10 GPPSOA 15
DB 7 GYPSA 12

RESULT 4
A61392
brain-associated small cell lung cancer antigen - human (fragment)
N:Alternate names: BASCA
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Sep-1994
C:Accession: A61392
R:Umezawa, Y.; Kuge, S.; Kikyo, N.; Shirai, T.; Watanabe, J.; Fujiwara, M.; Okabe, T.
Jpn. J. Clin. Oncol. 21, 251-255, 1991
A:Title: Identity of brain-associated small cell lung cancer antigen and the CD56 (NKH-1
A:Reference number: A61392; MUID:92046737
A:Accession: A61392
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <UME>

Query Match 25.5%; Score 26; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 12 PSQAQVTV 19
DB 7 PSQGEISV 14

RESULT 5
C34917
catechol 1,2-dioxygenase (EC 1.13.11.1) beta chain - Pseudomonas sp. (fragment)
N:Alternate names: pyrocatechase beta chain
C:Species: Pseudomonas sp.
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 10-Feb-1995
C:Accession: C34917
R:Nakai, C.; Horike, K.; Kuramitsu, S.; Kagamiyama, H.; Nozaki, M.
J. Biol. Chem. 265, 660-665, 1990
A:Title: Three isozymes of catechol 1,2-dioxygenase (pyrocatechase), alphaalpha, alpha
A:Reference number: A34917; MUID:90110118
A:Accession: C34917
A:Molecule type: protein
A:Residues: 1-20 <NAK>
C:Keywords: heterodimer; homodimer; oxidoreductase

Query Match 25.5%; Score 26; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 4.8e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 QEFQEVVG 9

DB 11 QQFFENAG 19

RESULT 6
S29636
jacalin beta-1 chain - Artocarpus champeden (fragment)
C:Species: Artocarpus champeden
C:Date: 19-Mar-1997 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
C:Accession: S29636
R:Ngoc, L.D.; Brillard, M.; Hoebeke, J.
Biochim. Biophys. Acta 1156, 219-222, 1993
A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17
A:Reference number: S29635; MUID:93152601
A:Accession: S29636
A:Molecule type: protein
A:Residues: 1-20 <NGO>
A:Experimental source: seed
C:Complex: heterotetramer; two alpha and two beta chains
C:Function: seed storage protein
A:Description: seed storage protein
A:Note: lectin for D-galactosyl-beta-1-3-N-acetylglactosamine, a tumor-associated T
C:Keywords: heterotetramer; lectin; seed; storage protein

Query Match 25.0%; Score 25.5; DB 2; Length 20;
Best Local Similarity 56.2%; Pred. No. 5.9e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

OY 3 IFQEVGFPQAQVTV 18
DB 6 ISQTVIVG-PWGAQVTV 20

RESULT 7
B61168
cocoonase (EC 3.4.21.-) - Chinese oak silkworm (fragment)
C:Species: Anthrenaea pernyi (Chinese oak silkworm)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C:Accession: B61168
R:Kramer, K.J.; Pelsted, R.L.; Law, J.H.
J. Biol. Chem. 248, 3021-3028, 1973
A:Title: Cocoonase. V. Structural studies on an insect serine protease.
A:Reference number: A61168; MUID:7316540
A:Accession: B61168
A:Molecule type: protein
A:Residues: 1-5 <KRA>
C:Keywords: hydrolase; serine proteinase; zymogen
F:1-5/Product: cocoonase (fragment) #status experimental <MAT>

Query Match 24.5%; Score 25; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 VWGFF 11
DB 1 IVGGF 5

RESULT 8
PH1436
T-cell receptor alpha chain (clone A24/PEF5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1436
R:Casanova, J.L.; Martinon, F.; Gounlief, H.; Barra, C.; Pannetier, C.; Regnault, A.;
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompa
A:Reference number: PH1430; MUID:93171821
A:Accession: PH1436
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2000, 08:30:07 ; Search time 112.59 Seconds

(without alignments)
11.273 Million cell updates/sec

Title: US-08-934-367-32

Perfect score: 102

Sequence: 1 OEIPEVVGCGFPSQAQVTVH 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues 3930

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_65:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	28.4	16	2	A60551
2	27	26.5	17	2	A61557
3	26	25.5	12	2	S61622
4	26	25.5	18	2	A61392
5	26	25.5	20	2	C34917
6	25.5	25.0	20	2	S29636
7	25	24.5	5	2	B61168
8	25	24.5	15	2	PH1436
9	25	24.5	16	2	A20180
10	24.5	24.0	20	2	A45806
11	24	23.5	15	4	I52698
12	24	23.5	17	2	PC2241
13	23	22.5	14	2	PH1448
14	23	22.5	15	2	PA0026
15	23	22.5	18	2	A35704
16	23	22.5	20	2	S50022
17	23	22.5	20	2	P00033
18	22.5	22.1	20	2	A56900
19	22	21.6	9	2	B20569
20	22	21.6	12	2	PH1183
21	22	21.6	14	2	PH0747
22	22	21.6	15	2	S26527
23	22	21.6	16	2	C53113
24	22	21.6	16	2	A44897
25	22	21.6	17	2	B61334
26	22	21.6	18	2	P00022
27	22	21.6	19	2	S29167
28	22	21.6	19	2	S74087
29	22	21.6	20	2	S50023

30	22	21.6	20	2	S71601	recombination prot
31	21.5	21.1	20	2	S29108	glutathione transf
32	21.5	21.1	20	2	A61327	trypsin (EC 3.4.21
33	21.5	21.1	20	2	D34817	collagenolytic pro
34	21	20.6	12	2	PH1189	T-cell receptor al
35	21	20.6	12	2	PH1180	T-cell receptor al
36	21	20.6	12	2	PH1188	T-cell receptor al
37	21	20.6	12	2	PH1172	T-cell receptor al
38	21	20.6	12	2	PH1175	T-cell receptor al
39	21	20.6	13	2	A32734	enkephalin precurs
40	21	20.6	14	2	PA0015	seed storage prote
41	21	20.6	14	2	PS0278	ribulose-bisphosph
42	21	20.6	14	2	PH1450	T-cell receptor al
43	21	20.6	15	2	S26516	T-cell receptor al
44	21	20.6	15	2	S26524	T-cell receptor al
45	21	20.6	15	2	S26528	T-cell receptor al

ALIGNMENTS

RESULT 1
A60551
Leukocyte elastase (EC 3.4.21.37) - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 17-Mar-1999
C:Accession: A60551
R:Axelsson, L.; Bengenfeldt, M.; Bjoerk, P.; Olsson, R.; Ohlsson, K.
Scand. J. Clin. Lab. Invest. 50, 35-42, 1990
A:Title: Release of immunoreactive canine leukocyte elastase normally and in endotoxi
A:Reference number: A60551; MUID:90193608
A:Accession: A60551
A:Molecule type: protein
A:Residues: 1-16 <AXP>
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; leukocyte; lysosome; serine proteinase

Query Match 28.4%; Score 29; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 VVGGRPSQ 14
DB 1 IVGGRPAQ 8

RESULT 2
A61557
Major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (strain FC
C:Species: Plasmodium falciparum
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C:Accession: A61557
R:Heidrich, H.G.
Biol. Cell 64, 205-214, 1988
A:Title: Isolation and functional characterization of Plasmodium falciparum merozoite
A:Reference number: A61557; MUID:89150734
A:Accession: A61557
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <HEI>
C:Keywords: surface antigen

Query Match 26.5%; Score 27; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 EEIFGVGCGFPS 13
DB 4 ESYQELVAVTPS 15

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-286-889-15

Query Match 26.5%; Score 27; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 IFQEVVGF 11
:111 11
DB 1 VFQEXGAGF 9

RESULT 15
US-08-485-618-15
Sequence 15, Application US/08485618
Patent No. 5728531
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5728531el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-485-618-15

Query Match 26.5%; Score 27; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 IFQEVVGF 11
:111 11
DB 1 VFQEXGAGF 9

Search completed: December 21, 2000, 08:31:50
Job time: 373 sec

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-666-473-114

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Query Match          27.5%; Score 28; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Oy      12 PSQAQVTV 19
        | 11111
Db       1 PHMAQVTV 8

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RESULT 12
US-08-669-284B-26
; Sequence 26, Application US/08669284B
; Patent No. 5939534
; GENERAL INFORMATION:
; APPLICANT: Inoue, Makoto
; APPLICANT: Kikuchi, Kaoru
; APPLICANT: Ishige, Yoko
; APPLICANT: Ito, Akira
; APPLICANT: Kimura, Toru
; APPLICANT: Nakayama, Chikao
; TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUROTROPHIC FACTORS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,284B
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/02269
; FILING DATE: 27-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 06-268281
; FILING DATE: 05-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 06-201504
; FILING DATE: 02-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 05-350934
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: Q-42041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-669-284B-26

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Query Match          26.5%; Score 27; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.2e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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```

Oy      4 FOEVVGG 10
        | 1111
Db       2 FQQVGG 8

```

```

RESULT 13
US-08-173-497-15
; Sequence 15, Application US/08173497
; Patent No. 5437958
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van Der Vlieten, Monica
; TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
; TITLE OF INVENTION: Subunit
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,497
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5437958and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31363
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-173-497-15

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Query Match          26.5%; Score 27; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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```

Oy      3 IFQEVVGGF 11
        : 111 11
Db       1 VFQEXGAGF 9

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RESULT 14
US-08-286-889-15
; Sequence 15, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Mich
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:

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Query Match	28.4%	Score 29	DB 2	Length 17
Best Local Similarity	75.0%	Pred. No. 32		
Matches	6	Conservative	0	Mismatches 2
				Indels 0
				Gaps 0

10 IFQEDAGG 17

; sequence 114, Application US/0866647.3
; Patent No. 5843713

```

; APPLICANT: YOSH
; APPLICANT: TAKE

```

;	TITLE OF INVENTI
;	NUMBER OF SEQUEN

STREET: 3000
CITY: Washing

STATE: D.C.
COUNTRY: USA

; COUNTRY: USA
; ZIP: 20007-51
;

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;      ZIP:  20007-51
;      COMPUTER READABLE
;

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COMPUTER READABLE
MEDIUM TYPE:

COMPUTER: IBM

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/      OPERATING SYST
;
SOFTWARE:  Dat

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```

; SOFTWARE: Pat
CURRENT APPLICAT

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;	CURRENT APPLICAT
;	APPLICATION NU

; APPLICATION NUMBER
; FILING DATE:

CLASSIFICATION ;
FILING DATE ;

CLASSIFICATION
PRIOR APPLICATION

APPLICATION NUMBER

FILING DATE: 11/11/2010

PRIOR APPLICATION NUMBER _____

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; APPLICATION NUMBER
; FILING DATE:

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;
; FILING DATE:
; PRIOR APPLICATION NO.:

; PRIOR APPLICATION NUMBER
 ; APPLICATION NUMBER

APPLCATION NO. _____
FILING DATE: _____
RECORDING DATE: _____

ATTORNEY/AGENT I

NAME: BENT, S
REGISTRATION NREGISTRATION NUMBER
REFERENCE/DOCK NUMBER; REFERENCE/DOCK
; TELECOMMUNICATIO; TELECOMMUNICATIO
; TELEPHONE: (2

TELEPHONE: (202) 343-3444
TELEFAX: (202) 343-3444

TELEFAX: (202) 696-1111
TELEX: 904136
INFORMATION FOR COUNTRIES

; INFORMATION FOR SE

```

: STREET: 6300 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: US
: ZIP: 98104-7092
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/466,348A
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Sharkey, Richard G.
: REGISTRATION NUMBER: 32,629
: REFERENCE/DOCKET NUMBER: 920010.448C6
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 41:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-08-466-348A-41

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Query Match          30.4%; Score 31; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 9 GGPSQAQVTV 19
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Db 1 GAMPNOQMRI 11

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RESULT 7
: US-08-466-545B-41
: Sequence 41, Application US/08466545B
: Patent No. 5876712
: GENERAL INFORMATION:
: APPLICANT: Cheever, Martin A.
: ATTORNEY/AGENT INFORMATION:
: NAME: Sharkey, Richard G.
: REGISTRATION NUMBER: 32,629
: REFERENCE/DOCKET NUMBER: 920010.448C6
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 41:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-08-466-545B-41

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: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-08-466-545B-41

```

```

Query Match          30.4%; Score 31; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 9 GGPSQAQVTV 19
   | 1:11111:
Db 1 GAMPNOQMRI 11

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```

RESULT 8
: US-08-466-680B-41
: Sequence 41, Application US/08466680B
: Patent No. 6075122
: GENERAL INFORMATION:
: APPLICANT: Cheever, Martin A.
: ATTORNEY/AGENT INFORMATION:
: NAME: Sharkey, Richard G.
: REGISTRATION NUMBER: 32,629
: REFERENCE/DOCKET NUMBER: 920010.448C4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 41:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-08-466-680B-41

```

```

Query Match          30.4%; Score 31; DB 3; Length 15;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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```

QY 9 GGPSQAQVTV 19
   | 1:11111:
Db 1 GAMPNOQMRI 11

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RESULT 9
: US-08-622-720A-23
: Sequence 23, Application US/08622720A
: Patent No. 5814508
: GENERAL INFORMATION:
: APPLICANT: Zhang, Ke

```

Db 1 VVGGXPGNSPXTV 13

RESULT 3

Patent No. 5219991
; APPLICANT: LEONARD, EDWARD; SKEEL, ALISON H.; YOSHIMURA,
; TEIZO; APPELLA, ETTORE
; TITLE OF INVENTION: MACROPHAGE STIMULATING PROTEIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/586,085
; FILING DATE: 21-SEP-1990
; SEQ ID NO: 8
; LENGTH: 20
5219991-8

Query Match 31.4%; Score 32; DB 5; Length 20;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 7 VVGGFSPQAQVTV 19
| | | | | : | |
Db 1 VVGGHPGNSPMTV 13

RESULT 4

US-08-467-083-41
; Sequence 41, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEDDANBERY
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-467-083-41

Query Match 30.4%; Score 31; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 9 GGFPSQAQVTV 19
| | | | | : | |
Db 1 GAMPNQAQMRI 11

RESULT 5

US-08-414-417B-41
; Sequence 41, Application US/08414417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-414-417B-41

Query Match 30.4%; Score 31; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 9 GGFPSQAQVTV 19
| | | | | : | |
Db 1 GAMPNQAQMRI 11

RESULT 6

US-08-486-348A-41
; Sequence 41, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
US-08-486-348A-41

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:31:50 ; Search time 99.91 Seconds
(without alignments)
3.355 Million cell updates/sec

Title: US-08-934-367-32

Perfect score: 102
Sequence: 1 GEFDEVVGGFPSQAQVTVH 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 1676186 residues

Total number of hits satisfying chosen parameters: 87906

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	35.3	14	3	US-09-120-365-87
2	34	33.3	19	5	5219991-12
3	32	31.4	20	5	5219991-8
4	31	30.4	15	1	US-08-467-083-41
5	31	30.4	15	1	US-08-414-417B-41
6	31	30.4	15	2	US-08-486-348A-41
7	31	30.4	15	2	US-08-468-545B-41
8	31	30.4	15	3	US-08-466-680B-41
9	30	29.4	17	2	US-08-622-720A-23
10	29	28.4	17	2	US-08-943-363-112
11	28	27.5	12	2	US-08-666-473-114
12	27	26.5	8	2	US-08-669-284B-26
13	27	26.5	11	1	US-08-173-497-15
14	27	26.5	11	1	US-08-286-889-15
15	27	26.5	11	1	US-08-485-618-15
16	27	26.5	11	1	US-08-362-652-15
17	27	26.5	11	2	US-08-605-672-15
18	27	26.5	11	2	US-08-482-293A-15
19	27	26.5	11	2	US-08-943-363-15
20	27	26.5	14	3	US-09-120-365-85
21	27	26.5	16	2	US-08-474-696A-7
22	27	26.5	17	3	US-08-256-747C-22
23	27	26.5	19	2	US-08-474-696A-1
24	27	26.5	19	2	US-08-474-696A-3
25	27	26.5	20	1	US-08-221-816B-11
26	26	25.5	6	1	US-07-890-422B-15
27	26	25.5	10	1	US-07-890-422B-19
28	26	25.5	11	1	US-08-081-539-106

29	26	25.5	11	1	US-08-466-647-106	Sequence 106, App
30	26	25.5	13	3	US-08-834-314-5	Sequence 5, Appl
31	26	25.5	14	3	US-09-120-365-82	Sequence 82, Appl
32	26	25.5	14	3	US-09-120-365-83	Sequence 83, Appl
33	26	25.5	16	2	US-09-120-365-84	Sequence 84, Appl
34	26	25.5	16	2	US-08-480-190-175	Sequence 175, App
35	26	25.5	16	2	US-08-488-379-175	Sequence 175, App
36	26	25.5	16	4	PCT-US93-07545-175	Sequence 175, App
37	25.5	25.0	20	1	US-08-218-025A-63	Sequence 63, Appl
38	25	24.5	5	3	US-08-570-761-3	Sequence 3, Appl
39	25	24.5	6	1	US-07-890-422B-14	Sequence 14, Appl
40	25	24.5	6	3	US-08-570-761-2	Sequence 2, Appl
41	25	24.5	7	1	US-08-482-880-32	Sequence 32, Appl
42	25	24.5	7	2	US-08-273-274-32	Sequence 32, Appl
43	25	24.5	7	2	US-08-475-041-32	Sequence 32, Appl
44	25	24.5	7	2	US-08-484-773-32	Sequence 32, Appl
45	25	24.5	9	2	US-08-934-222-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-09-120-365-87
; Sequence 87, Application US/09120365
; Patent No. 6103514
; GENERAL INFORMATION:
; APPLICANT: Natori, Shunji
; TITLE OF INVENTION: NEW PROTEASE
; FILE REFERENCE: 32290-144749
; CURRENT APPLICATION NUMBER: US/09/120, 365
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: JP 9-333 474
; EARLIER FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Nicotiana
; US-09-120-365-87

Query Match 35.3%; Score 36; DB 3; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ETFDEVVGFP 13
Db 3 ETFDEVVGFP 14

RESULT 2
5219991-12
; Patent No. 5219991
; APPLICANT: LEONARD, EDWARD;SKEEL, ALISON H.;YOSHIMURA,
; TIEZO;APPELLA, ETTORE
; TITLE OF INVENTION: MACROPHAGE STIMULATING PROTEIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/586, 085
; FILING DATE: 21-SEP-1990
; SEQ ID NO:12:
; LENGTH: 19
5219991-12

Query Match 33.3%; Score 34; DB 5; Length 19;
Best Local Similarity 53.8%; Pred. No. 4.4;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 VVGGFPSQAQVTV 19
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1.
:

OY 7 FPRPDGREA 15
 111 1 11
 DB 6 FPRITGHEA 14

RESULT 10
 ID 006946 PRELIMINARY; PRT; 17 AA.
 AC 006946;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE HYPOTHETICAL PROTEIN (ORF238) (FRAGMENT).
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-L72;
 RX MEDLINE: 98036037.
 RA Hayes F., Lubetzki S.A., Sherratt D.J.;
 RT "Salmonella typhimurium specifies a circular chromosome dimer
 resolution system which is homologous to the Xer site-specific
 recombination system of Escherichia coli.";
 RL Gene 198:105-110(1997).
 DR EMBL: U92525; AAC45779.1; -.
 KM Hypothetical protein.
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 2072 MW; BEB65CE8F0F9F529 CRC64;

Query Match 25.7%; Score 27; DB 2; Length 17;
 Best Local Similarity 75.0%; Pred. No. 5.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 FPRPDGR 13
 11 11 11
 DB 2 FPRYPLGR 9

RESULT 11
 ID 09UC91 PRELIMINARY; PRT; 17 AA.
 AC 09UC91;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE ONCOPETAL-LAMININ BINDING COLLAGEN ALPHA 1(II)CHAIN, OF-LB COLLAGEN
 DE ALPHA 1(II).
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 95169134.
 RA Minfra I.P., Andriolo M., Basirico L., Aquino A., Minafra S.,
 RA Boutillon M.M., van der Rest M.;
 RT "Onco-fetal/laminin-binding collagen from colon carcinoma: detection
 of new sequences.";
 RL Biochem. Biophys. Res. Commun. 207:852-859(1995).
 SQ SEQUENCE 17 AA; 1710 MW; E68058D0A20B55E CRC64;

Query Match 23.8%; Score 25; DB 4; Length 17;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 FPRPDGR 14
 11 11 11
 DB 2 FPRPKGND 9

RESULT 12

09TWL3
 ID 09TWL3 PRELIMINARY; PRT; 20 AA.
 AC 09TWL3;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE INITIATORIN (FRAGMENT).
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Bombycoidea; Bombycidae; Bombyx.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 95218779.
 RA Aigaki T., Kasuga H., Nagaoka S., Osanai M.;
 RT "Purification and partial amino acid sequence of Initiatorin, a
 prostatic endopeptidase of the silkworm, Bombyx mori.";
 RL Insect Biochem. Mol. Biol. 24:969-975(1994).
 DR INTERPRO: IPR001254; -.
 DR PRAM: PF00089; trypsin: 1.
 SQ SEQUENCE 20 AA; 2205 MW; 8BE047E96CFF1BA CRC64;

Query Match 23.8%; Score 25; DB 5; Length 20;
 Best Local Similarity 55.6%; Pred. No. 1.3e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 12 GREAVAYRF 20
 11 11 11
 DB 4 GRRAVPHSF 12

RESULT 13
 ID 014001 PRELIMINARY; PRT; 17 AA.
 AC 014001;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAY-1997 (TREMBlrel. 03, Last annotation update)
 DE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE (FRAGMENT).
 GN CGIPDEL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97079687.
 RA Loebbert R.W., Winterpacht A., Seipel B., Zabel B.U.;
 RT "Molecular cloning and chromosomal assignment of the human homologue
 of the rat cGMP-inhibited phosphodiesterase 1 (PDE3A)--a gene involved
 in fat metabolism located at 11p15.1.";
 RL Genomics 37:211-218(1996).
 DR EMBL: X95522; CAA64776.1; -.
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 2057 MW; 69D117C4FAE11540 CRC64;

Query Match 22.9%; Score 24; DB 4; Length 17;
 Best Local Similarity 54.5%; Pred. No. 1.6e+03;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 9 RPDGREAVAYR 19
 11 11 11
 DB 2 RRDROKAKMR 12

RESULT 14
 ID 016231 PRELIMINARY; PRT; 17 AA.
 AC 016231;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE ALCOHOL DEHYDROGENASE (EC 1.1.1.1) (ALDEHYDE REDUCTASE) (FRAGMENT).
GN ADH.
OS Fragaria linumae.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Rosales; Rosaceae;
OC Fragaria.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRA 377;
RA Yu H., Davis T.M.;
RT "Genetic relationships among Fragaria species based on RAPDs and an
RT alcohol dehydrogenase (ADH) gene.";
RL Genome 0:0-0(1997).
CC -1- CATALYTIC ACTIVITY: AN ALCOHOL + NAD(+) = AN ALDEHYDE OR KETONE +
CC NADH.
CC -1- COFACTOR: ZINC OR IRON.
DR EMBL: AF000218; AAC36545.1; -.
KW Oxidoreductase.
FT NON_TER 1 16
FT SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 25.7%; Score 27; DB 10; Length 16;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 FPRPDGREA 15
DB 6 FPRYICGHEA 14
RESULT 7
ID 082406 PRELIMINARY; PRT; 16 AA.
AC 082406;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE ALCOHOL DEHYDROGENASE (EC 1.1.1.1) (ALDEHYDE REDUCTASE) (FRAGMENT).
GN ADH.
OS Fragaria moschata.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Rosales; Rosaceae;
OC Fragaria.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRA 157;
RA Yu H., Davis T.M.;
RT "Genetic relationships among Fragaria species based on RAPDs and an
RT alcohol dehydrogenase (ADH) gene.";
RL Genome 0:0-0(1997).
CC -1- CATALYTIC ACTIVITY: AN ALCOHOL + NAD(+) = AN ALDEHYDE OR KETONE +
CC NADH.
CC -1- COFACTOR: ZINC OR IRON.
DR EMBL: AF000219; AAC36546.1; -.
KW Oxidoreductase.
FT NON_TER 1 16
FT SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 25.7%; Score 27; DB 10; Length 16;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 FPRPDGREA 15
DB 6 FPRYICGHEA 14

RESULT 8

082407
ID 082407 PRELIMINARY; PRT; 16 AA.
AC 082407;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE ALCOHOL DEHYDROGENASE (EC 1.1.1.1) (ALDEHYDE REDUCTASE) (FRAGMENT).
GN ADH.
OS Fragaria viridis.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Rosales; Rosaceae;
OC Fragaria.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRA 341;
RA Yu H., Davis T.M.;
RT "Genetic relationships among Fragaria species based on RAPDs and an
RT alcohol dehydrogenase (ADH) gene.";
RL Genome 0:0-0(1997).
CC -1- CATALYTIC ACTIVITY: AN ALCOHOL + NAD(+) = AN ALDEHYDE OR KETONE +
CC NADH.
CC -1- COFACTOR: ZINC OR IRON.
DR EMBL: AF000220; AAC36547.1; -.
KW Oxidoreductase.
FT NON_TER 1 16
FT SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 25.7%; Score 27; DB 10; Length 16;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 FPRPDGREA 15
DB 6 FPRYICGHEA 14
RESULT 9
ID 082781 PRELIMINARY; PRT; 16 AA.
AC 082781;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE ALCOHOL DEHYDROGENASE (EC 1.1.1.1) (ALDEHYDE REDUCTASE) (FRAGMENT).
GN ADH.
OS Fragaria vesca.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Rosales; Rosaceae;
OC Fragaria.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-YELLOW WONDER, BARON SOLEMACHER (BS);
RA Yu H., Davis T.M.;
RT "Genetic relationships among Fragaria species based on RAPDs and an
RT alcohol dehydrogenase (ADH) gene.";
RL Genome 0:0-0(1997).
CC -1- CATALYTIC ACTIVITY: AN ALCOHOL + NAD(+) = AN ALDEHYDE OR KETONE +
CC NADH.
CC -1- COFACTOR: ZINC OR IRON.
DR EMBL: AF000216; AAC36543.1; -.
DR EMBL: AF000214; AAC36541.1; -.
KW Oxidoreductase.
FT NON_TER 1 16
FT SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 25.7%; Score 27; DB 10; Length 16;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87213162.
 RA Kolval O., Kaneda T., Morishita R.;
 RT "Analysis of human terminal deoxynucleotidyl transferase cDNA
 RT expressible in mammalian cells."
 RL Biochem. Biophys. Res. Commun. 144:185-190(1987).
 DR EMBL: M26144; AAA74588.1; -
 KM Transferase.
 FT NON_TER
 SQ SEQUENCE 13 AA; 1442 MW; 25B7D365F34FC408 CRC64;

Query Match
 Best Local Similarity 25.7%; Score 27; DB 4; Length 13;
 Pred. No. 3.9e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 9 FPPDGRA 14
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 DB 3 GPDGRQ 8

RESULT 3
 082402 PRELIMINARY; PRT: 16 AA.
 ID 082402:
 AC 082402:
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE ALCOHOL DEHYDROGENASE (EC 1.1.1.1) (ALDEHYDE REDUCTASE) (FRAGMENT).
 GN ADH.
 OS Fragaria nubicola.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Rosales; Rosaceae;
 OC Fragaria.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRA520;
 RA Yu H., Davis T.M.;
 RT "Genetic relationships among Fragaria species based on RAPDs and an
 RT alcohol dehydrogenase (ADH) gene."
 RL Genome 0:0-0(1997).
 CC -1- CATALYTIC ACTIVITY: AN ALCOHOL + NAD(+) -> AN ALDEHYDE OR KETONE +
 CC NADH.
 CC -1- COFACTOR: ZINC OR IRON.
 DR EMBL: AF000213; AAC36540.1; -
 KW Oxidoreductase.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match
 Best Local Similarity 25.7%; Score 27; DB 10; Length 16;
 Pred. No. 4.9e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 FPPDGRA 15
 :||| |||
 DB 6 FPRITGHEA 14

RESULT 4
 082403 PRELIMINARY; PRT: 16 AA.
 ID 082403:
 AC 082403:
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE ALCOHOL DEHYDROGENASE (EC 1.1.1.1) (ALDEHYDE REDUCTASE) (FRAGMENT).
 GN ADH.
 OS Fragaria vesca.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Rosales; Rosaceae;
 OC Fragaria.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PAWTUCKAWAY;
 RA Yu H., Davis T.M.;
 RT "Genetic relationships among Fragaria species based on RAPDs and an
 RT alcohol dehydrogenase (ADH) gene."
 RL Genome 0:0-0(1997).
 CC -1- CATALYTIC ACTIVITY: AN ALCOHOL + NAD(+) -> AN ALDEHYDE OR KETONE +
 CC NADH.
 CC -1- COFACTOR: ZINC OR IRON.
 DR EMBL: AF000215; AAC36542.1; -
 KW Oxidoreductase.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 16 AA; 1666 MW; CEF73B5B28AACAB7 CRC64;

Query Match
 Best Local Similarity 25.7%; Score 27; DB 10; Length 16;
 Pred. No. 4.9e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 FPPDGRA 15
 :||| |||
 DB 6 FPRITGHEA 14

RESULT 5
 082404 PRELIMINARY; PRT: 16 AA.
 ID 082404:
 AC 082404:
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE ALCOHOL DEHYDROGENASE (EC 1.1.1.1) (ALDEHYDE REDUCTASE) (FRAGMENT).
 GN ADH.
 OS Fragaria nilgerrensis.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Rosales; Rosaceae;
 OC Fragaria.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERLIN 1;
 RA Yu H., Davis T.M.;
 RT "Genetic relationships among Fragaria species based on RAPDs and an
 RT alcohol dehydrogenase (ADH) gene."
 RL Genome 0:0-0(1997).
 CC -1- CATALYTIC ACTIVITY: AN ALCOHOL + NAD(+) -> AN ALDEHYDE OR KETONE +
 CC NADH.
 CC -1- COFACTOR: ZINC OR IRON.
 DR EMBL: AF000217; AAC36544.1; -
 KW Oxidoreductase.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match
 Best Local Similarity 25.7%; Score 27; DB 10; Length 16;
 Pred. No. 4.9e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 FPPDGRA 15
 :||| |||
 DB 6 FPRITGHEA 14

RESULT 6
 082405 PRELIMINARY; PRT: 16 AA.
 ID 082405:
 AC 082405:
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:35:33 ; Search time 157.2 Seconds
(without alignments)
11.880 Million cell updates/sec

Title: US-08-934-367-3
Perfect score: 105
Sequence: 1 VAVTFRRPRPDGREAAYRF 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	32.4	13	2 Q9R517	Q9R517 mycobacteri
2	27	25.7	13	4 Q14182	Q14182 homo sapien
3	27	25.7	16	10 O82402	O82402 fragaria nu
4	27	25.7	16	10 O82403	O82403 fragaria ve
5	27	25.7	16	10 O82404	O82404 fragaria ni
6	27	25.7	16	10 O82405	O82405 fragaria ii
7	27	25.7	16	10 O82406	O82406 fragaria mo
8	27	25.7	16	10 O82407	O82407 fragaria vi
9	27	25.7	16	10 O82781	O82781 fragaria ve
10	27	25.7	17	2 O06946	O06946 salmonella
11	25	23.8	17	4 O9UC91	O9UC91 homo sapien
12	25	23.8	20	5 O9TWL3	O9TWL3 bombyx mori
13	24	22.9	17	4 Q14001	Q14001 homo sapien
14	24	22.9	17	4 Q16231	Q16231 homo sapien
15	24	22.9	17	6 O9TRH5	O9TRH5 bos taurus
16	24	22.9	17	12 O78328	O78328 human immun
17	24	22.9	19	2 O9RAJ9	O9RAJ9 mycobacteri
18	23	21.9	12	8 Q31851	Q31851 arabidopsis
19	23	21.9	15	2 Q9R519	Q9R519 bacillus st

20	23	21.9	15	2 Q9R518	Q9R518 bacillus th
21	23	21.9	15	4 O00604	O00604 homo sapien
22	23	21.9	19	6 O9TRH3	O9TRH3 sus scrofa
23	22	21.0	17	6 O9TOZ8	O9TOZ8 sus scrofa
24	22	21.0	18	12 O87589	O87589 chimpanzee
25	22	21.0	18	12 O87591	O87591 chimpanzee
26	22	21.0	18	12 O87593	O87593 chimpanzee
27	22	21.0	20	3 P82263	P82263 aspergillus
28	22	21.0	20	6 O9TR52	O9TR52 sus scrofa
29	21	20.0	10	11 O9QVJ7	O9QVJ7 mus sp. mep
30	21	20.0	11	7 O77899	O77899 oreochromis
31	21	20.0	11	7 O77900	O77900 oreochromis
32	21	20.0	11	7 O77901	O77901 oreochromis
33	21	20.0	11	7 O77902	O77902 oreochromis
34	21	20.0	11	7 O77903	O77903 oreochromis
35	21	20.0	11	7 O77904	O77904 oreochromis
36	21	20.0	11	7 O77905	O77916 oreochromis
37	21	20.0	11	7 O77916	O77917 oreochromis
38	21	20.0	11	7 O77917	O77921 pseudotroph
39	21	20.0	11	7 O77921	O50959 neisseria g
40	21	20.0	12	2 O50959	O9um84 homo sapien
41	21	20.0	13	4 O9UM84	O9uee2 homo sapien
42	21	20.0	13	4 O9UEE2	O63940 ratus norv
43	21	20.0	14	2 O52636	O52636 escherichia
44	21	20.0	14	2 O52636	O52636 escherichia
45	21	20.0	15	2 O52304	O52304 escherichia

ALIGNMENTS

RESULT 1
Q9R517 PRELIMINARY; PRT; 19 AA.
ID O9R517
AC O9R517;
DT 01-MAY-2000 (TREMUREL. 13, Created)
DT 01-MAY-2000 (TREMUREL. 13, Last sequence update)
DT 01-JUN-2000 (TREMUREL. 14, Last annotation update)
DE ISONICOTINATE DEHYDROGENASE (FRAGMENT).
OS Mycobacterium.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae.
RN [1]
RP SEQUENCE.
RX MEDLINE: 94103749.
RA Kretzer A., Frunzke K., Andreesen J.R.;
RT "Catabolism of isonicotinate by Mycobacterium sp. INAI: extended
RT description of the pathway and purification of the molybdoenzyme
RT isonicotinate dehydrogenase.";
RL J. Gen. Microbiol. 139:2763-2772(1993).
SQ SEQUENCE 19 AA; 2215 MW; 6A4FB97459902F0B CRC64;

Query Match 32.4%; Score 34; DB 2; Length 19;
Best Local Similarity 58.3%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 FRFPRPDGREAV 16
Db 6 YRFAEDDGRIV 17

RESULT 2
Q14182 PRELIMINARY; PRT; 13 AA.
ID Q14182;
AC Q14182;
DT 01-NOV-1996 (TREMUREL. 01, Created)
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)
DT 01-MAY-1999 (TREMUREL. 10, Last annotation update)
DE DIOXYNUCLEOTIDYLTRANSFERASE (FRAGMENT).
GN DNMT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR INTERPRO: IPR002181; -
 DR PROSITE: PS00514; FIBRIN-AG-C-DOMAIN; PARTIAL.
 KW Blood coagulation; Plasma; Sulfatation.
 FT MOD_RES 3
 FT NON_TER 19
 FT SEQUENCE 19 AA; 2296 MW; 921A2B02D5F6891D CRC64;
 QY Query Match 21.0%; Score 22; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 1e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Db 9 DGRKVTTF 16
 QY 11 DGRAVAV 18
 Db 9 DGRKVTTF 16
 RESULT 13
 LIGA_TRAVE STANDARD; PRT; 13 AA.
 AC P20011;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LIGNINASE A (EC 1.11.1.-) (LIGNIN PEROXIDASE) (FRAGMENT).
 OS Trameetes versicolor (White-rot fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Aphylliphorales;
 OC Coriolaceae; Trameetes.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 89211432.
 RA Joenasson L., Karlsson O., Lundquist K., Nyman P.O.;
 RT "Trameetes versicolor ligninase: Isozyme sequence homology and
 RT substrate specificity.";
 RL FEMS Lett. 247:143-146(1989).
 CC -1- CATALYTIC ACTIVITY: DEPOLYMERIZATION OF LIGNIN. CATALYSES THE
 CC (ALPHA)-C(BETA) CLEAVAGE OF THE PROPYL SIDE CHAINS OF LIGNIN.
 CC -1- PATHWAY: FIRST STEP IN LIGNIN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. LIGNINASE SUBFAMILY.
 DR INTERPRO: IPR002016; -
 DR PROSITE: PS00435; PEROXIDASE_1; PARTIAL.
 DR PROSITE: PS00436; PEROXIDASE_2; PARTIAL.
 KW Oxidoreductase; Peroxidase; Heme; Glycoprotein; Multigene family;
 KW Lignin degradation.
 FT NON_TER 13
 FT SEQUENCE 13 AA; 1298 MW; 22C50ED5872A4338 CRC64;
 QY Query Match 20.0%; Score 21; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 9.9e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 10 PDGR 13
 Db 4 PDGK 7
 RESULT 14
 MK2A_PALPR STANDARD; PRT; 15 AA.
 AC P80409;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE METALNIKOWIN IIA.
 OS Palomena prasina.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
 OC Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomidae;
 OC Pentatomidae; Palomena.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-HEMOLYMPH;
 RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 RT Palomena prasina. Identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin.";
 RL J. Insect Physiol. 42:81-89(1996).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
 CC BACTERIA.
 CC -1- INDUCTION: BY BACTERIAL INFECTION.
 CC Antibiotic; Insect immunity.
 KW SEQUENCE 15 AA; 1893 MW; 23835D063B946299 CRC64;
 QY Query Match 20.0%; Score 21; DB 1; Length 15;
 Best Local Similarity 60.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Db 11 WPRPN 15
 QY 7 FPRPD 11
 Db 11 WPRPN 15

RESULT 15
 SODM_STRGR STANDARD; PRT; 15 AA.
 ID SODM_STRGR
 AC P80733;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SUPEROXIDE DISMUTASE [MN] (EC 1.15.1.1) (FRAGMENT).
 GN SOD2.
 OS Streptomyces griseus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=KCTC 9006;
 RX MEDLINE: 97056064.
 RA Youn H.-D., Youn H., Lee J.-W., Yim Y.-I., Lee J.K., Hah Y.C.,
 RA Kang S.-O.;
 RT "Unique isozymes of superoxide dismutase in Streptomyces griseus.";
 RL Arch. Biochem. Biophys. 334:341-348(1996).
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
 CC -1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) -> O(2) + H(2)O(2).
 CC -1- SUBUNIT: Tetramer (Potential).
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR HSSP: P80293; IAR4.
 DR INTERPRO: IPR001189; -
 DR PFAM: PF00081; sodfe; 1.
 DR PROSITE: PS00088; SOD_MN; PARTIAL.
 KW Oxidoreductase; Manganese.
 FT NON_TER 15
 FT SEQUENCE 15 AA; 1685 MW; 327993F710861372 CRC64;
 QY Query Match 20.0%; Score 21; DB 1; Length 15;
 Best Local Similarity 42.9%; Pred. No. 1.2e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 4 TFRFPRP 10
 Db 2 TYTLPEP 8

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PHSL_DESBN
ID PHSL_DESBN STANDARD: PRT: 19 AA.
AC P13066;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DIC-1998 (Rel. 37, Last annotation update)
DE PERIPLASMIC [NIFESE] HYDROGENASE LARGE SUBUNIT (EC 1.18.99.1) (NIFESE
DE HYDROGENYLASE LARGE CHAIN) (FRAGMENT)
OS Desulfotribrio baculatus (strain Norway 4).
OC Bacteria; Proteobacteria; delta subdivision; Desulfotomicrobium.
RN [1]
RP SEQUENCE:
RX MEDLINE: 88106446.
RA Pickrel B.C., He S.H., Li C., Menon N., Choi E.S., Przybyla A.E.,
RA Derwentian D.V., Peck H.D., Jr., Fauque G., le Gall J., Teixeira M.,
RA Moura I., Moura J.U.G., Pali D., Huynh B.H.;
RT Identification of three classes of hydrogenase in the genus,
RT Desulfotribrio.
RL Biochem. Biophys. Res. Commun. 149:369-377(1987).
CC -1- CATALYTIC ACTIVITY: 2 REDUCED FERREDOXIN + 2 H(+) = 2 OXIDIZED
CC FERREDOXIN + H(2)
CC -1- COFACTOR: ONE NICKEL ION, TWO 4FE-4S CLUSTERS AND ONE
CC SELENOCYSTEINE.
CC -1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL SUBUNIT.
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE [NIFE]/[NIFESE] HYDROGENASE LARGE
CC SUBUNIT FAMILY.
PIR: H27480; H27480.
DR INTERPRO: IPR001501;
DR PROSITE: PS00507; NI_HGENASE_L.1; PARTIAL.
DR PROSITE: PS00508; NI_HGENASE_L.2; PARTIAL.
KW Oxidoreductase; Periplasmic; Nickel; Selenium; Selenocysteine.
FT NON_TER 19
FT MOD_RES 19
SQ SEQUENCE 19 AA: 1942 MW: 28RCDD2D360F00367 CRC64:

Query Match 21.9%; Score 23; DB 1; Length 19;
Best Local Similarity 30.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 PRDGRAVA 17
DB 6 PAADGKRRIS 15

RESULT 10
UXX6_CHLTR STANDARD: PRT: 10 AA.
ID UXX6_CHLTR
AC P38007;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
RN [1]
RP SEQUENCE:
RC STRAIN-12/434/80;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christensen G., Birkelund S., Vitreou E., Ratti G.,
RL Pallini V.;
DE Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.44, ITS MW IS: 38.6 KDA.
FT NON_TER 10
FT MOD_RES 10
SQ SEQUENCE 10 AA: 1243 MW: DAD39A33304B5339 CRC64:

Query Match 21.0%; Score 22; DB 1; Length 10;
Best Local Similarity 30.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 VTFPRPRPDG 12

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DB 1 MNFKYIKKDG 10

RESULT 11
TKNL_KASMA STANDARD: PRT: 12 AA.
ID TKNL_KASMA
AC P08613;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HYLAMARES KASSININ (GLU(2)-PRO(5) KASSININ).
OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Hyperoliidae;
OC Kassina.
RN [1]
RP SEQUENCE:
RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
RT "New tachykinins, Glu2, pro5-kassinin (hylambates-kassinin) and
RT hylambatin, in the skin of the African rhacophorid frog Hylambates
RT maculatus."
RL Biomed. Res. 2:613-617(1981).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE PORENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
PIR: S10059; S10059.
DR INTERPRO: IPR002040;
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Amphibian skin.
FT MOD_RES 12
FT MOD_RES 12
SQ SEQUENCE 12 AA: 1376 MW: 3E756D279DD6DAB7 CRC64:

Query Match 21.0%; Score 22; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PRPD 11
DB 3 PKPD 6

RESULT 12
FIBB_HORSE STANDARD: PRT: 19 AA.
ID FIBB_HORSE
AC P14471;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-JAN-1990 (Rel. 13, Last annotation update)
DE FIBRINOPEPTIDE B.
OS Equus caballus (Horse), and Equus asinus (Donkey).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
RN [1]
RP SEQUENCE:
RC SPECIES-EQUUS;
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals."
RL Acta Chem. Scand. 19:1789-1791(1965).
RN [2]
RP SEQUENCE:
RC SPECIES-EQUUS;
RA Blomback B., Blomback M., Grondahl N.J., Holmberg E.;
RT "Structure of fibrinopeptides-its relation to enzyme specificity and
RT phylogeny and classification of species."
RL Ark. Kemi 25:411-428(1966).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS

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Best Local Similarity 50.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 11 DGRAVAYRF 20
| | : | | |
Db 2 DGSDAVGGEF 11

RESULT 6
CAQS_RAT
ID CAQS_RAT STANDARD: PRT: 20 AA.
AC P19633.
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CALSEQUESTERIN, SKELETAL MUSCLE ISOFORM (ASPARTACTIN) (LAMININ-BINDING PROTEIN) (FRAGMENT).
GN CASQ1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE.
RX MEDLINE; 88331073.
RA Hall D.E., Frazer K.A., Hann B.C., Reichardt L.F.?
RT "Isolation and characterization of a laminin-binding protein from rat and chick muscle."
RT and chick muscle."
RL J. Cell Biol. 107:687-697(1988).
CC -1- FUNCTION: CALSEQUESTERIN IS A HIGH-CAPACITY, MODERATE AFFINITY, CALCIUM-BINDING PROTEIN AND THUS ACTS AS AN INTERNAL CALCIUM STORE IN MUSCLE. THE RELEASE OF CALCIUM BOUND TO CALSEQUESTERIN THROUGH A CALCIUM RELEASE CHANNEL TRIGGERS MUSCLE CONTRACTION. BINDS 40 TO 50 MOLES OF CALCIUM. ALSO BINDS LAMININ.
CC -1- SUBCELLULAR LOCATION: THIS ISOFORM OF CALSEQUESTERIN OCCURS IN THE SARCOPLASMIC RETICULUM'S TERMINAL CISTERNAE LUMINAL SPACES OF FAST SKELETAL MUSCLE CELLS. ASPARTACTIN IS FOUND IN THE BASAL LAMINA SURROUNDING INDIVIDUAL MUSCLE FIBERS.
CC -1- TISSUE SPECIFICITY: SKELETAL AND HEART MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE CALSEQUESTERIN FAMILY.
DR PIR: A31049; A31049.
DR INTERPRO: IPR001393; -.
DR PROSITE: PS00864; CALSEQUESTERIN_2, PARTIAL.
DR PROSITE: PS00863; CALSEQUESTERIN_1; 1.
DR Muscle; Glycoprotein; Calcium-binding.
FT NON_TER 20
FT SEQUENCE 20 AA; 2238 MW; 92ADE04FC2A69280 CRC64;

Query Match 22.9%; Score 24; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 PPRPGREAV 16
| | : | | |
Db 6 PPEYDGVDRV 15

RESULT 7
CEP1_ACHFU
ID CEP1_ACHFU STANDARD: PRT: 11 AA.
AC P22790.
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARDIO-EXCITATORY PEPTIDE-1 (ACEP-1).
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylomatophora;
OC Achatinacea; Achatinidae; Achatina.
RN [1]
RP SEQUENCE.
RX STRAIN=FERUSSAC; TISSUE=HEART ATRIUM;
RX MEDLINE; 90211261.
RX Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;

RT "A novel cardio-excitatory peptide isolated from the atria of the African giant snail, Achatina fulica."
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
CC -1- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE MOVEMENT OF ACHATINA.
CC -1- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
DR PIR: A34662; A34662.
KW Hormone; Amidation.
FT MOD_RES 11
FT SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 21.9%; Score 23; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 RPDGR 13
| | : | | |
Db 6 RPDGR 10

RESULT 8
ATPB_CANFA
ID ATPB_CANFA STANDARD: PRT: 19 AA.
AC P99504.
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL (EC 3.6.1.34) (FRAGMENT).
GN ATP5B.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE.
RX MEDLINE; 98163340.
RX Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins."
RT Electrophoresis 18:2795-2802(1997).
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC SUBUNIT.
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
DR HSC-2DPAGE; P99504; DOG.
DR INTERPRO: IPR00194; -.
DR PROSITE: PS00152; ATPASE ALPHA_BETA; PARTIAL.
KW ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; ATP-binding; Mitochondrion.
FT UNSURE 8
FT UNSURE 17
FT NON_TER 19
FT SEQUENCE 19 AA; 1871 MW; BB9C163FDC60B842 CRC64;

Query Match 21.9%; Score 23; DB 1; Length 19;
Best Local Similarity 41.7%; Pred. No. 7.1e+02;
Matches 5; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 8 PPRDGEAVAYR 19
| | : | | |
Db 6 PSPKGAAXXR 17

RESULT 9

OS Halocynthia roretzi (Sea squirt).
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Pyrosidae; Halocynthia.
 RN (1)
 RP SEQUENCE:
 RC TISSUE=HEMOLYMPH;
 RX MEDLINE: 96321313.
 RA Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;
 RT "Purification and characterization of a 58,000-Da proteinase
 inhibitor from the hemolymph of a solitary ascidian, Halocynthia
 roretzi.";
 RL Comp. Biochem. Physiol. 114B:1-9(1996).
 CC -1- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR INTERPRO: IPR000215.
 DR PROSITE: PS00284; SERPIN: PARTIAL.
 KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.
 FT NON_TER 10
 SO SEQUENCE 10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;

Query Match 23.8%; Score 25; DB 1; Length 10;
 Best Local Similarity 55.6%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 9 RPDGRAVA 17
 : 1 1 1 1 1
 Db 2 KRDGEKVA 10

RESULT 3
 FIBA_BUBAR STANDARD; PRT; 19 AA.
 ID P14443;
 AC 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-JAN-1990 (Rel. 13, Last annotation update)
 DE FIBRINOPEPTIDE A.
 OS Bubalus arnee bubalis (Domestic water buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bubalus.
 RN (1)
 RP SEQUENCE:
 RC STRAIN=ITALIAN BREED;
 RX MEDLINE: 76040091.
 RA Balesrieri C., Colonna G., Irace G.;
 RT "Covalent structure of fibrinopeptides from buffaloes breeding in
 Italy.";
 RL Biochim. Biophys. Acta 405:517-521(1975).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR HSSP: P02671; IBBR.
 KW BLOOD coagulation; Plasma.
 FT NON_TER 19
 SO SEQUENCE 19 AA; 1852 MW; 9BA41F0F55A54C5 CRC64;

Query Match 23.8%; Score 25; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 3.3e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 11 DGRGAAYRP 20
 : 1 1 1 1 1
 Db 2 DGSDAVSGEF 11

RESULT 4
 MARI_ALTSP STANDARD; PRT; 14 AA.
 ID P29399;
 AC 01-DEC-1992 (Rel. 24, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE MARINOSTATIN C-2, C-1, AND D.
 OS Alteromonas sp. (strain B-10-31).
 OC Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 OC Alteromonas.
 RN (1)
 RP SEQUENCE, AND ACTIVE SITE.
 RX MEDLINE: 92176155.
 RA Takano R., Imada C., Kamel K., Hara S.;
 RT "The reactive site of marinostatin, a proteinase inhibitor from
 marine Alteromonas sp. B-10-31.";
 RL J. Biochem. 110:856-858(1991).
 CC -1- FUNCTION: INHIBITS SUBTILISIN, CHYMOTRYPSIN, AND ELASTASE, BUT
 CC NOT TRYPSIN.
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF MARINOSTATIN C-2.
 CC KW Serine protease inhibitor.
 FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
 FT VARIANT 1 2 MISSING (IN MARINOSTATIN C-1).
 FT ACT_SITE 1 3 MISSING (IN MARINOSTATIN D).
 FT ACT_SITE 6 7 REACTIVE BOND.
 SO SEQUENCE 14 AA; 1644 MW; 6E7CEBF92EF32E44 CRC64;

Query Match 22.9%; Score 24; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 4 TFRPRPD 11
 : 1 1 1 1
 Db 5 TMRPSDD 12

RESULT 5
 FIBA_BUBBU STANDARD; PRT; 19 AA.
 ID P14442;
 AC 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-JAN-1990 (Rel. 13, Last annotation update)
 DE FIBRINOPEPTIDE A.
 OS Bubalus bubalis (Water buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bubalus.
 RN (1)
 RP SEQUENCE:
 RA Moss G.A., Doolittle R.F.;
 RT "Amino acid sequence studies on artiodactyl fibrinopeptides.";
 RL Arch. Biochem. Biophys. 122:674-684(1967).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR HSSP: P02671; IBBR.
 KW BLOOD coagulation; Plasma.
 FT NON_TER 19
 SO SEQUENCE 19 AA; 1822 MW; 9BA41F1E11A54C5 CRC64;

Query Match 22.9%; Score 24; DB 1; Length 19;

RESULT 13

A34662

Achalina cardio-excitatory peptide-1 - giant African snail

C:Species: Achalina fulica (giant African snail)

C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 11-Jul-1997

C:Accession: A34662

R:Fujimoto, K.; Ohta, N.; Yoshida, M.; Kubota, I.; Muneoka, Y.; Kobayashi, M.

Biochem. Biophys. Res. Commun. 167, 777-783, 1990

A:Title: A novel cardio-excitatory peptide isolated from the atria of the African giant

A:Reference number: A34662; MUID:90211261

A:Accession: A34662

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <PU>

C:Keywords: amidated carboxyl end (Phe) #status experimental

Query Match 21.9%; Score 23; DB 2; Length 11;

Best Local Similarity 80.0%; Pred. No. 7.8e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 RPDGR 13

DB 6 RPDGR 10

RESULT 14

S21241

oligo-1,6-glucosidase (EC 3.2.1.10) - Bacillus "thermoamyloliquefaciens" (fragment)

C:Species: Bacillus "thermoamyloliquefaciens"

C:Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 21-Aug-1998

C:Accession: S21241

R:Suzuki, Y.; Yonezawa, K.; Hattori, M.; Takii, Y.

Eur. J. Biochem. 205, 249-256, 1992

A:Title: Assignment of Bacillus thermoamyloliquefaciens KP1071 alpha-glucosidase I to an

ence and in structural parameters calculated from the amino acid composition.

A:Reference number: S21202; MUID:92209510

A:Accession: S21241

A:Molecule type: protein

A:Residues: 1-15 <SU>

A:Experimental source: strain KP1071

C:Superfamily: alpha-glucosidase; alpha-amylase core homology

C:Keywords: glycosidase; hydrolase

Query Match 21.9%; Score 23; DB 2; Length 15;

Best Local Similarity 57.1%; Pred. No. 1.1e+03;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 13 REAVAYR 19

DB 7 KEAVVYQ 13

RESULT 15

S21202

glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - Bacillus stearothermophilus (fragment)

N:Alternate names: exo-alpha-1,4-glucosidase I

C:Species: Bacillus stearothermophilus

C:Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 21-Aug-1998

C:Accession: S21202

R:Suzuki, Y.; Yonezawa, K.; Hattori, M.; Takii, Y.

Eur. J. Biochem. 205, 249-256, 1992

A:Title: Assignment of Bacillus thermoamyloliquefaciens KP1071 alpha-glucosidase I to an

ence and in structural parameters calculated from the amino acid composition.

A:Reference number: S21202; MUID:92209510

A:Accession: S21202

A:Molecule type: protein

A:Residues: 1-15 <SU>

A:Experimental source: ATCC 12016

C:Superfamily: alpha-glucosidase; alpha-amylase core homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 21.9%; Score 23; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 1.1e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 13 REAVAYR 19
 DB 7 KEAVVYQ 13

Search completed: December 21, 2000, 08:30:03
 Job time: 267 sec

R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensions
A:Reference number: PA0001

A:Accession: PA0003

A:Molecule type: Protein

A:Residues: 1-15 <KAM>

A:Experimental source: leaf and callus

C:Superfamily: nucleoside-diphosphate kinase

C:Keywords: phosphotransferase

Query Match

Best Local Similarity 22.9%; Score 24; DB 2; Length 15;
Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 TFRPRPDG 12
| | | | |
Db 6 TFRPRPDG 14

RESULT

A28965 ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - spinach (fragments)

C:Species: Spinacia oleracea (spinach)

C>Date: 22-Dec-1988 #sequence_revision 22-Dec-1988 #text_change 23-Feb-1997

C:Accession: A28965

R;Mulligan, R.M.; Houtz, R.L.; Tolbert, N.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 1513-1517, 1988

A:Title: Reaction-intermediate analogue binding by ribulose biphosphate carboxylase/oxy
ceylated protein.

A:Reference number: A28965; MUID:88144466

A:Accession: A28965

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <MUL>

C:Keywords: carbon-carbon lyase; carboxy-lyase; chloroplast

Query Match

Best Local Similarity 22.9%; Score 24; DB 2; Length 15;
Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 VAVTFRPRPD 11
| | | | |
Db 3 VGRFRPRPD 13

RESULT

A509722 2S albumin small chain 1 nIV - rape (fragments)

C:Species: Brassica napus (rape)

C>Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998

C:Accession: S09722

R;Monalvie, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990

A:Title: Beta-Turns as structural motifs for the proteolytic processing of seed proteins

A:Reference number: S09720; MUID:90242974

A:Accession: S09722

A:Molecule type: protein

A:Residues: 1-9; 10-18 <MON>

A:Experimental source: seed

Query Match

Best Local Similarity 22.9%; Score 24; DB 2; Length 18;
Pred. No. 8.9e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 FRPRPDG 12
| | | | |
Db 5 FRPRPDG 12

RESULT

A31049 11

calsequestrin, fast skeletal muscle - rat (fragment)

N:Alternate names: 58K dihydropyridine-binding protein; aspartactin; calmitine; lamin

C:Species: Rattus norvegicus (Norway rat)

C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 16-Jul-1999

C:Accession: A31049; S46193; S46194; S46195

R;Hall, D.E.; Frazer, K.A.; Hann, B.C.; Reichardt, L.F.
J. Cell Biol. 107, 687-697, 1988

A:Title: Isolation and characterization of a laminin-binding protein from rat and chl

A:Reference number: A92751; MUID:88331073

A:Accession: A31049

A:Molecule type: protein

A:Residues: 1-20 <HAL>

R;Volpe, P.; Martini, A.; Furlan, S.; Meldolesi, J.
Biochem. J. 301, 465-469, 1994

A:Title: Calsequestrin is a component of smooth muscles: the skeletal- and cardiac-mu

A:Reference number: S46193; MUID:94318050

A:Accession: S46193

A:Molecule type: protein

A:Residues: 1-9 <VOL>

A:Accession: S46194

A>Status: preliminary

A:Molecule type: protein

A:Residues: 'XXX', 4-10, 'X', 12 <VO2>

A:Accession: S46195

A>Status: preliminary

A:Molecule type: protein

A:Residues: 'XE', 3-12 <VO3>

C:Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding pro

C:Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound t

C:Superfamily: calsequestrin

C:Keywords: calcium binding; glycoprotein; skeletal muscle

Query Match 22.9%; Score 24; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 FPRPDGREA 16
| | | | |
Db 6 FPRPDGREA 15

RESULT

A58839 ribulose-bisphosphate carboxylase activase I - rice (fragment)

N:Alternate names: RUBISCO activase I, 44K

C:Species: Oryza sativa (rice)

C>Date: 17-Jun-1998 #sequence_revision 02-Jul-1998 #text_change 02-Jul-1998

C:Accession: A58839

R;To, K.Y.; Shen, D.F.; Chen, L.F.O.; Chen, S.C.G.
submitted to the Protein Sequence Database, June 1998

A:Description: Characterization of rice leaf cDNA encoding rubisco activase.

A:Reference number: A58839

A:Accession: A58839

A:Molecule type: protein

A:Residues: 1-15 <TOK>

A:Experimental source: strain Taihong 67; leaf

A:Note: RUBISCO activase I has an additional 33 residues at the carboxyl end compared

C:Keywords: leaf

Query Match 22.4%; Score 23.5; DB 2; Length 15;
Best Local Similarity 53.8%; Pred. No. 8.9e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 5 FRPRPDG-REAV 16
| | | | |
Db 1 FQAPTGDGTHEAV 13

Db 8 FPPVDCCEAM 17

RESULT 3

PT0091

H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Aug-1998

C:Accession: PT0091

R:Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.

Submitted to JIPID, July 1998

A:Description: Proteome analysis of mouse brain.

A:Reference number: PT0091

A:Accession: PT0091

A:Molecule type: protein

A:Residues: 1-15 <KMW>

A:Experimental source: brain, striatum

C:Keywords: hydrolase

Query Match 24.8%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 PDGREA 15
| | | | |
Db 3 PDGREA 8

RESULT 4

E39419

collagen alpha 5(IV) chain - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 19-Oct-1995

C:Accession: E39419

R:Gunwar, S.; Ballester, F.; Kalluri, R.; Timoneda, J.; Chonko, A.M.; Edwards, S.J.; Nog

J. Biol. Chem. 266, 15318-15324, 1991

A:Title: Glomerular basement membrane. Identification of dimeric subunits of the noncoll

A:Reference number: A39419; MUID:91332055

A:Accession: E39419

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <GUN>

C:Superfamily: collagen alpha 1(IV) chain

C:Keywords: coiled coll; extracellular matrix; glycoprotein; trimer; triple helix

Query Match 24.8%; Score 26; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 10 PDGREA 20
| | | | |
Db 2 PDGREA 12

RESULT 5

S09721

2S albumin small chain nIII - rape (fragments)

C:Species: Brassica napus (rape)

C>Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998

C:Accession: S09721

R:Monalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.

FEBS Lett. 263, 209-212, 1990

A:Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins

A:Reference number: S09720; MUID:90242974

A:Accession: S09721

A:Molecule type: protein

A:Residues: 1-9;10-14 <MON>

A:Experimental source: seed

Query Match 23.8%; Score 25; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 FRPFRPDG 12
| | | | |
Db 5 FRPFRPDG 12

RESULT 6

I54264

rhodopsin single base deletion frame shift mutant - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence_revision 08-Nov-1996 #text_change 20-Apr-2000

C:Accession: I54264

R:Horn, M.; Humphries, P.; Kunisch, M.; Marchese, C.; Apfelstedt-Sylla, E.; Fugl, L.;

Hum. Genet. 90, 255-257, 1992

A:Title: Deletions in exon 5 of the human rhodopsin gene causing a shift in the readi

A:Reference number: I54264; MUID:93138610

A:Accession: I54264

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-19 <HOR>

A:Cross-references: GB:S55843; NID:g266287; PIDN:AAB25673.1; PID:g266288

C:Genetics:

A:Gene: GDB:RHO

A:Cross-references: GDB:120347

A:Map position: 3q21.3-3q24

Query Match 23.8%; Score 25; DB 4; Length 19;
Best Local Similarity 80.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 RFRPP 10
| | | | |
Db 5 RFRPP 9

RESULT 7

S68402

NAD(+)-glycohydrolase - bovine (fragments)

C:Species: Bos primigenius taurus (cattle)

C>Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 12-Dec-1997

C:Accession: S68402

R:Zhang, J.; Ziegler, M.; Schneider, R.; Klocker, H.; Auer, B.; Schweizer, M.

FEBS Lett. 377, 530-534, 1995

A:Title: Identification and purification of a bovine liver mitochondrial NAD(+)-glyco

A:Reference number: S68402; MUID:96140583

A:Accession: S68402

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-7;8-12 <ZHA>

C:Genetics:

A:Gene: nuclear

C:Keywords: mitochondrion; NAD

Query Match 22.9%; Score 24; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 11 DGRGAVAY 18
| | | | |
Db 5 DGRGELAH 12

RESULT 8

PA0003

nucleoside-diphosphate kinase (EC 2.7.4.6) - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 18-Nov-1994 #sequence_revision 06-Jan-1995 #text_change 15-Mar-1996

C:Accession: PA0003

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:30:01 ; Search time 112.59 seconds
(without alignments)
11.273 Million cell updates/sec

Title: US-08-934-367-3
Perfect score: 105
Sequence: 1 VAVTFRPPRPGREAVAYRF 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_65:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	25.7	13	2	184603
2	27	25.7	17	2	C37520
3	26	24.8	15	2	PT0091
4	26	24.8	20	2	E39419
5	25	23.8	14	2	S09721
6	25	23.8	19	4	I54264
7	24	22.9	12	2	S68402
8	24	22.9	15	2	PA0003
9	24	22.9	15	2	A28965
10	24	22.9	18	2	S09722
11	24	22.9	20	2	A31049
12	23.5	22.4	15	2	A58839
13	23	21.9	11	2	A34662
14	23	21.9	15	2	S21241
15	23	21.9	15	2	S21202
16	23	21.9	17	1	A61339
17	23	21.9	19	2	H27480
18	23	21.9	20	2	S13274
19	22	21.0	12	2	S10059
20	22	21.0	13	2	T08533
21	22	21.0	13	2	S22995
22	22	21.0	16	2	PS0210
23	22	21.0	17	2	B25348
24	22	21.0	19	2	A92058
25	21	20.0	9	2	S66607
26	21	20.0	10	2	A61007
27	21	20.0	10	2	PH0926
28	21	20.0	11	2	H54346
29	21	20.0	13	2	S04013

30	21	20.0	14	2	S60353	amylopullulanase -
31	21	20.0	14	2	I54284	C1-inhibitor - hum
32	21	20.0	15	2	F57789	gallbladder stone
33	21	20.0	17	2	A34835	ribosomal protein
34	21	20.0	19	2	P00548	capsid protein VP2
35	20	19.0	8	2	S66646	cardiacceleratory
36	20	19.0	9	2	A37027	macrophage chemola
37	20	19.0	9	2	I46023	growth hormone rec
38	20	19.0	10	1	XAV168	angiogenesis-conver
39	20	19.0	11	2	B60409	kassinin-like pept
40	20	19.0	11	2	C60409	kassinin-like pept
41	20	19.0	11	2	E60409	substance P-like p
42	20	19.0	11	2	D56979	collagen alpha 1(I
43	20	19.0	13	1	XAV198	bradykinin-conver
44	20	19.0	13	2	A37196	bradykinin-potentl
45	20	19.0	14	1	LFECFS	pheST operon leade

ALIGNMENTS

Result 1
184603
deoxynucleotidyltransferase - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 29-Aug-1997
C:Accession: 184603
R:Koizumi, O.; Kaneda, T.; Morishita, R.
Biochem. Biophys. Res. Commun. 144, 185-190, 1987
A:Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in
A:Reference number: I45884; MUID:87213162
A:Accession: 184603
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-13 <RES>
A:Cross-references: GB:M26144; NID:9951194; PID:9951195
A:Genetics:
A:Gene: GDB:DNMT
A:Cross-references: GDB:119100; OMIM:187410
A:Map position: 10q23-10q24

Query Match
Best Local Similarity 25.7%; Score 27; DB 2; Length 13;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 RPDGR 14
DB 3 QPDGRQ 8

Result 2
C37520
glutathione transferase (EC 2.5.1.18) MII - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 30-Sep-1993
R:Mannervik, B.; Alin, P.; Guttenberg, C.; Jenson, H.; Tahir, M.K.; Wahlstrom, M.; Jor
Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985
A:Title: Identification of three classes of cytosolic glutathione transferase common
A:Reference number: A24735; MUID:86042634
A:Accession: C37520
A:Molecule type: protein
A:Residues: 1-17 <MAN>
C:Superfamily: glutathione transferase
C:Keywords: transferase

Query Match
Best Local Similarity 25.7%; Score 27; DB 2; Length 17;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 FPRPDGREAV 16

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DB 1 FPRPGG 6

RESULT 14
5196404-4
; Patent No. 5196404
; APPLICANT: MARAGANORE, JOHN M.; FENTON II, JOHN M.; KLINE, TONI
; TITLE OF INVENTION: INHIBITORS OF THROMBIN
; NUMBER OF SEQUENCES: 18
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/549,388
; FILING DATE: 06-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 395,482
; FILING DATE: 18-AUG-1989
; SEQ ID NO:4:
; LENGTH: 20
5196404-4

Query Match 28.6%; Score 30; DB 5; Length 20;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 FPRPGG 6

RESULT 15
5425936-1
; Patent No. 5425936
; APPLICANT: MARAGANORE, JOHN M.; JABLONSKI, JO-ANN M.; BOURDON,
; PAUL R.
; TITLE OF INVENTION: INHIBITORS OF THROMBIN
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/924,549
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 652,929
; FILING DATE: 08-FEB-1991
; APPLICATION NUMBER: 549,388
; FILING DATE: 06-JUL-1990
; APPLICATION NUMBER: 395,482
; FILING DATE: 18-AUG-1989
; SEQ ID NO:1:
; LENGTH: 20
5425936-1

Query Match 28.6%; Score 30; DB 5; Length 20;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 FPRPDG 12
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DB 1 FPRPGG 6

Search completed: December 21, 2000, 08:31:45
Job time: 368 sec

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,052
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5788960nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-V
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 715 1000
TELEFAX: 312 715 1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label=D-Phe
OTHER INFORMATION: /note="The amino terminal phenylalanine residue
OTHER INFORMATION: is in the D stereochemical configuration"
US-08-463-052-29

Query Match 28.6%; Score 30; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 FPRPDG 12
|||||
Db 1 FPRPDG 6

RESULT 12
US-08-480-551-29
Sequence 29, Application US/08480551
Patent No. 5811394
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Wilcoff, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,551
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/264,176
FILING DATE:
APPLICATION NUMBER: US 07/653,012
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949

REFERENCE/DOCKET NUMBER: 90,1104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 715 1000
TELEFAX: 312 715 1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label=D-Phe
OTHER INFORMATION: /note="The amino terminal phenylalanine residue
OTHER INFORMATION: is in the D stereochemical configuration"
US-08-480-551-29

Query Match 28.6%; Score 30; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 FPRPDG 12
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Db 1 FPRPDG 6

RESULT 13
PCT-US91-09108-18
Sequence 18, Application PC/TUS9109108
GENERAL INFORMATION:
APPLICANT: Biogen, Inc.
TITLE OF INVENTION: *'\, BIFUNCTIONAL INHIBITORS OF THROMBIN ANDPLATELET ACTIVA
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue - 29th Floor
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09108
FILING DATE: 19911205
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 715-0600
TELEFAX: (212) 715-0674
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-09108-18

Query Match 28.6%; Score 30; DB 4; Length 20;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: Linear
US-08-058-699-9

Query Match 28.6%; Score 30; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FPRPG 12
11111
DB 1 FPRPG 6

RESULT 9
US-08-464-456-29
Sequence 29, Application US/08464456
Patent No. 5681541
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,456
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5681541nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-V
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 715 1000
TELEFAX: 312 715 1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label-D-Phe
OTHER INFORMATION: /note-"The amino terminal phenylalanine residue
OTHER INFORMATION: is in the D stereochemical configuration"
US-08-464-456-29

Query Match 28.6%; Score 30; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 FPRPG 12
11111
DB 1 FPRPG 6

RESULT 10
US-08-286-748B-6
Sequence 6, Application US/08286748B
Patent No. 5759542
GENERAL INFORMATION:
APPLICANT: Victor Gurevich
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
OF DRUGS BY PLATELETS FOR THE TREATMENT OF
CARDIOVASCULAR AND OTHER DISEASES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,748B
FILING DATE: August 5, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: J. Peter Fasse
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04547/013001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-286-748B-6

Query Match 28.6%; Score 30; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FPRPG 12
11111
DB 1 FPRPG 6

RESULT 11
US-08-463-052-29
Sequence 29, Application US/08463052
Patent No. 5788960
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:

Patent No. 5242810
GENERAL INFORMATION:
APPLICANT: Maragano, John M.
APPLICANT: Chao, Betty H.
APPLICANT: Strauch, Kathryn L.
APPLICANT: Thompson, Jeffrey S.
TITLE OF INVENTION: BIFUNCTIONAL INHIBITORS OF THROMBIN AND
NUMBER OF INVENTION: PLATELET ACTIVATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue - 29th Floor
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/623,611
FILING DATE: 19901207
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 715-0600
TELEFAX: (212) 715-0674
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-623-611-18

Query Match 28.6%; Score 30; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FPRPG 12
Db 1 FPRPG 6

RESULT 7
US-07-831-780-2
Sequence 2, Application US/07831780
Patent No. 5371184
GENERAL INFORMATION:
APPLICANT: Dunn, Jeffrey
APPLICANT: Lyle, Leon R.
APPLICANT: Rajagopalan, Raghavan
TITLE OF INVENTION: Radiolabelled Peptide Compounds
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rita D. Vacca
STREET: Wallinckrodt Medical, Inc., 675 McDonnell
STREET: Blvd.
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63134
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/831,780
FILING DATE: 19920502
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Vacca, Rita D.
REGISTRATION NUMBER: 33,624
REFERENCE/DOCKET NUMBER: 0754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-895-7215
TELEFAX: 314-895-2156
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: Human
US-07-831-780-2

Query Match 28.6%; Score 30; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FPRPG 12
Db 1 FPRPG 6

RESULT 8
US-08-058-699-9
Sequence 9, Application US/08058699
Patent No. 5443827
GENERAL INFORMATION:
APPLICANT: Edgar Haber
APPLICANT: Christoph Bode
APPLICANT: Marshall S. Runge
TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555x
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/058,699
FILING DATE: 19930503
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Janis K. Fraser, Ph.D.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:

RESULT 2
5433940-7
; Patent No. 5433940
; APPLICANT: MARGANORE, JOHN M.; FENTON II, JOHN M.; KLINE, TONI
; TITLE OF INVENTION: INHIBITORS OF THROMBIN
; NUMBER OF SEQUENCES: 25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,259
; FILING DATE: 17-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 548,388
; FILING DATE: 06-JUL-1989
; APPLICATION NUMBER: 395,482
; FILING DATE: 18-AUG-1989
; SEQ ID NO: 7:
; LENGTH: 10
5433940-7

Query Match 28.6%; Score 30; DB 5; Length 10;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 FPRPG 6

RESULT 3
US-08-101-041A-4
; Sequence 4, Application US/08101041A
; Patent No. 5541101
; GENERAL INFORMATION:
; APPLICANT: Saji, Fumitaka
; APPLICANT: AZUMA, Chihito
; APPLICANT: KIMURA, Tadashi
; TITLE OF INVENTION: ANTI-OXYTOCIN RECEPTOR ANTIBODIES AND
; NUMBER OF SEQUENCES: 7
; TITLE OF INVENTION: METHODS FOR THEIR PRODUCTION
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/101,041A
; FILING DATE: 03-AUG-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-206854
; FILING DATE: 03-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 002258-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:

; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note="Amino acids 102-119 of the
; OTHER INFORMATION: oxytocin receptor polypeptide."
US-08-101-041A-4

Query Match 28.6%; Score 30; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 TFRFPGD 8

RESULT 4
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; Patent No. 5196404
; APPLICANT: MARGANORE, JOHN M.; FENTON II, JOHN M.; KLINE, TONI
; TITLE OF INVENTION: INHIBITORS OF THROMBIN
; NUMBER OF SEQUENCES: 18
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/549,388
; FILING DATE: 06-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 395,482
; FILING DATE: 18-AUG-1989
; SEQ ID NO: 6:
; LENGTH: 18
5196404-6

Query Match 28.6%; Score 30; DB 5; Length 18;
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Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 FPRPG 6

RESULT 5
5433940-2
; Patent No. 5433940
; APPLICANT: MARGANORE, JOHN M.; FENTON II, JOHN M.; KLINE, TONI
; TITLE OF INVENTION: INHIBITORS OF THROMBIN
; NUMBER OF SEQUENCES: 25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,259
; FILING DATE: 17-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 548,388
; FILING DATE: 06-JUL-1989
; APPLICATION NUMBER: 395,482
; FILING DATE: 18-AUG-1989
; SEQ ID NO: 2:
; LENGTH: 19
5433940-2

Query Match 28.6%; Score 30; DB 5; Length 19;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 FPRPG 12
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DB 1 FPRPG 6

RESULT 6
US-07-623-611-18
; Sequence 18, Application US/07623611

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:31:43 ; Search time 99.91 Seconds
(without alignments)
3.355 Million cell updates/sec

Title: US-08-934-367-3

Perfect score: 105

Sequence: 1 VAVYFRPRPDGREAAYRFR 20

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 87906

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	30	28.6	10	5	5433940-7
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6	30	28.6	20	1	US-07-623-611-18
7	30	28.6	20	1	US-07-831-780-2
8	30	28.6	20	1	US-08-058-659-9
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10	30	28.6	20	1	US-08-286-748B-6
11	30	28.6	20	1	US-08-463-052-29
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13	30	28.6	20	4	PCT-US91-09108-18
14	30	28.6	20	5	5196404-4
15	30	28.6	20	5	5425936-1
16	29	27.6	10	3	US-08-159-339A-102
17	29	27.6	11	3	US-08-893-526A-17
18	29	27.6	15	3	US-08-630-916A-96
19	29	27.6	20	1	US-08-173-116-2
20	28.5	27.1	20	1	US-08-974-775-12
21	28	26.7	14	3	US-08-974-775-11
22	27	25.7	10	1	US-07-602-847C-1
23	27	25.7	14	2	US-08-622-720A-10
24	27	25.7	14	2	US-08-622-720A-21
25	27	25.7	14	3	US-08-974-775-19
26	27	25.7	15	1	US-07-602-847C-6
27	27	25.7	15	1	US-08-683-262B-70
28	27	25.7	17	5	5219991-5

29	26	24.8	12	2	US-08-556-597-138	Sequence 138, App
30	26	24.8	13	5	5196523-19	Patent No. 5196523
31	26	24.8	14	2	US-08-531-662B-21	Sequence 21, Appl
32	26	24.8	14	3	US-08-669-161A-21	Sequence 21, Appl
33	26	24.8	15	3	US-08-669-161A-24	Sequence 24, Appl
34	26	24.8	15	3	US-07-978-895-8	Sequence 8, Appl
35	26	24.8	15	2	US-08-473-119-8	Sequence 8, Appl
36	26	24.8	15	2	US-08-475-352-8	Sequence 8, Appl
37	26	24.8	15	2	US-08-726-306A-176	Sequence 176, App
38	26	24.8	16	2	US-08-448-600-5	Sequence 5, Appl
39	26	24.8	16	3	US-08-937-610-9	Sequence 18, Appl
40	26	24.8	19	1	US-08-392-828C-18	Sequence 18, Appl
41	26	24.8	19	3	US-09-330-945-18	Sequence 18, Appl
42	26	24.8	20	1	US-07-956-848A-16	Sequence 16, Appl
43	26	24.8	20	1	US-08-471-956-16	Sequence 16, Appl
44	26	24.8	20	2	US-08-637-759B-413	Sequence 413, App
45	26	24.8	20	3	US-08-871-355A-413	Sequence 413, App

ALIGNMENTS

RESULT 1
US-08-713-885-6
; Sequence 6, Application US/08713885
; Patent No. 5985833
; GENERAL INFORMATION:
; APPLICANT: Mosesson, Michael W.
; APPLICANT: Meh, David A.
; TITLE OF INVENTION: THROMBIN INHIBITOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,885
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 960296.93740
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ. ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-713-885-6

Query Match 28.6%; Score 30; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RFRP 10
Db 3 RFRP 7

FT NON TER 1 1
SQ SEQUENCE 22 AA; 2292 MW; 2E05FE169844236D CRC64;

Query Match 19.4%; Score 26; DB 6; Length 23;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 9 MDGFPPE 15
DB 3 MDICGPE 9

RESULT 12

ID 046081 PRELIMINARY; PRT; 24 AA.
AC 046081;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE NITROGENASE 3 SUBUNIT H (FRAGMENT).
GN ANFH.
OS Clostridium hungatei.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B3B;
RA Chen T., Leschine S.B.;
RA Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59415; AAB02934.1; -
DR INTERPRO: IPR000392; -
DR PPM: PF00142; fer4_N1FH; 1.
FT NON_TER 1 1
SQ SEQUENCE 24 AA; 2752 MW; C014801651E11BFC CRC64;

Query Match 19.4%; Score 26; DB 2; Length 24;
Best Local Similarity 31.2%; Pred. No. 2e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 10 DFGFPEHLVDFLOSL 25
DB 1 EFVYPRKPLTFMDQLEDM 16

RESULT 13

ID P82401 PRELIMINARY; PRT; 25 AA.
AC P82401;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE AUREIN 5.1.
OS Litoria raniformis, and Litoria aurea (Australian frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
RN [1]
RP SEQUENCE.
RA Rozeq T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
RA "The antibiotic and anticancer aurein peptides from the Australian
RT bell frogs Litoria aurea and Litoria raniformis";
RL Eur. J. Biochem. 0:0-0(2000).
CC -1. FUNCTION: HAS NO ANTIMICROBIAL OR ANTICANCER ACTIVITY.
SQ SEQUENCE 25 AA; 2547 MW; 15C6169CD98AFC27 CRC64;

Query Match 19.4%; Score 26; DB 13; Length 25;
Best Local Similarity 38.9%; Pred. No. 2.1e+03;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 6 LLOMDGFPPEHLVDFLO 23
DB 2 LLDIVTGILGNLIVDYLK 19

RESULT 14

ID 094554 PRELIMINARY; PRT; 16 AA.
AC 094554;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE CALMODULIN KINASE 2 (FRAGMENT).
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RA Alemany V., Alligne R.;
RA Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U57982; AAD09466.1; -
KW Kinase.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1846 MW; 4A673B1FAC3288D9 CRC64;

Query Match 18.7%; Score 25; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 FGFP 14
DB 5 FGFP 8

RESULT 15

ID 09PS70 PRELIMINARY; PRT; 19 AA.
AC 09PS70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE.
RX MEDLINE: 92011685.
RA Stifani S., Barber D.L., Aebbersold R., Steyrer E., Shen X., Nimpf J.,
RA Schneider W.J.;
RA "The laying hen expresses two different low density lipoprotein
RT receptor-related proteins";
RL J. Biol. Chem. 265:19079-19087(1991).
SQ SEQUENCE 19 AA; 1861 MW; 4EEC9311205620608 CRC64;

Query Match 18.7%; Score 25; DB 13; Length 19;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 6 LLOMDGFPPEHLVD 20
DB 1 LLAQGLGXPTALALD 15

Search completed: December 21, 2000, 08:40:02
Job time: 125 sec

AC 09TRO7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CALCYCLIN-ASSOCIATED PROTEIN PEPTIDE L-8, CAP-50-ANNEXIN.
 OS Bos taurus (Bovine)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP MEDLINE: 92317074.
 RA Mitutani A., Usuda N., Tokumitsu H., Minami H., Yasui K.,
 RA Kobayashi R., Hidaka H.,
 RT "CAP-50, a newly identified annexin, localizes in nuclei of cultured
 RT fibroblast 3Y1 cells."
 RL J. Biol. Chem. 267:13498-13504(1992).
 SO SEQUENCE 14 AA; 1446 MW; C8322EB96DD9C6C6 CRC64;

Query Match 20.1%; Score 27; DB 6; Length 14;
 Best Local Similarity 41.7%; Pred. No. 7.7e+02;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 11 FGPEHLVDFL 22
 Db 2 FGDEQATITDXL 13

RESULT 8
 09S8E1 PRELIMINARY; PRT; 22 AA.
 AC 09S8E1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE ANNEXIN (FRAGMENT).
 OS Capsicum annuum (Bell pepper).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
 OC Solanaceae; Capsicum.
 RN [1]
 RP MEDLINE: 95353219.
 RA Hoshino T., Mizutani A., Chida M., Hidaka H., Mizutani J.,
 RT "Plant annexin form homodimer during Ca(2+)-dependent liposome
 RT aggregation."
 RL Biochem. Mol. Biol. Int. 35:749-755(1995).
 SO SEQUENCE 22 AA; 2465 MW; A36D11AF311F0F CRC64;

Query Match 20.1%; Score 27; DB 10; Length 22;
 Best Local Similarity 41.7%; Pred. No. 1.3e+03;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 11 FGPEHLVDFL 22
 Db 3 WGTDEKLIIDIL 14

RESULT 9
 09TRC2 PRELIMINARY; PRT; 20 AA.
 AC 09TRC2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE HEMOPROTEIN P-30 (FRAGMENT).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE.

RX MEDLINE: 94245717.
 RA Escrivu V., Laporte F., Garin J., Brandolin G., Vignats P.V.;
 RT "Purification and physical properties of a novel type of cytochrome b
 RT from rabbit peritoneal neutrophils."
 RL J. Biol. Chem. 269:14007-14014(1994).
 SO SEQUENCE 20 AA; 2198 MW; 2301B618163DMA19 CRC64;

Query Match 19.8%; Score 26.5; DB 6; Length 20;
 Best Local Similarity 45.0%; Pred. No. 1.4e+03;
 Matches 9; Conservative 2; Mismatches 4; Indels 5; Gaps 1;

OY 3 GFLIQMDFGPEHLVDFL 22
 Db 6 GFLVLLV-----SALLVGL 20

RESULT 10
 09ZG55 PRELIMINARY; PRT; 21 AA.
 AC 09ZG55;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE ATP-BINDING PROTEIN (FRAGMENT).
 GN RECF.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-L2 434B;
 RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
 RT "Gene identification of Chlamydia trachomatis by random DNA
 RT sequencing."
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF087306; AAD04082.1; .
 KW ATP-binding.
 FT NON_TER 1 1
 FT 21 21
 SO SEQUENCE 21 AA; 2336 MW; 0185D9AC428276D9 CRC64;

Query Match 19.8%; Score 26.5; DB 2; Length 21;
 Best Local Similarity 41.7%; Pred. No. 1.4e+03;
 Matches 5; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

OY 6 LLQMDFGPEHL 17
 Db 8 ILQL-ISFPKH 18

RESULT 11
 002830 PRELIMINARY; PRT; 22 AA.
 AC 002830;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE PRO ALPHA1 TYPE II COLLAGEN (FRAGMENT).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96377339.
 RA Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
 RA Vuorio E.;
 RT "Evidence for insufficient chondrocytic differentiation during repair
 RT of full-thickness defects of articular cartilage."
 RL Matrix Biol. 15:39-47(1996).
 DR EMBL: S83370; AAB50773.1; .
 DR INTERPRO: IPR00085; .
 DR Pfam: PF01410; COL1F1; 1.

RN [1]
 RP SEQUENCE.
 RX MEDLINE: 92250478.
 RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hatake H.,
 RT "A calyculin-associated protein is a newly identified member of the
 RT Ca2+/phospholipid-binding proteins, annexin family.".
 RL J. Biol. Chem. 267:8919-8924(1992).
 SQ SEQUENCE 19 AA; 2018 MW; 9A54062504B8322E CRC64;

Query Match 23.1%; Score 31; DB 6; Length 19;
 Best Local Similarity 43.8%; Pred. No. 2.7e+02;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 11 FGPEHLVDFLOSLS 26
 Db 2 FGPEQAIIDXLGSR 17

RESULT 3
 O9UHI PRELIMINARY; PRT; 17 AA.
 AC O9UHI;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE DJ436M1.2 (RETINOSCHISIS (X-LINKED, JUVENILE) 1 (XLRSL)) (FRAGMENT).
 GN RSL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Grafham D.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z94056; CAB40073.1; .
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 2029 MW; 8100E1B78C52C7FB CRC64;

Query Match 22.8%; Score 30.5; DB 4; Length 17;
 Best Local Similarity 58.3%; Pred. No. 2.8e+02;
 Matches 7; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

OY 2 DGFLLMDFGF 13
 Db 6 EGFLLLL-FCY 16

RESULT 4
 P70861 PRELIMINARY; PRT; 21 AA.
 ID P70861;
 AC P70861;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE THDF (FRAGMENT).
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-212;
 RC MEDLINE: 97312006.
 RA Ge Y., Old I.G., Girons I.S., Charon N.W.;
 RT "The flag motility operon of Borrelia burgdorferi is initiated by a
 RT sigma 70-like promoter.".
 RL Microbiology 143:1681-1690(1997).
 DR EMBL: U62901; AAB62742.1; .
 FT NON_TER 21
 SQ SEQUENCE 21 AA; 2432 MW; F33E1EC548BD5B33 CRC64;

Query Match 22.4%; Score 30; DB 2; Length 21;

Best Local Similarity 50.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 9 MDEGFPEHL 18
 Db 7 IEFDFEGIL 16

RESULT 5
 O9TWH5 PRELIMINARY; PRT; 20 AA.
 ID O9TWH5
 AC O9TWH5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE 40 KDA GAP JUNCTION PROTEIN (FRAGMENT).
 OS Heliothis virescens (Noctuid moth) (Owl moth).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Preygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Dicitryla;
 OC Noctuoidea; Noctuidae; Heliothinae; Heliothis.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 95347000.
 RA Ryerse J.S.;
 RT "Immunocytochemical, electrophoresis, and immunoblot analysis of
 RT Heliothis virescens gap junctions isolated in the presence and absence
 RT of protease inhibitors.";
 RL Cell Tissue Res. 281:179-186(1995).
 SQ SEQUENCE 20 AA; 2304 MW; A298D3EB3E89586B CRC64;

Query Match 21.6%; Score 29; DB 5; Length 20;
 Best Local Similarity 35.3%; Pred. No. 5.7e+02;
 Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 5 LLLMDFGPEHLVDF 21
 Db 3 VIFNIDGYLEFLTRDF 19

RESULT 6
 O9UGS1 PRELIMINARY; PRT; 12 AA.
 ID O9UGS1;
 AC O9UGS1;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE DJ796117.4 (NOVEL PROTEIN SIMILAR TO GS2) (FRAGMENT).
 GN DJ796117.4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barlow K.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL035398; CAB63074.1; .
 FT NON_TER 1
 SQ SEQUENCE 12 AA; 1430 MW; AF7740ABECB69A6 CRC64;

Query Match 20.1%; Score 27; DB 4; Length 12;
 Best Local Similarity 44.4%; Pred. No. 6.5e+02;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 5 LLLMDFGF 13
 Db 1 MILEDMSF 9

RESULT 7
 O9TRO7 PRELIMINARY; PRT; 14 AA.
 ID O9TRO7

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:37:57 ; Search time 28.23 Seconds

(without alignments)
85.998 Million cell updates/sec

Title: US-08-934-367-29

Perfect score: 134

Sequence: 1 RDGFLLQMDFGFPEHLVDFLQSLs 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 6467

Minimum DB seq length: 0

Maximum DB seq length: 26

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPTREMBL_14:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.tentent:*
13: sp.virus:*
14: sp.vertebrate:*
15: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	24.6	24	6 Q9TR30	Q9tr30 ovis aries
2	31	23.1	19	6 Q9TRR6	Q9trr6 oryctolagus
3	30.5	22.8	17	4 Q9UJH1	Q9ujh1 homo sapien
4	30	22.4	21	4 P70861	P70861 borrelia bu
5	29	21.6	20	5 Q9TWH5	Q9twh5 heliothis v
6	27	20.1	12	4 Q9UGS1	Q9ugs1 homo sapien
7	27	20.1	14	6 Q9TR07	Q9trq7 bos taurus
8	27	20.1	22	10 Q9S8E1	Q9s8e1 capsicum an
9	26.5	19.8	20	6 Q9TRC2	Q9trc2 oryctolagus
10	26.5	19.8	21	2 Q9ZG55	Q9zgs5 chlamydia t
11	26	19.4	22	6 Q02830	Q02830 oryctolagus
12	26	19.4	24	2 Q46081	Q46081 clostridium
13	26	19.4	25	13 P82401	P82401 litorea ran
14	25	18.7	16	3 Q94554	Q94554 schizosacch
15	25	18.7	19	13 Q9PS70	Q9ps70 gallus gall
16	25	18.7	20	10 Q9S878	Q9s878 petunia hyb
17	25	18.7	21	12 Q93044	Q93044 maize strea
18	25	18.7	21	12 Q93046	Q93046 maize strea
19	25	18.7	21	12 Q93047	Q93047 maize strea

20	25	18.7	23	6 Q9TR28	Q9tr28 canis famli
21	25	18.7	24	4 Q13661	Q13661 homo sapien
22	25	18.7	24	12 Q69137	Q69137 humo herpe
23	24.5	18.3	22	13 Q9PS42	Q9ps42 gallus gall
24	24.5	18.3	23	12 Q10423	Q10423 influenza a
25	24.5	18.3	25	13 Q9PS41	Q9ps41 gallus gall
26	24	17.9	13	2 Q31364	Q31364 borrelia ga
27	24	17.9	13	2 Q31365	Q31365 borrelia ga
28	24	17.9	13	2 Q34622	Q34622 borrelia bu
29	24	17.9	18	1 Q9UYK7	Q9uyk7 pyrococcus
30	24	17.9	19	5 Q9W508	Q9w508 drosophila
31	24	17.9	20	6 Q9TR63	Q9tr63 atelea delz
32	24	17.9	21	2 Q9X3D0	Q9x3d0 prochloroco
33	24	17.9	21	12 Q93050	Q93050 maize strea
34	24	17.9	22	4 Q9UQ31	Q9uq31 homo sapien
35	24	17.9	22	6 Q9XTA7	Q9xta7 cercopithe
36	24	17.9	22	6 Q9XTA6	Q9xta6 canis famli
37	24	17.9	22	11 Q9WV72	Q9wv72 cricetus
38	24	17.9	22	11 Q9WV71	Q9wv71 ratcus norv
39	24	17.9	22	11 Q9R1U8	Q9rlu8 mus musculu
40	24	17.9	26	8 Q79846	Q79846 asplenium n
41	24	17.9	26	10 Q9S8P2	Q9s8p2 rapanus sa
42	23.5	17.5	22	2 Q50082	Q50082 mycobacteri
43	23	17.2	8	2 Q85406	Q85406 coxiella bu
44	23	17.2	9	5 Q96417	Q96417 drosophila
45	23	17.2	10	2 Q9X534	Q9x534 leclercia a

ALIGNMENTS

RESULT 1
Q9TR30 PRELIMINARY; PRT; 24 AA.
AC Q9TR30:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT VIA-L (FRAGMENT).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
RN [1]
RP SEQUENCE.
RX MEDLINE; 96092035.
RA Linder D., Freund R., Kadenbach B.;
RT *Species-specific expression of cytochrome c oxidase isozymes.*;
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 112:461-469(1995).
SQ SEQUENCE 24 AA; 2795 MW; D49D27C03B61F803 CRC64;

Query Match 24.6%; Score 33; DB 6; Length 24;
Best Local Similarity 58.3%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 LQMDFGFPEHL 17
DB 11 LQEDNGIPVHL 22
RESULT 2
Q9TRR6 PRELIMINARY; PRT; 19 AA.
AC Q9TRR6:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CALICYCLIN-ASSOCIATED PROTEIN, CAP50=CA2+/PHOSPHOLIPID-BINDING PROTEIN
DE L-14 FRAGMENT.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

Query Match 17.2%; Score 23; DB 1; Length 25;
 Best Local Similarity 44.4%; Pred. No. 1.7e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 8 QMDGPEFH 16
 : | | | |
 DB 17 ECDXGTPEN 25

RESULT 13
 UC03_MAIZE STANDARD; PRT; 18 AA.
 AC P80609;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 146)
 DE (FRAGMENT).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 RN (1)
 RP SEQUENCE.
 RC TISSUE=COLEOPTILE;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Perrollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program."
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.1, ITS MW IS: 29.3 KDA.
 CC -1- CAUTION: THE ORDER OF THE PEPTIDES SHOWN IS UNCERTAIN.
 DR MAIZE-2DPAGE: P80609; COLEOPTILE.
 DR MAIZEDB: 123924; -.
 FT NON_TER 1 1
 FT NON_CONS 9 10
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 1938 MW; 6F513BEB035881C0 CRC64;

Query Match 16.4%; Score 22; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGFL 5
 : | | | |
 DB 13 DGFL 16

RESULT 14
 CAOS_RAT STANDARD; PRT; 20 AA.
 ID CAOS_RAT
 AC P19633;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CALSQUESTRIN, SKELETAL MUSCLE ISOFORM (ASPARTACTIN) (LAMININ-BINDING
 DE PROTEIN) (FRAGMENT).
 GN CASQ1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN (1)
 RP SEQUENCE.
 RX MEDLINE: 88331073.
 RA Hall D.E., Frazer K.A., Hann B.C., Reichardt L.F.;
 RT "Isolation and characterization of a laminin-binding protein from rat
 RT and chick muscle."
 RL J. Cell Biol. 107:687-697(1988).
 CC -1- FUNCTION: CALSQUESTRIN IS A HIGH-CAPACITY, MODERATE AFFINITY,
 CC CALCIUM-BINDING PROTEIN AND THIS ACTS AS AN INTERNAL CALCIUM STORE
 CC IN MUSCLE. THE RELEASE OF CALCIUM BOUND TO CALSQUESTRIN THROUGH

CC A CALCIUM RELEASE CHANNEL TRIGGERS MUSCLE CONTRACTION. BINDS 40
 CC TO 50 MOLES OF CALCIUM. ALSO BINDS LAMININ.
 CC -1- SUBCELLULAR LOCATION: THIS ISOFORM OF CALSQUESTRIN OCCURS IN THE
 CC SARCOPLASMIC RETICULUM'S TERMINAL CISTERNAE LUMINAL SPACES OF
 CC FAST SKELETAL MUSCLE CELLS. ASPARTACTIN IS FOUND IN THE BASAL
 CC LAMINA SURROUNDING INDIVIDUAL MUSCLE FIBERS.
 CC -1- TISSUE SPECIFICITY: SKELETAL AND HEART MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE CALSQUESTRIN FAMILY.
 DR PIR, A31049; A31049.
 DR INTERPRO: IPR001393; -.
 DR PROSITE: PS00864; CALSQUESTRIN_2; PARTIAL.
 DR PROSITE: PS00863; CALSQUESTRIN_1; 1.
 KW Muscle; Glycoprotein; Calcium-binding.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2238 MW; 92ADE04FC2A69280 CRC64;

Query Match 16.4%; Score 22; DB 1; Length 20;
 Best Local Similarity 62.5%; Pred. No. 1.9e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 FPEHLLVD 20
 : | | | | |
 DB 6 FPEYDGV 13

RESULT 15
 MIF_PIG STANDARD; PRT; 20 AA.
 ID MIF_PIG
 AC P80928;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE MACROPHAGE MIGRATION INHIBITORY FACTOR (MIF) (GLYCOSYLATION-INHIBITING
 DE FACTOR) (GIF) (FRAGMENT).
 GN MIF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN (1)
 RP SEQUENCE.
 RA Riviere S., Bouet F., Menez A., Galat A.;
 RL Submitted (MAR-1997) to the SWISS-PROT data bank.
 CC -1- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST
 CC A ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE
 CC IN HOST DEFENSE (BY SIMILARITY).
 CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MIF FAMILY.
 DR HSSP; P14174; MIF.
 DR INTERPRO: IPR001398; -.
 DR PROSITE: PS01158; MIF; PARTIAL.
 KW Macrophage; Inflammatory response; Cytokine.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2147 MW; 3517AF60F3012A61 CRC64;

Query Match 16.4%; Score 22; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGFL 5
 : | | | |
 DB 16 DGFL 19

Search completed: December 21, 2000, 08:40:18
 Job time: 116 sec

RA Linder D., Freund R., Kadenbach B.;
 RT "Species-specific expression of cytochrome c oxidase isozymes.";
 CC Comp. Biochem. Physiol. 112B:461-469(1995).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 F(2)O +
 4 FERROCYTOCHROME C.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VITA FAMILY.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 23
 SQ SEQUENCE 23 AA: 2627 MM: AD3EA34B61FF73CE CRC64;

Query Match 18.7%; Score 25; DB 1; Length 23;
 Best Local Similarity 50.0%; Pred. No. 7.8e+02;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 6 LLOMDFGFEHL 17
 DB 11 LFGDNGLPVXL 22

RESULT 10
 ANGT_HORSE STANDARD; PRT: 14 AA.
 AC P01016;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE ANGIOTENSINOGEN (FRAGMENT).
 GN AGT.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 RN (1)
 RA SEQUENCE.
 RA Skeggs L.T., Kahn J.R., Lentz K., Shumway N.P.;
 RT "The preparation, purification, and amino acid sequence of a
 RT polypeptide renin substrate.";
 J. Exp. Med. 106:439-453(1957).
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 BALANCE OF BODY FLUIDS.
 CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR: A01250; A01250.
 DR INTERPRO: IPR000215; .
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT NON_TER 14 8 ANGIOTENSIN II.
 SQ SEQUENCE 14 AA: 1759 MM: 2E9921F8EEFBDD7 CRC64;

Query Match 17.9%; Score 24; DB 1; Length 14;
 Best Local Similarity 83.3%; Pred. No. 6.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 14 PEHLIV 19
 DB 7 PPHILV 12

RESULT 11
 SCX2_MESTA STANDARD; PRT: 24 AA.
 AC P45668;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE NEUROTOXIN II (BT-II) (FRAGMENT).
 CC Mesobuthus tamulus (Eastern Indian scorpion) (Butus tamulus).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butiridae; Butiridae; Mesobuthus.
 RN (1)
 RP SEQUENCE.
 RC TISSUE-VEINOM;
 RX MEDLINE: 94287436.
 RA Lala K., Narayanan P.;
 RT "Purification, N-terminal sequence and structural characterization of
 RT a toxic protein from the Indian scorpion venom Butus tamulus.";
 RL Toxicon 32:325-338(1994).
 CC -1- FUNCTION: BINDS TO SODIUM CHANNELS AND INHIBIT THE INACTIVATION OF
 CC THE ACTIVATED CHANNELS, THEREBY BLOCKING NEURONAL TRANSMISSION.
 CC THIS TOXIN IS ACTIVE AGAINST MAMMALS. LD(50) IS 2.25 MG/KG IN MICE
 CC BY SUBCELLULAR LOCATION: SECRETED.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
 KW Alpha-toxin; Sodium channel inhibitor.
 FT NON_TER 24
 SQ SEQUENCE 24 AA: 2686 MM: DA190C8FF8E2769 CRC64;

Query Match 17.2%; Score 23; DB 1; Length 24;
 Best Local Similarity 80.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLL 6
 DB 2 DGYLL 6

RESULT 12
 BOTR_BOTJA STANDARD; PRT: 25 AA.
 AC P22028;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE BOTROCETIN (PLATELET COAGGLUTININ) (FRAGMENT).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubridae;
 OC Viperidae; Crotalinae; Bothrops.
 RN (1)
 RA SEQUENCE.
 RP TISSUE-VEINOM;
 RX MEDLINE: 91129280.
 RA Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
 RA Fukui H., Sugimoto M., Ruggeri Z.M.;
 RT "Isolation and chemical characterization of two structurally and
 RT functionally distinct forms of botrocetin, the platelet coagglutinin
 RT isolated from the venom of Bothrops jararaca.";
 RL Biochemistry 30:1957-1964(1991).
 CC -1- FUNCTION: THERE ARE TWO DISTINCT FORMS OF THE VON WILLEBRAND
 CC FACTOR-DEPENDENT PLATELET COAGGLUTININ. THE DIMERIC FORM IS
 CC 34-TIMES MORE ACTIVE THAN THE ONE-CHAIN BOTROCETIN IN PROMOTING
 CC VWF BINDING TO PLATELETS.
 CC -1- SUBUNIT: MONOMER. VWF AND BOTROCETIN FORM A SOLUBLE COMPLEX.
 CC -1- PTM: CONTAINS NUMEROUS INTRACHAIN DISULFIDE BONDS.
 CC -1- SIMILARITY: NO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
 DR INTERPRO: IPR001304; .
 DR PROSITE: PS00615; C_TYPE_LECTIN_1; PARTIAL.
 DR PROSITE: PS00641; C_TYPE_LECTIN_2; PARTIAL.
 KW Glycoprotein; Venom.
 FT VARIANT 2 2 I -> V.
 FT NON_TER 25 25
 SQ SEQUENCE 25 AA: 2655 MM: D25D9031A705CAF8 CRC64;

AC P12662;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE INTERPHOTORECEPTOR RETINOID-BINDING PROTEIN (IRBP) (INTERSTITIAL
 DE RETINOL-BINDING PROTEIN) (FRAGMENT).
 GN IRBP3.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 86301171.
 RA Feng S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A.,
 RA Bridges C.D.B.;
 RT "N-terminal sequence homologues in interstitial retinol-binding
 RT proteins from 10 vertebrate species.";
 RL FEBS Lett. 205:309-312(1986)
 CC -1- FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN
 CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
 CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
 CC -1- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
 CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
 CC EPITHELIUM CELLS.
 DR PIR; B24417; B24417.
 KW Vitamin A; Transport.
 FT NON_TER 25
 SQ SEQUENCE 25 AA; 2813 MW; 4E751DPA160231B7 CRC64;

Query Match 19.4%; Score 26; DB 1; Length 25;
 Best Local Similarity 38.5%; Pred. No. 6e+02;
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 6 LLQMDFGPPEHL 18
 Db 12 ILLDNTTFPESLM 24

RESULT 7
 ARCD_PSEPU STANDARD; PRT; 16 AA.
 AC P11147;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ARGININE/ORNITHINE ANTIporter (FRAGMENT).
 GN ARCD.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=ATCC 4359;
 RA Wilson S.D., Wang M., Filpula D.;
 RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES AN ELECTRONEUTRAL EXCHANGE BETWEEN ARGININE
 CC AND ORNITHINE TO ALLOW HIGH-EFFICIENCY ENERGY CONVERSION IN THE
 CC ARGININE DEIMINASE PATHWAY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 CC (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
 CC PERMEASES.
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 CC -----
 DR EMBL; 007185; AAA16963.1; -.

KW Transport; Amino-acid transport; Transmembrane; Inner membrane.
 FT NON_TER 1
 SQ SEQUENCE 16 AA; 1644 MW; 90B48A7C8FAA9705 CRC64;

Query Match 18.7%; Score 25; DB 1; Length 16;
 Best Local Similarity 83.3%; Pred. No. 5.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 DGFLL 7
 Db 11 DGFLL 16

RESULT 8
 COXN_THUOB STANDARD; PRT; 20 AA.
 AC P80980;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE VIIB-HEART (EC 1.9.3.1) (FRAGMENT).
 OS Thunnus obesus (Bigeye tuna).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphi; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 RN [1]
 RP SEQUENCE.
 RX TISSUE=HEART;
 RA MEDLINE; 97454291.
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver.";
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
 CC 4 FERRICYTOCHROME C.
 KW Oxidoreductase; Mitochondrion.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2303 MW; 0A33BD34006E5AA6 CRC64;

Query Match 18.7%; Score 25; DB 1; Length 20;
 Best Local Similarity 46.2%; Pred. No. 6.7e+02;
 Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4 FLLQMDFGPPEH 16
 Db 8 FLLFGDGMMPVH 20

RESULT 9
 COXK_CANFA STANDARD; PRT; 23 AA.
 AC Q9TRZ8;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-HEART, MITOCHONDRIAL
 DE (EC 1.9.3.1) (CYTOCHROME C OXIDASE SUBUNIT VIIA-H) (COX VIIA-M)
 DE (FRAGMENT).
 GN COX7A1 OR COX7AH.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN, AND HEART;
 RX MEDLINE; 96092035.

RN (1)
 RP SEQUENCE.
 RX MEDLINE: 86301171.
 RA Fong S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A.,
 RA Bridges C.D.B.;
 RA "N-terminal sequence homologues in interstitial retinol-binding
 RT proteins from 10 vertebrate species.";
 RL FEBS Lett. 205:309-312(1986).
 CC -1- FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN
 CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
 CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
 CC -1- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
 CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
 CC EPITHELIUM CELLS.
 CC PIR: A24417; A24417.
 DR Vitamin A; Transport.
 KW NON_TER 24
 FT SEQUENCE 24 AA: 2799 MW: 02EDBE61A8E4523 CRC64;
 SQ

Query Match 20.1%; Score 27; DB 1; Length 24;
 Best Local Similarity 35.0%; Pred. No. 2.8e+02;
 Matches 7; Conservative 5; Mismatches 2; Indels 6; Gaps 1;

QY 5 LLLQW-----DFGPFPHL 18
 DB 5 LVLDMAQVLLDNTYTPENLM 24

RESULT 3
 COX2_ONCMY STANDARD: PRT; 23 AA.
 ID COX2_ONCMY
 AC P80333;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER (EC 1.9.3.1) (VIIC)
 DE (FRAGMENT).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 RN (1)
 RP SEQUENCE.
 RC TISSUE=LIVER;
 RX MEDLINE: 94237150.
 RA Freund R., Kadenbach B.;
 RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
 RT of cytochrome c oxidase isolated from rainbow trout.";
 RL Eur. J. Biochem. 221:1111-1116(1994).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O +
 CC 4 FERROCYTOCHROME C.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
 DR PIR: S43632; S43632.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 KW NON_TER 23
 FT SEQUENCE 23 AA: 2635 MW: BCBED43FBAD9C509 CRC64;
 SQ

Query Match 20.1%; Score 27; DB 1; Length 23;
 Best Local Similarity 50.0%; Pred. No. 3.8e+02;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 LQMDGPFPHL 17
 DB 11 LFOAXNGIPVHL 22

CCA-STRT
 ID CCA-STRT
 AC P80436;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CHINOXALIN-2-CARBOXYLIC ACID ACTIVATING ENZYME (FRAGMENT).
 OS Streptomyces tiosolicus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 RN (1)
 RP SEQUENCE.
 RA Pahl A., Schlumbohm W., Keller U.;
 RL Submitted (MAR-1995) to the SWISS-PROT data bank.
 CC -1- FUNCTION: INVOLVED IN TRIOSTIN BIOSYNTHESIS.
 KW Antibiotic biosynthesis.
 KW NON_TER 24
 FT SEQUENCE 24 AA: 2900 MW: 91C222B657CEB6D1 CRC64;
 SQ

Query Match 20.1%; Score 27; DB 1; Length 24;
 Best Local Similarity 30.0%; Pred. No. 4e+02;
 Matches 6; Conservative 5; Mismatches 3; Indels 6; Gaps 1;

QY 2 DGFLLQMDGPFPHLVDF 21
 DB 3 DGFV-----PWPDLADEY 16

RESULT 5
 YCXB_ODOSI STANDARD: PRT; 26 AA.
 ID YCXB_ODOSI
 AC P49839;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE HYPOTHEICAL 3.2 KDA PROTEIN IN RPOC2-RPS2 INTERGENIC REGION (ORF26B).
 OS Odontella sinensis.
 OC Chloroplast.
 OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
 OC Biddulphiophycidae; Eupodiscaceae; Eupodiscaceae; Odontella.
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.;
 RT "The chloroplast genome of a chlorophyll a+c-containing alga,
 RT Odontella sinensis".
 RL Plant Mol. Biol. Rep. 13:336-342(1995).
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 CC -----
 DR EMBL: Z67753; CAA01747.1;
 KW Chloroplast; Hypothetical protein.
 KW NON_TER 26
 FT SEQUENCE 26 AA: 3137 MW: 83058587C0A30B36 CRC64;
 SQ

Query Match 20.1%; Score 27; DB 1; Length 26;
 Best Local Similarity 42.9%; Pred. No. 4.4e+02;
 Matches 6; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 2 DGFLLQMDGPFPHLVDF 13
 DB 11 DGFIECLMLNLYKF 24

RESULT 6
 IRBP_PIG STANDARD: PRT; 25 AA.
 ID IRBP_PIG

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:38:22 ; Search time 12.36 Seconds

(without alignments)
67.204 Million cell updates/sec

Title: US-08-934-367-29

Perfect score: 134

Sequence: 1 RDGFLILQMDGFEPEHLVDVFLQSLIS 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues 1478

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 26

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	24.6	24	1	Q9TR30 ovis aries
2	28	20.9	24	1	IRBP_SHEEP
3	27	20.1	23	1	COXJ_ONCMY
4	27	20.1	24	1	CCAA_STRTI
5	27	20.1	26	1	YCXD_ODOSI
6	26	19.4	25	1	IRBP_PIG
7	25	18.7	16	1	ARCD_PSEPU
8	25	18.7	20	1	COXN_THUOB
9	25	18.7	23	1	COXK_CANFA
10	24	17.9	14	1	AMGT_HORSE
11	23	17.2	24	1	SCX2_MESTA
12	23	17.2	25	1	BOTR_BOTJA
13	22	16.4	18	1	UCO3_MAIZE
14	22	16.4	20	1	CAOS_RAT
15	22	16.4	20	1	MTF_PIG
16	22	16.4	24	1	FIBG_CANFA
17	22	16.4	24	1	KPYK_CLOPA
18	22	16.4	26	1	CATG_RAT
19	22	16.4	25	1	CT21_LITCI
20	21.5	16.0	25	1	ALR_PSEFL
21	21	15.7	9	1	FARD_CALVO
22	21	15.7	9	1	SAMP_MUSCA
23	21	15.7	25	1	AMP3_MELGA
24	20	14.9	11	1	CH60_DROME
25	20	14.9	11	1	TEML_RANTE
26	20	14.9	14	1	DCMM_PSECF
27	20	14.9	16	1	MDH_SYNY4
28	20	14.9	21	1	ATPB_PHYPA
29	20	14.9	23	1	SODM_RANCA
30	19.5	14.6	19	1	NIO6_SOLTU
31	19.5	14.6	20	1	DPP4_BOVIN
32	19	14.2	19	1	OXLA_OPHHA
33	19	14.2	19	1	UP21_URETN

34	19	14.2	19	1	UP25_UREIN
35	19	14.2	20	1	ITRA_ALBUJ
36	19	14.2	20	1	SUCB_CANFA
37	19	14.2	21	1	DCMS_PSECA
38	19	14.2	21	1	YD90_HAEIN
39	19	14.2	23	1	CH60_THIFE
40	19	14.2	25	1	ACP_ERYLO
41	19	14.2	25	1	CR21_LITSP
42	19	14.2	25	1	CR22_LITGI
43	19	14.2	25	1	CR23_LITGE
44	19	14.2	25	1	CR25_LITGI
45	19	14.2	25	1	FLAA_TREPH

ALIGNMENTS

RESULT 1	COXJ_SHEEP	STANDARD;	PRT;	24 AA.
ID	COXJ_SHEEP			
AC	O9TR30:			
DT	01-OCT-2000 (Rel. 40, Created)			
DT	01-OCT-2000 (Rel. 40, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	CYTOCHROME C OXIDASE POLYPEPTIDE VILIA-LIVER/HEART, MITOCHONDRIAL			
DE	(EC 1.9.3.1) (CYTOCHROME C OXIDASE SUBUNIT VILIA-L) (FRAGMENT).			
GN	COX7A2 OR COX7AL.			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Caprinae; Ovis.			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=LIVER, AND HEART;			
RX	MEDLINE; 96092035.			
RA	Linder D., Freund R., Kadenbach B.;			
RT	*Species-specific expression of cytochrome c oxidase isozymes.*;			
RL	Comp. Biochem. Physiol. 112B:461-469(1995).			
CC	-1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE			
CC	CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN			
CC	MITOCHONDRIAL ELECTRON TRANSPORT.			
CC	-1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O +			
CC	4 FERRICYTOCHROME C.			
CC	-1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.			
CC	-1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VILIA FAMILY.			
CC	Oxidoreductase; Inner membrane; Mitochondrion.			
FT	NON_TER 24			
SO	SEQUENCE 24 AA; 2795 MW; D49D27C03B61F803 CRC64;			
QY	6	24.6%; Score 33; DB 1; Length 24;		
Db	11 LFQEDNGIPVHL 22	Best local similarity 58.3%; Pred. No. 48;		
		Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;		
RESULT 2	IRBP_SHEEP	STANDARD;	PRT;	24 AA.
ID	IRBP_SHEEP			
AC	P12663:			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	01-FEB-1996 (Rel. 33, Last annotation update)			
DE	INTERPROTECTOR RETINOID-BINDING PROTEIN (IRBP) (INTERSTITIAL			
DE	RETINOL-BINDING PROTEIN) (FRAGMENT).			
GN	IRBP.			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Caprinae; Ovis.			

!!: !!:
 Db 8 DGYYYYAMDY 17

RESULT 14

S77989
 cytochrome-c oxidase (EC 1.9.3.1) chain VIIb - bigeye tuna (fragment)
 C:Species: Thunnus obesus (bigeye tuna)
 C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
 C:Accession: S77989
 R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
 submitted to the Protein Sequence Database, June 1997
 A:Reference number: S77980
 A:Accession: S77989
 A:Molecule type: protein
 A:Residues: 1-20 <ARN>
 A:Experimental source: heart
 C:Genetics:
 A:Genome: nuclear
 C:Function:
 A:Pathway: oxidative phosphorylation; respiratory chain
 C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 18.7%; Score 25; DB 2; Length 20;
 Best Local Similarity 46.2%; Pred. No. 1e+03;
 Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4 FILLQMDPGEPEH 16
 | | | | | | | | | |
 Db 8 FILEYGDNGMPVH 20

RESULT 15

PC4030
 rRNA endonuclease (EC 3.1.27.10) - shiitake mushroom (fragment)
 M:Alternate names: nuclease Le3
 C:Species: Lentinula edodes (shiitake mushroom)
 C:Date: 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 20-Mar-1996
 C:Accession: PC4030
 R: Kobayashi, H.; Inokuchi, N.; Koyama, T.; Tomita, M.; Irie, M.
 Biosci. Biotechnol. Biochem. 59, 1169-1171, 1995
 A:Title: Purification and characterization of the 2nd 5'-nucleotide-forming nuclease from
 A:Reference number: PC4030; MUID:95337563
 A:Accession: PC4030
 A:Molecule type: DNA
 A:Residues: 1-23 <KOB>
 C:Comment: This enzyme has 3'-nucleotidase activity.
 C:Keywords: endonuclease; hydrolase

Query Match 18.7%; Score 25; DB 2; Length 23;
 Best Local Similarity 42.9%; Pred. No. 1.2e+03;
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 11 FGPEHLLVDFLOS 24
 : | | | | | : |
 Db 1 WGMIGHETLVGFTAS 14

Search completed: December 21, 2000, 08:39:30
 Job time: 134 sec

A:Title: Structural and immunological studies on the soluble formate dehydrogenase from
 A:Accession number: S59492; MUID:96145736
 A:Accession: S59492
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <FRI>

Query Match 19.4%; Score 26; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 5e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 8 QMDFGF 14
 : : : : :
 Db 6 EIDFCTP 12

RESULT 9
 B24417
 Interphotoreceptor retinoid-binding protein - pig (fragment)
 N:Alternate names: interstitial retinol-binding protein
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Nov-1997
 C:Accession: B24417
 R:Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
 FEBS Lett. 205, 309-312, 1986
 A:Title: N-terminal sequence homologues in interstitial retinol-binding proteins from 10
 A:Reference number: A91365; MUID:86301171
 A:Accession: B24417
 A:Molecule type: protein
 A:Residues: 1-25 <FON>
 C:Superfamily: Interphotoreceptor retinoid-binding protein
 C:Keywords: duplication

Query Match 19.4%; Score 26; DB 2; Length 25;
 Best Local Similarity 38.5%; Pred. No. 9e+02;
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 6 LIQMFGRPEHL 18
 : : : : :
 Db 12 ILIDNYTPEESIM 24

RESULT 10
 S71306
 heat shock protein 90 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
 C:Accession: S71306
 R:Conconi, M.; Szveda, L.I.; Levine, R.L.; Stadman, E.R.; Friguet, B.
 Arch. Biochem. Biophys. 331, 232-240, 1996
 A:Title: Age-related decline of rat liver multicatalytic proteinase activity and protect
 A:Reference number: S71306; MUID:96299287
 A:Accession: S71306
 A:Molecule type: protein
 A:Residues: 1-15 <CON>
 A:Experimental source: liver
 C:Keywords: heat shock; phosphoprotein; stress-induced protein

Query Match 18.7%; Score 25; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 7.2e+02;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 14 PEHLVDFLQ 23
 : : : : :
 Db 6 PDPIVETLR 15

RESULT 11
 T44936
 calmodulin kinase 2 - fission yeast (Schizosaccharomyces pombe) (fragment)

C:Species: Schizosaccharomyces pombe
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
 C:Accession: T44936
 R:Alemamy, V.; Alique, R.
 Submitted to the EMBL Data Library, May 1996
 A:Reference number: 22873
 A:Accession: T44936
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-16 <ALE>
 A:Cross-references: EMBL:U57982; PIDN:AAD09466.1

Query Match 18.7%; Score 25; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 FGFP 14
 : : : : :
 Db 5 FGFP 8

RESULT 12
 C49048
 T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragmen
 C:Species: Homo sapiens (man)
 C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
 C:Accession: C49048
 R:Stoud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
 Eur. J. Immunol. 22, 2413-2418, 1992
 A:Title: Limited heterogeneity of T cell receptor variable region gene usage in juven
 A:Reference number: A49048; MUID:92387250
 A:Accession: C49048
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-16 <SID>
 A:Experimental source: patient EV, IL-2R+ synovial T-cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:113265)
 C:Keywords: T-cell receptor

Query Match 18.7%; Score 25; DB 2; Length 16;
 Best Local Similarity 54.5%; Pred. No. 7.7e+02;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 GFLIQMDPGF 13
 : : : : :
 Db 3 GFLIQGPPGV 13

RESULT 13
 P11607
 Ig H chain V-D-J region (wild-type clone 333) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: P11607
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less m
 A:Reference number: P11580; MUID:93301609
 A:Accession: P11607
 A:Molecule type: DNA
 A:Residues: 1-17 <LEV>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: Immunoglobulin

Query Match 18.7%; Score 25; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 8.3e+02;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 DGLLIQMDF 11

RESULT 3

B59018

MUC1 enhancer binding protein 85k chain MUC1EBP-85 - human (fragments)

C:Species: Homo sapiens (man)

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998

C:Accession: B59018

R:Abbe, M.; Smith, C.J.; Larson, C.J.

submitted to the Protein Sequence Database, May 1998

A:Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a bre

A:Reference number: A59018

A:Accession: B59018

A:Molecule type: protein

A:Residues: 1-17:18-26 <ABE>

A:Experimental source: breast cancer cell line MCF-7

C:Keywords: DNA binding; heterodimer

Query Match

Best Local Similarity 20.9%; Score 28; DB 2; Length 26;

Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 LLLQMDGFPPEHLVD 20

DB 9 VLXMDVGFLEPLTE 24

RESULT 4

A32521

hexokinase (EC 2.7.1.1) I peptide III - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 12-Apr-1995

C:Accession: A32521

R:Schlrich, D.M.; Wilson, J.E.

Arch. Biochem. Biophys. 257, 1-12, 1987

A:Title: Rat brain hexokinase: amino acid sequence at the substrate hexose binding site

A:Reference number: A90080; MOID:87324917

A:Accession: A32521

A:Molecule type: protein

A:Residues: 1-21 <SCH>

C:Superfamily: human hexokinase I; hexokinase homology

C:Keywords: ATP; glycolysis; phosphotransferase

Query Match

Best Local Similarity 20.1%; Score 27; DB 2; Length 21;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 LQMDGFPPEH 16

DB 3 LGFTSFSPXH 12

RESULT 5

S43632

cytochrome-c oxidase (EC 1.9.3.1) chain VIIa, hepatic - rainbow trout (fragment)

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997

C:Accession: S43632

R:Freund, R.; Kadenbach, B.

Eur. J. Biochem. 221, 1111-1116, 1994

A:Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochr

A:Reference number: S43624; MOID:94237150

A:Accession: S43632

A:Molecule type: protein

A:Residues: 1-23 <FRE>

A:Note: the source is designated as Salmo gairdneri

C:Genetics:

A:Genome: nuclear

C:Superfamily: mammalian cytochrome-c oxidase chain VIIa

C:Keywords: liver; membrane-associated complex; mitochondrion; oxidoreductase

Query Match

20.1%; Score 27; DB 2; Length 23;

Best Local Similarity 50.0%; Pred. No. 5.7e+02;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 LQMDGFPPEHL 17

DB 11 LFGXNXGIPVHL 22

RESULT 6

S78374

hypothetical protein 26b - Odontella sinensis chloroplast

C:Species: chloroplast Odontella sinensis

C:Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 24-Apr-1998

C:Accession: S78374

R:Kowallik, K.V.; Scoabe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.

Plant Mol. Biol. Rep. 13, 336-342, 1995

A:Title: The Chloroplast Genome of a chlorophyll a+c-containing Alga, Odontella sine

A:Reference number: S78238

A:Accession: S78374

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-26 <KOW>

A:Cross-references: EMBL:267753; NID:g1185127; PID:e211900; PID:g1185264

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995

C:Genetics:

A:Genome: chloroplast

C:Keywords: chloroplast

Query Match

Best Local Similarity 20.1%; Score 27; DB 2; Length 26;

Matches 6; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 2 DGFLL-LQMDGFP 13

DB 11 DGFIECLMLMYK 24

RESULT 7

A54077

cytochrome b558 - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995

C:Accession: A54077

R:Escrivou, V.; Laporte, F.; Garin, J.; Brandolin, G.; Vignais, P.V.

J. Biol. Chem. 269, 14007-14014, 1994

A:Title: Purification and Physical Properties of a novel type of cytochrome b from ra

A:Reference number: A54077; MOID:94245717

A:Accession: A54077

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <ESC>

A:Experimental source: peritoneal neutrophils

A:Note: sequence extracted from NCBI backbone (NCBIP:148739)

Query Match

Best Local Similarity 19.8%; Score 26.5; DB 2; Length 20;

Matches 9; Conservative 2; Mismatches 4; Indels 5; Gaps 1;

QY 3 GFLLLQMDGFPPEHLVD 22

DB 6 GFLVLLV-----SALLVGF 20

RESULT 8

S59492

formate dehydrogenase alpha chain - Alcaligenes eutrophus (fragment)

C:Species: Alcaligenes eutrophus

C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999

C:Accession: S59492

R:Riedelbold, J.; Mayer, F.; Bill, F.; Trautwein, A.X.; Bowlen, B.

Biol. Chem. Hoppe-Seyler 376, 561-568, 1995

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:37:16 ; Search time 19.49 Seconds
(without alignments)
\$4.657 Million cell updates/sec

Title: US-08-934-367-29

Perfect score: 134
Sequence: 1 RDGFLLMQDMFGPEPHLLVDFLQSL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 5255

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_65:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	20.9	19	2 A39504	octamer-binding pr
2	28	20.9	24	2 A24417	interphotoreceptor
3	28	20.9	26	2 B59018	MOC1 enhancer bind
4	27	20.1	21	2 A32521	hexokinase (EC 2.7
5	27	20.1	23	2 S43632	cytochrome-c oxida
6	27	20.1	26	2 S78374	hypothetical prote
7	26.5	19.8	20	2 A54077	cytochrome b558 -
8	26	19.4	15	2 S59492	formate dehydrogen
9	26	19.4	25	2 B24417	interphotoreceptor
10	25	18.7	15	2 S71306	heat shock protein
11	25	18.7	16	2 T49366	calmodulin kinase
12	25	18.7	16	2 C94048	T-cell receptor be
13	25	18.7	17	2 PH1607	Ig H chain V-D-J r
14	25	18.7	20	2 S77989	cytochrome-c oxida
15	25	18.7	23	2 PC4030	rRNA endonuclease
16	25	18.7	25	2 A60502	myonexin - northern
17	24.5	18.3	14	2 B61597	cytochrome P450 AL
18	24.5	18.3	13	2 S03879	6-phosphofructokin
19	24	17.9	14	2 A01250	angiotensin precur
20	24	17.9	15	2 A60834	angiotensin I prec
21	24	17.9	17	2 B31769	T-cell receptor de
22	24	17.9	18	2 PN0175	glutathione transf
23	24	17.9	18	2 H75063	hypothetical prote
24	24	17.9	20	2 A60822	cytochrome P450 PB
25	24	17.9	20	2 A37984	ADP,ATP carrier pr
26	23	17.2	7	2 S36662	dermorphin (uys-7)
27	23	17.2	14	2 PA0015	seed storage prote
28	23	17.2	17	2 S71864	glutathione transf
29	23	17.2	19	2 I46554	T-cell receptor de

30	23	17.2	21	2 T07683	proteinase inhibit
31	23	17.2	23	2 I39681	exeg protein - Aer
32	23	17.2	24	2 PC2199	alicyclic amine N-
33	23	17.2	24	2 T42257	phosphoprotein pho
34	23	17.2	24	2 A53357	neurotoxin Bt-II -
35	23	17.2	25	2 S35926	T-cell receptor ga
36	23	17.2	26	2 J70965	cytochrome-c oxida
37	23	17.2	26	2 A42218	early protein Sx1
38	22	16.4	7	1 A61324	dermorphin - Rohde
39	22	16.4	11	2 PT0250	Ig heavy chain CRD
40	22	16.4	12	2 C36201	1-aminocyclopropan
41	22	16.4	14	2 A61002	photosystem II oxy
42	22	16.4	19	2 B60822	cytochrome P450 UT
43	22	16.4	20	2 S72501	protein kinase C 1
44	22	16.4	20	2 A31049	calsequestrin, fas
45	22	16.4	20	2 A47105	dystroglycan - chl

ALIGNMENTS

RESULT 1
A39504
octamer-binding protein, Ku-like, 72K chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: A39504
R:May, G.; Sutton, C.; Gould, H.
J. Biol. Chem. 266, 3052-3059, 1991
A:Title: Purification and characterization of Ku-2, an octamer-binding protein relate
A:Reference number: A39504; MUID:91131605
A:Accession: A39504
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <MAX>

Query Match 20.9%; Score 28; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LQMDFGF 13
DB 11 LEMDVG 17

RESULT 2
A24417
interphotoreceptor retinoid-binding protein - sheep (fragment)
N:Alternate names: interstitial retinol-binding protein
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Nov-1997
C:Accession: A24417
R:Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
FEBS Lett. 205, 309-312, 1986
A:Title: N-terminal sequence homologies in interstitial retinol-binding proteins from
A:Reference number: A91365; MUID:86301171
A:Accession: A24417
A:Molecule type: protein
A:Residues: 1-24 <FON>
C:Superfamily: Interphotoreceptor retinoid-binding protein
C:Keywords: duplication

Query Match 20.9%; Score 28; DB 2; Length 24;
Best Local Similarity 35.0%; Pred. No. 4.2e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 1;

QY 5 LLLQW-----DEGPEPHLL 18
DB 5 LVLDMAQVLLNDYTPPENILM 24

FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lawyer
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 401:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-401

Query Match 20.9%; Score 28; DB 3; Length 10;
Best local Similarity 66.7%; Pred. No. 82;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 FPEHL 18
:||||:
DB 2 YPEHLV 7

RESULT 15
PCT-US91-02942-88
Sequence 88, Application PC/TUS9102942
GENERAL INFORMATION:
APPLICANT: ROTHLEIN, ROBERT
APPLICANT: ADAIR, JOHN R
APPLICANT: ATHWAL, DILJEET S
TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Ave. NW Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02942
FILING DATE: 19910429
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9009549.8
FILING DATE: 27-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAM L
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1011.0586600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-02942-88

Query Match 20.9%; Score 28; DB 4; Length 10;
Best local Similarity 55.6%; Pred. No. 82;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 GELLQMDP 11
:||||:
DB 2 GWLLSFDY 10

Search completed: December 21, 2000, 08:39:07
Job time: 141 sec

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 MDGFEHLL 18
: 11 : 11

Db 9 IDHYHNELL 18

RESULT 12

US-08-424-881-3

; Sequence 3, Application US/08424881

; Patent No. 5863782

; GENERAL INFORMATION:

; APPLICANT: John Joseph HOPWOOD

; APPLICANT: Hamish Steele SCOTT

; APPLICANT: Craig Geoffrey FREEMAN

; APPLICANT: Charles Phillip MORRIS

; APPLICANT: Lianne Cheryl BLANCH

; APPLICANT: Xiao-Nui GUO

; TITLE OF INVENTION: SYNTHETIC MAMMALIAN SULPHAMIDASE

; TITLE OF INVENTION: AND GENETIC SEQUENCES ENCODING SAME

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

; STREET: 400 GARDEN CITY PLAZA

; CITY: GARDEN CITY

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 11530-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/424,881

; FILING DATE: 19-APR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: DIGIGLIO, FRANK S.

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 9671

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: +516 742 4343

; TELEFAX: +516 742 4366

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 25 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-424-881-3

Query Match 21.6%; Score 29; DB 2; Length 25;

Best Local Similarity 53.8%; Pred. No. 1.7e+02;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RDGFLLQMDFGF 13
: 111 : 111

Db 3 RNALLLLADGGF 15

RESULT 13

US-08-874-763-3

; Sequence 3, Application US/08874763

; Patent No. 5972333

; GENERAL INFORMATION:

; APPLICANT: John Joseph HOPWOOD

; APPLICANT: Hamish Steele SCOTT

; APPLICANT: Craig Geoffrey FREEMAN

; APPLICANT: Charles Phillip MORRIS

; APPLICANT: Lianne Cheryl BLANCH

; APPLICANT: Xiao-Nui GUO

; TITLE OF INVENTION: SYNTHETIC MAMMALIAN SULPHAMIDASE

; TITLE OF INVENTION: AND GENETIC SEQUENCES ENCODING SAME

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

; STREET: 400 GARDEN CITY PLAZA

; CITY: GARDEN CITY

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 11530-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/874,763

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/424,881

; FILING DATE: 19-APR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: DIGIGLIO, FRANK S.

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 9671

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: +516 742 4343

; TELEFAX: +516 742 4366

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 25 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-874-763-3

Query Match 21.6%; Score 29; DB 2; Length 25;

Best Local Similarity 53.8%; Pred. No. 1.7e+02;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RDGFLLQMDFGF 13
: 111 : 111

Db 3 RNALLLLADGGF 15

RESULT 14

US-08-159-339A-401

; Sequence 401, Application US/08159339A

; Patent No. 6037135

; GENERAL INFORMATION:

; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.

; APPLICANT: Settle, Alessandro

; APPLICANT: Celis, Esteban

; TITLE OF INVENTION: HLA Binding peptides and their

; NUMBER OF SEQUENCES: 1254

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/159,339A

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H 32,140
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5858980e
US-08-468-540b-3

Query Match 21.6%; Score 29; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RDGFLLOMDFG 12
1:111 11
Db 5 RBGFLPRHRDTG 16

RESULT 10
US-08-827-618A-22
Sequence 22, Application US/08827618A
Patent No. 5998366
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Erlander, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,618A
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,725
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-12/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-618A-22

Query Match 21.6%; Score 29; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 MDGFPPEHL 18
:11:111
Db 9 IDFPHPNEL 18

RESULT 11
US-08-483-952A-22
Sequence 22, Application US/08483952A
Patent No. 6011139
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Erlander, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,952A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,859
FILING DATE: 17-SEP-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-7/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-952A-22

Query Match 21.6%; Score 29; DB 3; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;

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:   FEATURE:
:   NAME/KEY: Peptide
:   LOCATION: 1..22
:   OTHER INFORMATION: /note="motif C peptide from human
:   OTHER INFORMATION: telomerase core protein 1 (TCTP)"
US-08-851-043A-170

```

Query Match	22.0%	Score	29.5	DB	3	Length	22
Best Local	Similarity	40.9%	Pred. No.	1.2e+02			
Matches	9	Conservative	1	Mismatches	3	Indels	9
						Gaps	1

```

OY      1 RDGELLQMDFGFPEHLLVDL 22
          |||  || :|          |||
Db      2 RDGLLRLVD-----DFL 14

```

```

1  RESULT
2  7
3  US-08-399-696-85
4  : Sequence 85, Application US/08399696
5  : Patent No. 5756669
6  : GENERAL INFORMATION:
7  : APPLICANT:
8  : TITLE OF INVENTION: p53-BINDING POLYPEPTIDES AND
9  : TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME
10 : NUMBER OF SEQUENCES: 126
11 : COMPUTER READABLE FORM:
12 : MEDIUM TYPE: floppy disk
13 : COMPUTER: IBM PC compatible
14 : OPERATING SYSTEM: PC-DOS/MS-DOS
15 : SOFTWARE: Patent In Release #1.0, Version #1.25
16 : CURRENT APPLICATION DATA:
17 : APPLICATION NUMBER: US/08/399,696
18 : FILING DATE: 02-MAR-1995
19 : CLASSIFICATION: 435
20 : PRIOR APPLICATION DATA:
21 : APPLICATION NUMBER: US 08/156,671
22 : FILING DATE: 22-NOV-1993
23 : ATTORNEY/AGENT INFORMATION:
24 : NAME: Smith, William M.
25 : REGISTRATION NUMBER: 30,223
26 : REFERENCE/DOCKET NUMBER: 15522-000710
27 : TELECOMMUNICATION INFORMATION:
28 : TELEPHONE: (415) 326-2400
29 : TELEFAX: (415) 326-2422
30 : INFORMATION FOR SEQ ID NO: 85:
31 : SEQUENCE CHARACTERISTICS:
32 : LENGTH: 19 amino acids
33 : TYPE: amino acid
34 : STRANDEDNESS: unknown
35 : TOPOLOGY: unknown
36 : MOLECULE TYPE: peptide
37 : US-08-399-696-85

```

Query Match	21.6%	Score 29	DB 1	Length 19
Best local	Similarity 62.5%	Pred. NO	1.2e+02	
Matches	5	Conservative	2	Mismatches 1
				Indels 0
				Gaps 0

QY	15	EHLVDFL	22
		::	
Db	12	EHLIDGL	19

RESULT 8
 US-08-484-530-22
 ; Sequence 22, Application US/08484530
 ; Patent No. 5846740
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Tobin, Allan J
 ; APPLICANT: Erlanger, Mark G
 ; APPLICANT: Kaufman, Daniel L.
 ;
 ; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase

NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fleury, Hobdach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA

```

? ZIP: 94111-4187
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/484,550
? FILING DATE: 07-JUN-1995

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Query Match	21.6%	Score	29	DB	2	Length	20
Best Local Similarity	50.0%	Pred. No.	1.3e+02				
Matches	5	Conservative	2	Mismatches	3	Indels	0
						Gaps	0

```
Qy      9 MDEGFPEHLL 18
        :||:|  ||
Db      9 IDFHYPNELLL 18
```

```

1      RESULT 9
2      US-08-468-540B-3
3      Sequence 3, Application US/08468540B
4      Patent No. 5858980
5      GENERAL INFORMATION:
6      APPLICANT: Weiner, Howard
7      APPLICANT: Haffler, David
8      APPLICANT: Miller, Ariel
9      APPLICANT: Al-Sabbagh, Ahmad
10     TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
11     TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
12     NUMBER OF SEQUENCES: 25
13     CORRESPONDENCE ADDRESS:
14     ADDRESSEE: Darby & Darby P.C.
15     STREET: 805 Third Avenue
16     CITY: New York
17     STATE: NY
18     COUNTRY: USA
19     ZIP: 10022
20     COMPUTER READABLE FORM:
21     MEDIUM TYPE: Diskette
22     COMPUTER: IBM Compatible
23     OPERATING SYSTEM: DOS
24     SOFTWARE: FASTSEQ for Windows Version 2.0
25     CURRENT APPLICATION DATA:
26     APPLICATION NUMBER: US/08/468,540B
27     FILING DATE: 06-JUN-1995
28     CLASSIFICATION: 514
29     PRIOR APPLICATION DATA:
30     APPLICATION NUMBER:

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02942
FILING DATE: 19910429
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9009549.8
FILING DATE: 27-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAM L
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1011.0586600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: AMINO ACID
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US91-02942-98

Query Match 23.9% Score 32; DB 4; Length 26;
Best Local Similarity 54.5%; Pred. No. 57;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RGGFLLQMDP 11
| | | | | | |
Db 16 RGGWLLSFDY 26

RESULT 5
US-08-199-508-2
Sequence 2, Application US/08199508
Patent No. 5717058
GENERAL INFORMATION:
APPLICANT: Matthews, Maura-Ann H.
APPLICANT: Stettler, Gary L.
APPLICANT: Anthony-Cahill, Spencer J.
APPLICANT: Anderson, David C.
TITLE OF INVENTION: Modulators of Gene Expression
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Somatogen, Inc.
STREET: 5797 Central Avenue
CITY: Boulder
STATE: Colorado
ZIP: 80301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,508
FILING DATE: February 18, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,536
FILING DATE: February 23, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5717058ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 121 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3322
TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 20
TYPE: amino acid
TOPOLOGY: unknown to applicant
MOLECULE TYPE: peptide
HYPOTHETICAL: yes
US-08-199-508-2

Query Match 22.4% Score 30; DB 1; Length 20;
Best Local Similarity 38.5%; Pred. No. 88;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 11 RGFPHLLVDFLQ 23
| | | : | : |
Db 1 RGYPVYFGDCVQ 13

RESULT 6
US-08-851-843A-170
Sequence 170, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No.6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

Query Match 23.9%; Score 32; DB 3; Length 22;
Best Local Similarity 58.3%; Pred. No. 47;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 15 EHLVDFLOSLS 26
| | | | | : | :
DB 7 ERLEDDLQALN 18

RESULT 2

US-08-940-093-133
; Sequence 133, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cornuzel, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO. 6037323e
US-08-940-093-133

Query Match 23.9%; Score 32; DB 3; Length 22;
Best Local Similarity 58.3%; Pred. No. 47;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 15 EHLVDFLOSLS 26
| | | | | : | :
DB 7 ERLEDDLQALN 18

RESULT 3
US-08-940-096-133
; Sequence 133, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cornuzel, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO. 6046166e
US-08-940-096-133

Query Match 23.9%; Score 32; DB 3; Length 22;
Best Local Similarity 58.3%; Pred. No. 47;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 15 EHLVDFLOSLS 26
| | | | | : | :
DB 7 ERLEDDLQALN 18

RESULT 4
PCT-US91-02942-98
; Sequence 98, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: AFHAWL, DILBERT S
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:36:46 ; Search time 17.58 Seconds
(without alignments)
24.789 Million cell updates/sec

Title: US-08-934-367-29
Perfect score: 134
Sequence: 1 RDGFLLIQMDGFPEHLVDFLOSLS 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 99815

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/prodata/2/1aa/6.COMB.pep: *
4: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep: *
5: /cgn2_6/prodata/2/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	32	23.9	22	3	US-08-940-095-133 Sequence 133, App
2	32	23.9	22	3	US-08-940-093-133 Sequence 133, App
3	32	23.9	22	3	US-08-940-096-133 Sequence 133, App
4	32	23.9	26	4	PCT-US91-02942-98 Sequence 98, App1
5	30	22.4	20	1	US-08-199-508-2 Sequence 2, App1
6	29.5	22.0	22	3	US-08-851-843A-170 Sequence 170, App
7	29	21.6	19	1	US-08-399-696-85 Sequence 85, App1
8	29	21.6	20	2	US-08-484-530-22 Sequence 22, App1
9	29	21.6	20	2	US-08-468-540B-3 Sequence 3, App1
10	29	21.6	20	2	US-08-827-618A-22 Sequence 22, App1
11	29	21.6	20	3	US-08-483-952A-22 Sequence 22, App1
12	29	21.6	25	2	US-08-424-881-3 Sequence 3, App1
13	29	21.6	25	2	US-08-874-763-3 Sequence 3, App1
14	29	21.6	10	3	US-08-159-339A-401 Sequence 401, App
15	28	20.9	10	4	PCT-US91-02942-88 Sequence 88, App1
16	28	20.9	22	3	US-08-940-095-134 Sequence 134, App
17	28	20.9	22	3	US-08-940-093-134 Sequence 134, App
18	28	20.9	22	3	US-08-940-096-134 Sequence 134, App
19	28	20.9	26	2	US-08-482-142-22 Sequence 22, App1
20	28	20.9	26	2	US-08-482-142-37 Sequence 37, App1
21	28	20.9	26	2	US-08-482-142-134 Sequence 134, App
22	28	20.9	26	2	US-08-482-142-168 Sequence 168, App
23	28	20.9	26	2	US-08-478-572-22 Sequence 22, App1
24	28	20.9	26	2	US-08-478-572-37 Sequence 37, App1
25	28	20.9	26	2	US-08-478-572-134 Sequence 134, App
26	28	20.9	26	2	US-08-478-572-168 Sequence 168, App
27	28	20.9	26	2	PCT-US95-04481-13 Sequence 13, App1
28	28	20.9	26	4	PCT-US95-04481-30 Sequence 30, App1

ALIGNMENTS

29	27	20.1	9	2	US-08-765-783A-83	Sequence 83, App1
30	27	20.1	11	1	US-08-467-420A-14	Sequence 14, App1
31	27	20.1	11	1	US-08-470-110A-14	Sequence 14, App1
32	27	20.1	11	1	US-08-667-769A-14	Sequence 14, App1
33	27	20.1	11	2	US-08-940-371-14	Sequence 14, App1
34	27	20.1	11	4	PCT-US95-17082A-14	Sequence 14, App1
35	27	20.1	15	2	US-08-482-142-85	Sequence 85, App1
36	27	20.1	15	2	US-08-478-572-85	Sequence 85, App1
37	27	20.1	15	3	US-08-596-257A-10	Sequence 10, App1
38	27	20.1	15	3	US-08-860-339-10	Sequence 10, App1
39	27	20.1	20	1	US-07-678-974D-8	Sequence 8, App1
40	27	20.1	20	2	US-08-162-149-10	Sequence 10, App1
41	27	20.1	20	2	US-08-945-168-13	Sequence 13, App1
42	27	20.1	22	2	US-08-559-524A-12	Sequence 12, App1
43	27	20.1	22	3	US-08-749-707-12	Sequence 12, App1
44	27	20.1	26	2	US-08-482-142-84	Sequence 84, App1
45	27	20.1	26	2	US-08-482-142-99	Sequence 99, App1

RESULT 1
US-08-940-095-133
Sequence 133, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dassaux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6004925e
US-08-940-095-133

Best Local Similarity 66.7%; Pred. No. 3e+05; Indels 0; Caps 0;
Matches 4; Conservative 1; Mismatches 1;

Oy 8 RGLPTG 13
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Db 1 RQOPSG 6

Search completed: December 21, 2000, 08:35:33
Job time: 596 sec

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DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE PHOSPHONOSTIDE-SPECIFIC PHOSPHOLIPASE C ISOZYME C1 (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RX MEDLINE: 93280199.
RA Min D.S., Kim D.M., Lee Y.H., Seo J., Suh P.G., Ryu S.H.;
RT "Purification of a novel phospholipase C isozyme from bovine
RL cerebellum."
RL J. Biol. Chem. 268:12207-12212(1993).
SO SEQUENCE 18 AA; 1927 MW; 1E37AE00CFC2AFc1 CRC64;

Query Match
Best Local Similarity 24.0%; Score 24; DB 6; Length 18;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 GLPTGO 14
DB 7 GLPXGK 12

RESULT 12
Q9S8M8 PRELIMINARY; PRT; 19 AA.
AC Q9S8M8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE FRIT-2-VIII-GAMMA-GLIADIN (FRAGMENT).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
RN [1]
RP SEQUENCE.
RX MEDLINE: 94284958.
RA Fluge O., Sletten K., Akenes L., Elsayed S.;
RT "In vitro toxicity of purified gluten peptides tested by organ
RL culture."
RL J. Pediatr. Gastroenterol. Nutr. 18:186-192(1994).
SO SEQUENCE 19 AA; 2240 MW; FC0F56FCB41B5C81 CRC64;

Query Match
Best Local Similarity 24.0%; Score 24; DB 10; Length 19;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 PTGOAQ 16
DB 5 PSCQVQ 10

RESULT 13
Q9TRCO PRELIMINARY; PRT; 20 AA.
AC Q9TRCO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-JUN-2000 (TREMBLrel. 13, Last sequence update)
DE ENTEROTOXIN-BINDING GLYCOPROTEIN PP16K (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RX MEDLINE: 94259890.
RA Shida K., Takamizawa K., Nagaoka M., Kushiro A., Osawa T., Tsuji T.;
RT "Enterotoxin-binding glycoproteins in a protease-peptone fraction of

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RT heated bovine milk."
RL J. Dairy Sci. 77:930-939(1994).
SO SEQUENCE 20 AA; 2321 MW; C738FD14F55C74C3 CRC64;

Query Match
Best Local Similarity 24.0%; Score 24; DB 6; Length 20;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIFOEL 6
DB 7 EVEREL 12

RESULT 14
Q9PXE4 PRELIMINARY; PRT; 20 AA.
AC Q9PXE4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE VP1 PROTEIN (FRAGMENT).
OS Foot-and-mouth disease virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96100820.
RA Platt P., Hassard S., Newman J.F., Brown F.;
RT "Antigenic variants in a plaque-isolate of foot-and-mouth disease
RL virus: implications for vaccine production."
RL Vaccine 13:781-784(1995).
SO SEQUENCE 20 AA; 1925 MW; E91F87C99C19D7DB CRC64;

Query Match
Best Local Similarity 24.0%; Score 24; DB 12; Length 20;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 LSRGLP 11
DB 15 VARGLP 20

RESULT 15
Q08979 PRELIMINARY; PRT; 9 AA.
AC Q08979;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE DNA PROVIRUS INTEGRATION SITE IN TUMOR INDUCED BY MURINE LEUKEMIA
DE VIRUS SL3-3, ISOLATE GTT TUMOR03-3 (FRAGMENT).
GN AML1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MURIT; TISSUE-MURINE RETROVIRUS INDUCED TUMOR;
RX MEDLINE: 97332339.
RA Amtoft H.W., Sorensen A.B., Barell C., Schmidt J., Luz A.,
RA Pedersen F.S.;
RT "Stability of AML1 (core) site enhancer mutations in T lymphomas
RL induced by attenuated SL3-3 murine leukemia virus mutants."
RL J. Virol. 71:5080-5087(1997).
DR EMBL: Y11802; CAA72496.1; -.
FT NON_TER 1
FT NON_TER 9
SO SEQUENCE 9 AA; 981 MW; 293E01E865A776D8 CRC64;

Query Match
Best Local Similarity 23.0%; Score 23; DB 11; Length 9;

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Query Match 24.0%; Score 24; DB 10; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 10 LPTGOA 17
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 DB 1 MPTGCAI 8

RESULT 7
 O9S8V3 PRELIMINARY; PRT; 15 AA.
 AC O9S8V3:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE GAMMA 1 GLIADIN (FRAGMENT).
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
 RN [1]
 RP MEDLINE; 93009000.
 RA Sjoström H., Friis S.U., Noren O., Anthonsen D.;
 RT "Purification and characterisation of antigenic gliadins in coeliac
 RT disease.";
 RL Clin. Chim. Acta 207:227-237(1992).
 SO SEQUENCE 15 AA; 1664 MW; 2B5C932C3CCDA72E CRC64;

Query Match 24.0%; Score 24; DB 10; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.5e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 11 PTGOA 16
 :||| |
 DB 6 PSGOY 11

RESULT 8
 O9S8V2 PRELIMINARY; PRT; 15 AA.
 AC O9S8V2:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE GAMMA 2 GLIADIN (FRAGMENT).
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
 RN [1]
 RP MEDLINE; 93009000.
 RA Sjoström H., Friis S.U., Noren O., Anthonsen D.;
 RT "Purification and characterisation of antigenic gliadins in coeliac
 RT disease.";
 RL Clin. Chim. Acta 207:227-237(1992).
 SO SEQUENCE 15 AA; 1742 MW; 2B5C8365ACCB32E CRC64;

Query Match 24.0%; Score 24; DB 10; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.5e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 11 PTGOA 16
 :||| |
 DB 6 PSGOY 11

RESULT 9
 O9GUZ5

ID O9GUZ5 PRELIMINARY; PRT; 15 AA.
 AC O9GUZ5:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE 38-42 KDA COSTIMULATORY FACTOR (FRAGMENT).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP MEDLINE; 96007483.
 RA Viney D.S., Raju M., Verma R.K., Mishra G.C.;
 RT "Characterization of novel costimulatory molecules. A protein of 38-42
 RT kDa from B cell surface is concerned with T cell activation and
 RT differentiation.";
 RL J. Biol. Chem. 270:23429-23436(1995).
 SO SEQUENCE 15 AA; 1758 MW; F10C664C976A5D19 CRC64;

Query Match 24.0%; Score 24; DB 11; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.5e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ERFQEL 6
 :||| |
 DB 10 ELFEEL 15

RESULT 10
 O9UOG8 PRELIMINARY; PRT; 18 AA.
 AC O9UOG8:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ENDOPLASMIC RETICULUM-GOLGI INTERMEDIATE COMPARTMENT PROTEIN ERGIC-53
 DE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP MEDLINE; 99192442.
 RA Nichols W.C., Terry V.H., Wheatley M.A., Yang A., Zivelin A.,
 RA Ciavarella N., Stefanie C., Matsushita T., Saito H., de Bosch N.B.,
 RA Ruiz-Saez A., Torres A., Thompson A.R., Feinstein D.I., White G.C.,
 RA Negrier C., Vinciguerra C., Aktan M., Kaufman R.J., Ginsburg D.,
 RA Seligson U.;
 RT "ERGIC-53 gene structure and mutation analysis in 19 combined factors
 RT V and VIII deficiency families.";
 RL Blood 93:2261-2266(1999).
 DR EMBL; AF081879; AND32486.1; -.
 DR EMBL; AF081878; AND32486.1; JOINED.
 FT NON_TER 1
 FT NON_TER 1
 SO SEQUENCE 18 AA; 2070 MW; 34CC39BA56F8B53B CRC64;

Query Match 24.0%; Score 24; DB 4; Length 18;
 Best Local Similarity 42.9%; Pred. No. 1.9e+03;
 Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 5 ELRGLPTGOA 18
 :||| |
 DB 1 EFGKHPLDQCPA 14

RESULT 11
 O9TRG0 PRELIMINARY; PRT; 18 AA.
 AC O9TRG0:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)

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RESULT 2
O9S8W0 PRELIMINARY: PRT: 19 AA.
AC O9S8W0:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE HIGH-MOLECULAR-WEIGHT GLUTENIN SUBUNIT 7 (FRAGMENT).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
RN [1]
RP SEQUENCE: 93003354.
RX MEDLINE: 93003354.
RA Tao H.P., Adalsteins A.E., Kasarda D.D.;
RT "Intramolecular disulfide bonds link specific high-molecular-weight
RT glutenin subunits in wheat endosperm.";
RL Biochim. Biophys. Acta 1159:13-21(1992).
SQ SEQUENCE 19 AA; 2011 MW; 95880C10396419DA CRC64;
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Query Match 27.0%; Score 27; DB 10; Length 19;
Best Local Similarity 38.5%; Pred. No. 6.4e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
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OY 4 QELSRCLPTGOAQ 16
DB 1 QQAGCGCGGCGG 13

RESULT 3
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AC O9TR96:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MEGAPOLETIN-MEGAKARYOCYTE GROWTH AND PLATELET PRODUCTION REGULATOR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
RN [1]
RP SEQUENCE: 95062214.
RX MEDLINE: 95062214.
RA Kuter D.J., Beeler D.L., Rosenberg R.D.;
RT "The purification of megapoletin: a physiological regulator of
RT megakaryocyte growth and platelet production.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11104-11108(1994).
SQ SEQUENCE 17 AA; 1975 MW; DA3A5E835A755C9D CRC64;
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Query Match 26.0%; Score 26; DB 6; Length 17;
Best Local Similarity 71.4%; Pred. No. 8.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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OY 3 FOELSRG 9
DB 10 FOGLRNG 16

RESULT 4
O9R514 PRELIMINARY: PRT: 16 AA.
AC O9R514:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE 17 KDA LYSINE-SPECIFIC CYSTEINE PROTEINASE (FRAGMENT).
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; CFB group; Bacteroidaceae; Porphyromonas.
RN [1]
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RP SEQUENCE: 94103245.
RX MEDLINE: 94103245.
RA Pike R., McGraw W., Potempa J., Travis J.;
RT "Lysine- and arginine-specific proteinases from Porphyromonas
RT gingivalis. Isolation, characterization, and evidence for the
RL existence of complexes with hemagglutinins.";
RL J. Biol. Chem. 269:406-411(1994).
SQ SEQUENCE 16 AA; 1819 MW; D864F9BF367828C6 CRC64;
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```
Query Match 25.0%; Score 25; DB 2; Length 16;
Best Local Similarity 46.2%; Pred. No. 1.1e+03;
Matches 6; Conservative 3; Mismatches 2; Indels 2; Gaps 1;
```

```
OY 1 EIRFELSRGLPTG 13
DB 5 EIRFQVD-LPAG 15
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RESULT 5
Q28830 PRELIMINARY: PRT: 20 AA.
AC Q28830:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE FRUCTOSE 6-PHOSPHATE, 2-KINASE:FRUCTOSE 2,6-BISPHOSPHATASE
DE (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92062062.
RA Sakata J., Uyeda K.;
RT "Characterization of two isozymic forms of heart fructose 6-phosphate,
RT 2-kinase:fructose 2,6-bisphosphatase.";
RL Biochem. Biophys. Res. Commun. 180:470-474(1991).
FR EMBL: S62278; AAB20157.1; -.
DT NON_TER 1 1
SQ SEQUENCE 20 AA; 2231 MW; BD8F37CBB2470660 CRC64;
```

```
Query Match 25.0%; Score 25; DB 6; Length 20;
Best Local Similarity 38.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
```

```
OY 8 RGLPTGOAQYAVH 20
DB 6 RDKPRTAETSRRAH 18
```

```
RESULT 6
Q9S8Z2 PRELIMINARY: PRT: 15 AA.
AC Q9S8Z2:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PHOTOSYSTEM I REACTION CENTER SUBUNIT II, PSI-D.
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Caryophyllales; Caryophyllales;
OC Chenopodiaceae; Spinacia.
RN [1]
RP SEQUENCE: 92249324.
RX MEDLINE: 92249324.
RA Lagoutte B., Vallon O.;
RT "Purification and membrane topology of PSI-D and PSI-E, two subunits
RT of the photosystem I reaction center.";
RL Eur. J. Biochem. 205:1175-1185(1992).
SQ SEQUENCE 15 AA; 1515 MW; 1A7105AA0A04549A9 CRC64;
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:25:37 ; Search time 157.2 Seconds
(without alignments)
11.880 Million cell updates/sec

Title: US-08-934-367-2

Sequence: 1 EIF0ELSRGLPTGQACVAVH 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL.14:*
2: SP_archaea:*
3: SP_bacteria:*
4: SP_fungi:*
5: SP_human:*
6: SP_invertebrate:*
7: SP_mammal:*
8: SP_mhc:*
9: SP_organelle:*
10: SP_phage:*
11: SP_plant:*
12: SP_prodent:*
13: SP_virus:*
14: SP_vertebrate:*
15: SP_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	29.0	15	8	Q9T355	Q9T355	synaptobrevin b
2	27.0	19	10	Q9S8W0	Q9S8W0	trifolium ae
3	26.0	17	6	Q9TR96	Q9TR96	ovis aries
4	25.0	16	2	Q9R514	Q9R514	porphyromon
5	25.0	20	6	Q28830	Q28830	bos taurus
6	24.0	15	10	Q9S8Z2	Q9S8Z2	spinaclia ol
7	24.0	15	10	Q9S8V3	Q9S8V3	trifolium ae
8	24.0	15	10	Q9S8V2	Q9S8V2	trifolium ae
9	24.0	15	11	Q9QU25	Q9QU25	mus sp. 38-
10	24.0	18	4	Q9U0G8	Q9U0G8	homo sapien
11	24.0	18	6	Q9TRC0	Q9TRC0	bos taurus
12	24.0	19	10	Q9S8M8	Q9S8M8	trifolium ae
13	24.0	20	6	Q9PXK4	Q9PXK4	bos taurus
14	24.0	20	12	Q9PXK4	Q9PXK4	foot-and-mo
15	23.0	9	11	Q08979	Q08979	mus musculu
16	23.0	15	5	Q9TWF5	Q9TWF5	artemia (br
17	23.0	19	8	Q9TWN3	Q9TWN3	begonia for
18	23.0	20	6	Q9TRV8	Q9TRV8	oryctolagus
19	22.0	12	2	Q02128	Q02128	desulfovibri

20	22.0	12	10	P82328	pisum sativ
21	22.0	12	11	Q9QVK4	rattus sp.
22	22.0	15	4	Q00604	homo sapien
23	22.0	15	12	Q88954	vaccinia vi
24	22.0	17	2	Q9R512	porphyromon
25	22.0	19	4	Q07603	homo sapien
26	22.0	19	8	Q9TWN1	begonia tai
27	22.0	19	10	Q9S956	zea mays (m
28	22.0	19	11	Q9QV31	rattus sp.
29	22.0	19	12	Q84274	human papil
30	22.0	20	2	Q9R5R7	mycobacteri
31	22.0	9	13	Q9PRM4	gallus gall
32	21.0	10	12	Q88953	vaccinia vi
33	21.0	13	4	Q9UCM7	homo sapien
34	21.0	13	7	Q9TNO8	homo sapien
35	21.0	15	4	Q9UMZ6	homo sapien
36	21.0	16	6	Q9TR09	bos taurus
37	21.0	16	10	Q40656	oryza sativ
38	21.0	19	2	Q52033	pseudomonas
39	21.0	19	4	Q9UCG2	homo sapien
40	21.0	19	8	Q9TWN5	begonia for
41	21.0	19	8	Q9TWN2	begonia for
42	21.0	19	8	Q9T304	begonia apt
43	21.0	19	8	Q9T303	begonia apt
44	21.0	19	10	Q9S8E2	spinaclia ol
45	21.0	19	11	Q62637	rattus norv

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	15 AA.
Q9T355	Q9T355	Q9T355		
AC	Q9T355	Q9T355		
DT	01-MAY-2000 (TREMURREL. 13, Created)			
DT	01-MAY-2000 (TREMURREL. 13, Last sequence update)			
DT	01-MAY-2000 (TREMURREL. 13, Last annotation update)			
DT	NADH DEHYDROGENASE SUBUNIT 6 (FRAGMENT)			
DE	Synaptobrevin			
OS	Mitochondrion			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;			
OC	Percomorpha; Perciformes; Percoidae; Acropomatidae; Synaptops.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Donaldson K.A., Wilson R.R., Jr.;			
RT	"Amphi-Panamic geminates of snook (Percoidae: Centropomidae) provide a			
RT	calibration of the divergence rate in the mitochondrial DNA control			
RT	region of fishes."			
RT	Mol. Phylogenet. Evol. 0:0-0(2000).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	Donaldson K.A., Wilson R.R., Jr.;			
RA	"Amphi-Panamic geminates of snook (Percoidae: Centropomidae) provide a			
RT	calibration of the divergence rate in the mitochondrial DNA control			
RT	region of fishes."			
RT	Mol. Phylogenet. Evol. 13:208-213(1999).			
RL	EMBL: AF123592; AAF19093.1; -			
DR	EMBL: AF155907; AAF08478.1; -			
KW	Mitochondrion			
FT	NON-TRK			
SO	SEQUENCE			

Query Match: 29.0%; Score 29; DB 8; Length 15;
Best Local Similarity: 66.7%; Pred. No. 2.3e+02;
Matches: 6; Conservative: 1; Mismatches: 2; Indels: 0; Gaps: 0;

Thu Dec 21 08:51:19 2000

Search completed: December 21, 2000, 08:32:52
Job time: 435 sec

us-08-934-367-2.rsp

RL Biochem. J. 288:831-837(1992).
 CC -1- FUNCTION: DEGRADATION OF LYSOPHOSPHOLIPIDS. MAY PLAY AN IMPORTANT
 CC ROLE IN PROTECTING THESE CELLS FROM THE CYTOLYTIC EFFECTS OF THE
 CC LYSOPHOSPHOLIPIDS PRODUCED BY THE ACTIVATION OF PHOSPHOLIPASE A2.
 CC -1- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)O =
 CC GLYCEROPHOSPHOCHOLINE + A FATTY ACID ANION.
 CC -1- INDUCTION: INCREASED BY DIFFERENTIATION OF THE CELLS.
 CC -1- PTM: THE N-TERMINUS IS BLOCKED.
 KW Hydrolyase; Lipid degradation.
 FT NON_TER 1
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2138 MW; 15838FD23D89567 CRC64;

Query Match 21.0%; Score 21; DB 1; Length 20;
 Best Local Similarity 55.6%; Pred. No. 2.2e+03;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 SRIPTGQA 15
 | | | |
 Db 3 SISLPTSM 11

RESULT 13
 UC25_MAIZE
 ID UC25_MAIZE STANDARD; PRT; 15 AA.
 AC P80631;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 77)
 DE (FRAGMENT).
 OS Zea mays (Maize).
 OS Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 RN [1]
 RC SEQUENCE.
 RP TISSUE-COLEOPTILE;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huot J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program".
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.9, ITS MW IS: 31.6 KDA.
 CC MAIZE-2DPAGE; P80631; COLEOPTILE.
 DR MAIZEEDB: 123957; - -
 DR MAIZEEDB: 123957; - -
 FT NON_TER 1
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1580 MW; 83C54CF0CE1614D0 CRC64;

Query Match 20.0%; Score 20; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 LSRGLP 11
 | | | |
 Db 5 LSRSP 10

RESULT 14
 CERB_RAT
 ID CERB_RAT STANDARD; PRT; 16 AA.
 AC P23436; P02682;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CEREBELLIN.
 OS Rattus norvegicus (Rat), and Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]

RP SEQUENCE.
 RC SPECIES-RAT;
 RA Slemmon J.R., Blacher R., Danho W., Hempstead J.L., Morgan J.I.;
 RT "Isolation and sequencing of two cerebellum-specific peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:6866-6870(1984).
 RN [2]
 RC SEQUENCE.
 RP SPECIES-PIG; TISSUE-BRAIN;
 RX MEDLINE; 89341798.
 RA Yiangou Y., Burnet P., Nikou G., Chrysanthou B.J., Bloom S.R.;
 RT "Purification and characterisation of cerebellins from human and
 RT porcine cerebellum."; Neurochem. 53:886-889(1989).
 RL J. Neurochem. 53:886-889(1989).
 CC -1- FUNCTION: CEREBELLIN EXERTS NEUROMODULATORY FUNCTIONS. DIRECTLY
 CC STIMULATES NOREPINEPHRINE RELEASE VIA THE ADENYLATE CYCLASE/PKA-
 CC DEPENDENT SIGNALING PATHWAY; AND INDIRECTLY ENHANCES
 CC ADENOCORTICAL SECRETION IN VIVO, THROUGH A PARACRINE MECHANISM
 CC INVOLVING MEDULLARY CATECHOLAMINE RELEASE.
 CC -1- TISSUE SPECIFICITY: LOCALIZED IN THE PURKINJE CELLS.
 DR PIR; A03135; CORT.
 DR PIR; PLO124; PLO124.
 KW Synapsosome.
 SQ SEQUENCE 16 AA; 1633 MW; 3EFA16635343D518 CRC64;

Query Match 20.0%; Score 20; DB 1; Length 16;
 Best Local Similarity 57.1%; Pred. No. 2.5e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGOAOYA 18
 | | | |
 Db 1 SGRSAKVA 7

RESULT 15
 LEC3_MACPO
 ID LEC3_MACPO STANDARD; PRT; 20 AA.
 AC P18677;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-AUG-1991 (Rel. 19, Last annotation update)
 DE AGGLUTININ BETA-3 CHAIN (MPA).
 OS Maclura pomifera (Osage orange).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 CC Rosales; Moraceae; Maclura.
 RN [1]
 RC SEQUENCE.
 RP TISSUE-SEED;
 RX MEDLINE; 89206218.
 RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;
 RT "Homology of the D-galactose-specific lectins from Althoea
 RT integrifolia and Maclura pomifera and the role of an unusual small
 RT polypeptide subunit.";
 RL Arch. Biochem. Biophys. 270:596-603(1989).
 CC -1- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN
 CC STRUCTURE GAL-BETA1-3-GALNAC.
 CC -1- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.
 CC -1- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.
 DR PIR; S03988; S03988.
 KW Lectin.
 SQ SEQUENCE 20 AA; 2082 MW; AA38811BBD6370E0 CRC64;

Query Match 20.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 PPGQAO 16
 | | | |
 Db 2 PNGKSO 7

DE (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA) (FRAGMENT).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=HEART;
 RX MEDLINE: 98163340.
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins."
 RL Electrophoresis 18:2795-2802(1997).
 CC -1- CATALYTIC ACTIVITY: SUCCINATE + COA + GTP = SUCCINYL-COA + GDP +
 CC ORTHOPHOSPHATE.
 CC -1- PATHWAY: SUBSTRATE LEVEL PHOSPHORYLATION STEP OF THE TRICARBOXYLIC
 CC ACID CYCLE.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
 CC -1- SIMILARITY: TO OTHER BETA SUBUNITS OF SUCCINYL-COA SYNTHETASE,
 CC OF MALATE-COA LIGASE AND TO ATP CITRATE-LYASE.
 CC HSC-2DPAGE: P99507; DOG.
 DR INTERPRO: IPR000303;
 DR PROSITE: PS01217; SUCCINYL-COA_LIG_3; PARTIAL.
 KW Ligase; Glycolysis; Tricarboxylic acid cycle; Mitochondrion.
 FT NON_TER 20
 SO SEQUENCE 20 AA; 2248 MW; BE8AEFD54DB0AC2E CRC64;

QY 1 EIPFELSRLP 11
 Db 10 ELLEGACVSIIP 20

Query Match 22.0%; Score 22; DB 1; Length 20;
 Best Local Similarity 36.4%; Pred. No. 1.5e+03;
 Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

RESULT 10
 RS13_PARDE STANDARD; PRT; 17 AA.
 ID RS13_PARDE
 AC P2180;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 30S RIBOSOMAL PROTEIN S13 (FRAGMENT).
 GN RPSM.
 OS Paracoccus denitrificans.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
 OC Paracoccus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=71.11T;
 RA Perlier V., Boussec A., Meier O., Barzu O., Gilles A.M.;
 RT "Adenylate kinase from P. denitrificans, an iron and zinc binding
 RT protein, catalyzes phosphorylation of AMP and reduction of
 RT cytochrome C."
 RL Submitted (Jul-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN THE BINDING OF FMET-TRNA AND, HENCE, IN THE
 CC INITIATION OF TRANSLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U64204; AAB06329.1; ALT_INIT.
 DR INTERPRO: IPR001892;
 DR PROSITE: PS00646; RIBOSOMAL_S13; PARTIAL.
 KW Ribosomal protein.

FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1793 MW; 43F7F60DC8670B7D CRC64;

QY 10 LPTGQ 14
 Db 9 IPTGK 13

Query Match 21.0%; Score 21; DB 1; Length 17;
 Best Local Similarity 60.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 CUDE_VERCH STANDARD; PRT; 20 AA.
 ID CUDE_VERCH
 AC P80406;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CUTICLE-DEGRADING PROTEASE-LIKE PROTEIN (EC 3.4.21.-) (CHYMOTELASTASE)
 DE (FRAGMENT).
 OS Verticillium chlamydosporium.
 OC Eukaryota; Fungi; Ascomycota; anamorphic Ascomycota; Dimerospora.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=VC10;
 RX MEDLINE: 95247009.
 RA Segers R., Butt T.M., Keen J.N., Kerry B.R., Peberdy J.F.;
 RT "The subtilins of the invertebrate mycopathogens Verticillium
 RT chlamydosporium and Metarrhizium anisopliae are serologically and
 RT functionally related".
 RL FEMS Microbiol. Lett. 126:227-231(1995).
 CC -1- FUNCTION: CAPABLE OF BREACHING THE INSECT CUTICLE.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
 CC SUBTILASE FAMILY.
 DR INTERPRO: IPR000209;
 DR PROSITE: PS00136; SUBTILASE_ASP; PARTIAL.
 DR PROSITE: PS00137; SUBTILASE_HIS; PARTIAL.
 DR PROSITE: PS00138; SUBTILASE_SER; PARTIAL.
 KW Hydrolase; Serine protease.
 FT NON_TER 20
 SO SEQUENCE 20 AA; 2113 MW; 26744EC2F729B19 CRC64;

QY 8 RGLPTGQAOV 17
 Db 6 QGAPXGIGRI 15

Query Match 21.0%; Score 21; DB 1; Length 20;
 Best Local Similarity 30.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

RESULT 12
 LPP2_HUMAN STANDARD; PRT; 20 AA.
 ID LPP2_HUMAN
 AC P56642;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE LYSOGENOUS PHOSPHATASE HL-60 PEAK 2 (EC 3.1.1.5) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=LEUKEMIA;
 RX MEDLINE: 93111958.
 RA Garsenti D., Holtsberg F., Steiner M.R., Egan R.W., Clark M.A.;
 RT "Butyric acid-induced differentiation of HL-60 cells increases the
 RT expression of a single lysophospholipase.";

DT 01-NOV-1995 (Rel. 32, last annotation update)
 DE ANNETOCIN.
 OS Eisenia foetida (Common branding worm) (Common dung-worm).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haptotaxida;
 OC Lumbricina; Lumbricidae; Eisenia.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-PITUITARY;
 RX MEDLINE; 94121660.
 RA Omiti T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
 RA Nomoto K.;
 RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
 RT Eisenia foetida."
 RL Biochem. Biophys. Res. Commun. 198:393-399(1994).
 CC -1- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
 CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
 CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
 CC NEPHRIDIAL FUNCTION.
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR; PC2021; PC2021.
 DR INTERPRO; IPR000981; .
 DR PFAM; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
 KW hormone; Amidation.
 KM HORMONE.
 FT MOD_RES 1 9
 FT DISULFID 1 6
 FT SEQUENCE 9 AA; 996 MW; D4EEB76B45412C9 CRC64;

Query Match 22.0%; Score 22; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 8.8e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 8 RGLPTG 13
 DB 4 RNCPTG 9

RESULT 6
 ID TAIL3_TREME STANDARD; PRT; 13 AA.
 AC P01370;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 01-NOV-1991 (Rel. 20, last annotation update)
 DE TREMEROGEN A-13.
 OS Tremella mesenterica (Jelly fungus).
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
 OC Tremellaceae; Tremella.
 RN [1]
 RP SEQUENCE.
 RA Sakagami Y., Yoshida M., Isogai A., Suzuki A.;
 RT "peptide sex hormones inducing conjugation tube formation in
 RT compatible mating-type cells of Tremella mesenterica."
 RL Science 212:1525-1527(1981).
 CC -1- FUNCTION: TREMEROGEN A-13 IS PRODUCED BY THE A MATING-TYPE CELLS
 CC AND INDUCES FORMATION OF CONJUGATION TUBES IN A MATING-TYPE CELLS.
 DR PIR; A01641; JRG3
 KW Lipoprotein; Prenylation; Pheromone.
 FT LIPID 13
 FT FARNESYL 13
 FT SEQUENCE 13 AA; 1204 MW; 680304A9697BA864 CRC64;

Query Match 22.0%; Score 22; DB 1; Length 13;
 Best Local Similarity 57.1%; Pred. No. 9.6e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 SRGLPTG 13
 DB 5 NRGPDSG 11

RESULT 7

UN12_CLOPA
 ID UN12_CLOPA STANDARD; PRT; 13 AA.
 AC P81533;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, last sequence update)
 DT 15-JUL-1998 (Rel. 36, last annotation update)
 DE UNKNOWN PROTEIN CP 12 FROM 2D-PAGE (FRAGMENT).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-W5;
 RX MEDLINE; 98291870.
 RA Flensburg R., Skjeldal L.;
 RT "Two dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5."
 RL Electrophoresis 19:802-806(1998).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.8, ITS MW IS: 42.7 KDA.
 FT VARIANT 4 5
 FT NON_TER 13 13
 FT SEQUENCE 13 AA; 1465 MW; 70AA9E98455D405B CRC64;

Query Match 22.0%; Score 22; DB 1; Length 13;
 Best Local Similarity 33.3%; Pred. No. 9.6e+02;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 IFOLSRGL 10
 DB 3 VLOEINPGI 11

RESULT 8
 ID BULB_NARPS STANDARD; PRT; 20 AA.
 AC P80554;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 01-OCT-1996 (Rel. 34, last annotation update)
 DE BULB PROTEIN (FRAGMENT).
 OS Narcissus pseudonarcissus (Daffodil).
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Narcissus.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-CV. GOLDEN HARVEST; TISSUE-BULB;
 RA Parlis M.D., Barker P., Thomas B.;
 RL Submitted (FEB-1996) to the SWISS-PROT data bank.
 FT UNSTR 2 2
 FT NON_TER 20 20
 FT SEQUENCE 20 AA; 2077 MW; 76212FF3A468AD38 CRC64;

Query Match 22.0%; Score 22; DB 1; Length 20;
 Best Local Similarity 80.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 GLPTG 13
 DB 12 GLPPG 16

RESULT 9
 ID SUBC_CANPA STANDARD; PRT; 20 AA.
 AC P99507;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, last sequence update)
 DT 15-JUL-1998 (Rel. 36, last annotation update)
 DE PUTATIVE SUCCINYL-COA LIGASE [GDP-FORMING] BETA-CHAIN (EC 6.2.1.4)

```

RP SEQUENCE FROM N.A.
RX MEDLINE: 86235450.
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Saibuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HIV-1/LAV over time in patients with AIDS or
RT at risk for AIDS."
RL Science 232:1548-1553(1986).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -1- MISCELLANEOUS: ISOLATES MMJ1, MMJ2, AND MMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M12507; AAB12991.1; -.
DR HIV: M12507; TATSMWJ2.
KW AIDS.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1467 MW; 37CC737BFE67AA8 CRC64;

Query Match
Best Local Similarity 83.3%; Score 25; DB 1; Length 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 RGLPTG 13
DB 6 RGDPTG 11

RESULT 3
TAT_HV128 STANDARD; PRT: 14 AA.
AC P12511:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1988 (Rel. 12, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
GN TAT.
OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88281278.
RA Younou J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
RA Gallo R.C.;
RT "Nucleotide sequence analysis of the env gene of a new Zairian
RT isolate of HIV-1."
RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -1- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
CC ZAIRIAN MALE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: J03653; AAA44685.1; -.
DR HIV: J03653; TATSYJ1.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1453 MW; 37CC737BFE82D7AA8 CRC64;

Query Match
Best Local Similarity 83.3%; Score 25; DB 1; Length 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 RGLPTG 13
DB 6 RGDPTG 11

RESULT 4
COXB_THUOB STANDARD; PRT: 20 AA.
ID COXB_THUOB
AC P80974:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE VB (EC 1.9.3.1) (FRAGMENT).
OS Thunus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
RN [1]
RP SEQUENCE.
RC TISSUE=HEART, AND LIVER;
RX MEDLINE: 97454291.
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lotsepetch F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver."
RL Eur. J. Biochem. 248:99-103(1997).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
CC 4 FERROCYTOCHROME C.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.
DR INTERPRO: IPR002124.
DR PROSITE: PS00848; COX5B; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2158 MW; 76F1473E1F392BD7 CRC64;

Query Match
Best Local Similarity 44.4%; Score 25; DB 1; Length 20;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 8 RGLPTGQAQ 16
DB 4 KGLPTDDEQ 12

RESULT 5
OXYT_EISFO STANDARD; PRT: 9 AA.
ID OXYT_EISFO
AC P42988:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:25:37 ; Search time 62.7 Seconds
(without alignments)
10.191 Million cell updates/sec

Title: US-08-934-367-2

Perfect score: 100
Sequence: 1 EIFQELSRGLPTGQAQVAHV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27.0	27.0	20	1	COXF_ONCMY
2	25.0	25.0	14	1	TAT_HV1W2
3	25.0	25.0	14	1	TAT_HV1Z8
4	25.0	25.0	20	1	COXB_THUOB
5	22.0	22.0	9	1	OXYT_EISRO
6	22.0	22.0	13	1	TA13_TREME
7	22.0	22.0	13	1	UNI2_GLOPA
8	22.0	22.0	20	1	SUCB_NARPS
9	22.0	22.0	20	1	SUCB_CANPA
10	21.0	21.0	17	1	RS13_PARDE
11	21.0	21.0	20	1	CUDP_VERCH
12	21.0	21.0	20	1	LPP2_HUMAN
13	20.0	20.0	15	1	UC25_MAIZE
14	20.0	20.0	16	1	CERB_RAT
15	20.0	20.0	20	1	LEC3_MACPO
16	19.5	19.5	20	1	YOA4_KLEAE
17	19.0	19.0	10	1	GNL1_ALIMT
18	19.0	19.0	16	1	DHE2_THUTH
19	19.0	19.0	16	1	HTPG_ACICA
20	19.0	19.0	19	1	OXLA_OPNHA
21	19.0	19.0	20	1	ALAT_PIG
22	19.0	19.0	20	1	DNAK_MYCAV
23	18.0	18.0	5	1	PRCT_PPRAM
24	18.0	18.0	9	1	LMTP_LOCKI
25	18.0	18.0	11	1	BPPA_AKHA
26	18.0	18.0	13	1	ORCK_ORCLI
27	18.0	18.0	14	1	SODN_STRGR
28	18.0	18.0	15	1	C10A_RAT
29	18.0	18.0	17	1	EPG_THRAO
30	18.0	18.0	17	1	RM35_YEAST
31	18.0	18.0	19	1	COOT_SARBU
32	18.0	18.0	20	1	OXLA_AKRRH
33	17.5	17.5	18	1	CPAX_BOVIN

34	17	17.0	11	1	BPP_AKHP	P04562 agkistrodon
35	17	17.0	14	1	CRBL_VESOR	P17236 vespa orient
36	17	17.0	14	1	PSAG_CUCSA	P42049 cucumis sat
37	17	17.0	15	1	GLN2_STNPS	P41107 pinus pinas
38	17	17.0	15	1	RBS_PHTPA	P80657 physcomitre
39	17	17.0	15	1	TRP2_LEUMA	P81733 leucophaea
40	17	17.0	18	1	DRPH_UCAPU	P08871 uca pugilati
41	17	17.0	18	1	UC21_MAIZE	P80627 zea mays (m
42	17	17.0	19	1	PTRH_STRSA	P24365 streptococc
43	17	17.0	19	1	RECO_SALRY	P40724 salmonella
44	17	17.0	19	1	SCX6_TITBA	P56610 tillyus bali
45	17	17.0	19	1	TRP3_LEUMA	P81735 leucophaea

ALIGNMENTS

RESULT	1	STANDARD	PRT	20 AA
COXF_ONCMY	COXF_ONCMY	STANDARD	PRT	20 AA
ID	ID	ID	ID	ID
AC	P80329:			
DT	01-OCT-1994 (Rel. 30, Last sequence update)			
DT	01-OCT-1994 (Rel. 30, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	CYTCHROME C OXIDASE POLYPEPTIDE VB-HEART (EC 1.9.3.1) (FRAGMENT).			
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=HEART;			
RX	MEDLINE: 94237150.			
RA	Freund R., Kadenbach B.;			
RT	*Identification of tissue-specific isoforms for subunits Vb and Vlla			
RT	of cytochrome c oxidase isolated from rainbow trout.*;			
RL	Eur. J. Biochem. 221:1111-1116(1994).			
CC	-1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE			
CC	CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN			
CC	MITOCHONDRIAL ELECTRON TRANSPORT.			
CC	-1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +			
CC	4 FERRICYTOCHROME C.			
CC	-1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.			
CC	-1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.			
DR	HSSP: P00428; 10CC.			
DR	INTERPRO: IPR002124; -.			
DR	PROSITE: PS00848; COX5B; PARTIAL.			
KW	Oxidoreductase; Inner membrane; Mitochondrion.			
FT	NON_TER 20			
SC	SEQUENCE 20 AA; 2184 MW; 6ABE00CB33E92BD7 CRC64;			
QY	8 RGLPTGQAQ 16			
DB	4 KGIPTDEQ 12			
Query Match	27.0%; Score 27; DB 1; Length 20;			
Best Local Similarity	44.4%; Pred. No. 2.2e+02;			
Matches	4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;			
RESULT	2	STANDARD	PRT	14 AA
ID	TAT_HV1W2			
AC	P12509:			
DT	01-OCT-1988 (Rel. 12, Created)			
DT	01-OCT-1988 (Rel. 12, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).			
TAT				
OS	Human immunodeficiency virus type 1 (MN2 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
RN	[1]			

OY 8 RGLPTGO 14
:|:|:|:
Db 4 KGIPDE 10

RESULT 14

protein QA600027 - Arabidopsis thaliana (fragment)
PT0085
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 06-Jun-1997
C:Accession: PT0085
R:Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
submitted to JIPID, December 1995
A:Description: Two dimensional electrophoresis of plant proteins and standardization of
A:Reference number: PN0173
A:Accession: PT0085
A:Molecule type: protein
A:Residues: 1-15 <TSU>
A:Experimental source: leaf

Query Match 23.0%; Score 23; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 RGLPTGO 15
:|:|:|:
Db 1 KGGATGO 8

RESULT 15

PH0758
T-cell receptor beta chain (E22) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0758
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; KUID:92078846
A:Accession: PH0758
A:Molecule type: mRNA
A:Residues: 1-16 <CAS>
A:Cross-references: EMBL:X60853; NID:g50743; PIDN:CA43243.1; PID:g50744
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 23.0%; Score 23; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 11 PTGOAOVAV 19
|||:|:
Db 5 PTGKSNTREV 13

Search completed: December 21, 2000, 08:30:01
JOD Time: 265 sec

A:Molecule type: protein
A:Residues: 1-20 <ARK>
A:Experimental source: heart; liver
C:Genetics:
A:Genome: nuclear
C:Function:
A:Pathway: oxidative phosphorylation; respiratory chain
C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 25.0%; Score 25; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 8.9e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 8 RGLPTGOAQ 16
|:|:|:
Db 4 KGIPTDDEQ 12

RESULT 9
A:Accession: A56891
gamma 1 gliadin - wheat (fragment)
C:Species: Triticum sp. (wheat)
C:Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 08-Dec-1995
C:Accession: A56891
R:Sjostrom, H.; Friis, S.U.; Noren, O.; Anthonsen, D.
Clin. Chim. Acta 207, 227-237, 1992
A:Title: Purification and characterisation of antigenic gliadins in coeliac disease.
A:Reference number: A56891; MUID:93009000
A:Contents: Kadett
A:Accession: A56891
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <SJO>
A:Note: sequence extracted from NCBI backbone (NCBIP:119387)

Query Match 24.0%; Score 24; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 9.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 PTGOAQ 16
|:|:|:
Db 6 PSGOVQ 11

RESULT 10
A:Accession: B56891
gamma 2 gliadin - wheat (fragment)
C:Species: Triticum sp. (wheat)
C:Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 08-Dec-1995
C:Accession: B56891
R:Sjostrom, H.; Friis, S.U.; Noren, O.; Anthonsen, D.
Clin. Chim. Acta 207, 227-237, 1992
A:Title: Purification and characterisation of antigenic gliadins in coeliac disease.
A:Reference number: A56891; MUID:93009000
A:Contents: Kadett
A:Accession: B56891
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <SJO>
A:Note: sequence extracted from NCBI backbone (NCBIP:119388)

Query Match 24.0%; Score 24; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 9.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 PTGOAQ 16
|:|:|:
Db 6 PSGOVQ 11

RESULT 11
A:Accession: S52125
gamma2-gliadin p25-27 - poulard wheat
C:Species: Triticum turgidum (poulard wheat)
C:Date: 14-Jul-1995 #sequence_revision 03-Nov-1995 #text_change 16-Feb-1997
C:Accession: S52125
R:Roche, A.; Soriano, F.; Molina, E.; Gonzalez-Limas, G.; Mendez, E.
Biochim. Biophys. Acta 1247, 143-148, 1995
A:Title: Characterization of distinct alpha- and gamma-type gliadins and low molecular
A:Reference number: S52124; MUID:95178530
A:Accession: S52125
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <ROC>
C:Superfamily: gliadin

Query Match 24.0%; Score 24; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 PTGOAQ 16
|:|:|:
Db 6 PSGOVQ 11

RESULT 12
A:Accession: S33867
guinadic acid 4-oxidoeductase large chain - Serratia marcescens
C:Species: Serratia marcescens
C:Date: 02-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 07-May-1999
C:Accession: S33867
R:Felzner, S.; Lings, F.
Biol. Chem. Hoppe-Seyler 374, 363-376, 1993
A:Title: Microbial metabolism of quinoline and related compounds. XVIII. Purification
us 2CC-1.
A:Reference number: S33867; MUID:93363223
A:Accession: S33867
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <FET>

Query Match 24.0%; Score 24; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.3e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 PTGOAQ 17
|:|:|:
Db 10 PDGOAEL 16

RESULT 13
A:Accession: S43626
cytochrome-c oxidase (EC 1.9.3.1) chain Vb-H - trout (fragment)
C:Species: Salmo sp. (trout)
C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 02-Jul-1998
C:Accession: S43626
R:Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A:Title: Identification of tissue-specific isoforms for subunits Vb and Vira of cyto
A:Reference number: S43624; MUID:94237150
A:Accession: S43626
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <FRK>
C:Keywords: electron transfer; membrane-associated complex; oxidoreductase; respirato

Query Match 23.0%; Score 23; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 1e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 3
S43629
cytochrome-c oxidase (EC 1.9.3.1) chain Vb-L, cardiac - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999
C:Accession: S43629
R:Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A:Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase
A:Reference number: S43624; MUID:94237150
A:Accession: S43629
A:Molecule type: protein
A:Residues: 1-14 <FRE>
A:Note: the source is designated as Salmo gairdneri
C:Genetics:
A:Genome: nuclear
C:Keywords: cardiac muscle; heart; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 26.0%; Score 26; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 9 GLPTGQAO 16
DB 4 GIPTEXEQ 11
1:11:1

RESULT 4
B60278
24k antigen - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 18-Jun-1993
C:Accession: B60278
R:Flis, T.; Costopoulos, C.; Radford, A.J.; Baclic, A.; Wood, P.R.
Infect. Immun. 59, 800-807, 1991
A:Title: Purification and characterization of major antigens from a Mycobacterium bovis
A:Reference number: A60278; MUID:91147217
A:Accession: B60278
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <RFI>

Query Match 26.0%; Score 26; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 FOELSRGLPTGQ 14
DB 5 YKEELKGTDTGQ 16
::1:1111

RESULT 5
CS3113
Lys-gingipain form 2, 17k - Porphyromonas gingivalis (fragment)
N:Alternate names: lysine-specific cysteine proteinase 2, 17k
C:Species: Porphyromonas gingivalis
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C:Accession: CS3113
R:Pike, R.; McGraw, W.; Potempa, J.; Travis, J.
J. Biol. Chem. 269, 406-411, 1994
A:Title: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolation and characterization of the genes
A:Reference number: A53113; MUID:94103245
A:Accession: CS3113
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <PIK>
A:Experimental source: H66
A:Note: sequence extracted from NCBI backbone (NCBIP:141693)

Query Match 25.0%; Score 25; DB 2; Length 16;

Best Local Similarity 46.2%; Pred. No. 7e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 2; Gaps 1;
QY 1 EIFOELSRGLPTG 13
DB 5 EIFRQVD-LPAG 15
1111:111

RESULT 6
A41877
LcrK - Yersinia pseudotuberculosis (fragment)
C:Species: Yersinia pseudotuberculosis
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C:Accession: A41877
R:Rimpilainen, M.; Forsberg, A.; Wolf-Watz, H.
J. Bacteriol. 174, 3355-3363, 1992
A:Title: A novel protein, LcrK, involved in the low-calcium response of Yersinia pseudotuberculosis
A:Reference number: A41877; MUID:92250432
A:Contents: YP11, PIB102
A:Accession: A41877
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18 <RIM>
A:Note: sequence extracted from NCBI backbone (NCBIN:100533, NCBIP:100534)

Query Match 25.0%; Score 25; DB 2; Length 18;
Best Local Similarity 37.5%; Pred. No. 8e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 4 QELSRGLPTGQAVAV 19
DB 1 EALSRALSTTLGOMKV 16
:111:1111

RESULT 7
I46940
6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2,6-bisphosphate 2-phosphatase (EC 3.1.3.17)
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 31-Mar-2000
C:Accession: I46940
R:Sakata, J.; Oyeda, K.
Biochem. Biophys. Res. Commun. 180, 470-474, 1991
A:Title: Characterization of two isozymic forms of heart fructose 6-phosphate, 2-kinase
A:Reference number: I46940; MUID:92062062
A:Accession: I46940
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-20 <SAK>
A:Cross-references: GB:S62278; NID:9237973; PIDN:AAB20157.1; PID:9237974
A:Superfamily: 6-phosphofructo-2-kinase / fructose-2,6-bisphosphate 2-phosphatase; phosphatase; phosphoric monoester hydrolase; phosphotransferase

Query Match 25.0%; Score 25; DB 2; Length 20;
Best Local Similarity 38.5%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 8 RGLPTGQAVAVH 20
DB 6 RDKPTAETSRRAH 18
111:1111

RESULT 8
S77983
cytochrome-c oxidase (EC 1.9.3.1) chain Vb - bigeye tuna (fragment)
C:Species: Thunnus obesus (bigeye tuna)
C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
C:Accession: S77983
R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lotspeltch, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A:Reference number: S77980
A:Accession: S77983

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:25:36 ; Search time 112.59 Seconds
(without alignments)
11.273 Million cell updates/sec

Title: US-08-934-367-2
Perfect score: 100
Sequence: 1 EIFQELSRGLPTGQAVAVH 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_65:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	27.0	20	2	S43627 cytochrome-c oxida
2	27	27.0	20	2	P00537 arylhydroxamic aci
3	26	26.0	14	2	S43629 cytochrome-c oxida
4	26	26.0	16	2	B60278 24k antigen - Myco
5	25	25.0	16	2	C53113 Lys-gingipain form
6	25	25.0	18	2	A41877 LcrKC - Yersinia p
7	25	25.0	20	2	I46940 6-phosphofructo-2-
8	25	25.0	20	2	S77983 cytochrome-c oxida
9	24	24.0	15	2	A56891 gamma 1 gliadin -
10	24	24.0	15	2	B56891 gamma 2 gliadin -
11	24	24.0	18	2	S52125 gamma2-gliadin P25
12	24	24.0	20	2	S33867 quinaldic acid 4-o
13	23	23.0	11	2	S43626 cytochrome-c oxida
14	23	23.0	15	2	PH0085 protein QA600027 -
15	23	23.0	16	2	PH0758 T-cell receptor be
16	22	22.0	8	2	A35180 neutral proteinase
17	22	22.0	9	2	PC2021 oxytocin-related p
18	22	22.0	10	2	H60588 sperm-activating p
19	22	22.0	12	2	S29479 hypothetical prote
20	22	22.0	13	1	UTG3 tremmerogen a-13 -
21	22	22.0	15	2	A40634 orl1g 3' of eryk -
22	22	22.0	15	2	PH1455 T-cell receptor al
23	22	22.0	15	2	S08282 cytochrome P450K-2
24	22	22.0	16	2	A53337 regulatory protein
25	22	22.0	17	2	E53113 gingipain, 44k - p
26	22	22.0	19	2	I39327 pre-T/NK cell-asso
27	22	22.0	20	2	A54083 p190/210, fatty ac
28	22	22.0	20	2	A47105 dystroglycan - chi
29	21	21.0	9	2	PH1591 Ig H chain V-D-J r

30	21	21.0	10	2	PH0926 T-cell receptor be
31	21	21.0	12	2	PH0920 T-cell receptor be
32	21	21.0	13	2	PH0799 T-cell receptor al
33	21	21.0	16	2	A41170 photosystem II 6.1
34	21	21.0	17	1	A61339 vesplaklinin 1 - e
35	21	21.0	17	2	A61557 major merozoite su
36	21	21.0	20	2	S72501 protein kinase C 1
37	21	21.0	20	2	S27350 lysophospholipase
38	21	21.0	20	2	PU0033 aldose 1-epimerase
39	21	21.0	20	2	S65884 translaton initia
40	20	20.0	10	2	B39517 probable methionin
41	20	20.0	11	2	D56979 collagen alpha 1(I
42	20	20.0	12	2	B56049 urinary tract ston
43	20	20.0	13	2	S63492 dissimilatory sulf
44	20	20.0	14	2	PH1566 cerebrin 30 - huma
45	20	20.0	14	2	S39930 S-allele-associate

ALIGNMENTS

RESULT 1
S43627
cytochrome-c oxidase (EC 1.9.3.1) chain Vb-H - trout (fragment)
C:Species: Salmo sp. (trout)
C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 02-Jul-1998
C:Accession: S43627
R:Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A:Title: Identification of tissue-specific isoforms for subunits Vb and Vlla of cytochrome c oxidase
A:Reference number: S43624; MUID:94237150
A:Accession: S43627
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <FR>
C:Keywords: electron transfer; membrane-associated complex; oxidoreductase; respirato

Query Match 27.0%; Score 27; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 4.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 RGLPTGQAV 16
DB 4 KGIPTDEQ 12

RESULT 2
P00537
arylhydroxamic acid N,O-acetyltransferase (EC 2.3.1.-) - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: P00537
R:Stone, T.; Yamaguchi, T.; Isobe, M.; Takabatake, E.; Adachi, T.; Hirano, K.; Wang, C
Chem. Pharm. Bull. 40, 2857-2859, 1992
A:Title: Purification and characterization of hamster hepatic microsomal N,O-acetyltransferase
A:Reference number: P00537; MUID:93099627
A:Accession: P00537
A:Molecule type: protein
A:Residues: 1-20 <SON>
A:Experimental source: liver
C:Keywords: acyltransferase

Query Match 27.0%; Score 27; DB 2; Length 20;
Best Local Similarity 46.2%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 8 RGLPTGQAVAVH 20
DB 7 RMTHTGQVAVH 19

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RESULT 15
US-08-458-887-7
; Sequence 7, Application US/08458887
; Patent No. 5914261
;
GENERAL INFORMATION:
; APPLICANT: Boulton, Teri G. et al.
; TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,887
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,544
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
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US-08-458-887-7

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Query Match 27.0%; Score 27; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 94;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 IFQELSRGLP 11
   1111:11
Db 1 IFQETARFP 10

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Search completed: December 21, 2000, 08:31:43
Job time: 366 sec

Sequence 100, Application US/07794288D
Patent No. 5580953
GENERAL INFORMATION:
APPLICANT: ELISABETH ALBRECHT,
APPLICANT: HOWARD JONES,
APPLICANT: LAURA S.L. GAETA,
APPLICANT: KATHRYN S. PRICKEIT and
APPLICANT: KEVIN BEAUMONT
TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST
TITLE OF INVENTION: PEPTIDES AND USES THEREFOR
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: First Interstate World
STREET: Center
STREET: 633 West Fifth Street,
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
MEDIUM TYPE: Mb Storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: IBM M.S. DOS (Version
5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07794,288D
FILING DATE: Herewith
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/794,288
FILING DATE: 19-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Duft, Bradford, J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 193/153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
FEATURE:
OTHER INFORMATION:
US-07-794-288D-100

Query Match 28.0%; Score 28; DB 1; Length 14;
Best Local Similarity 45.5%; Pred. No. 53;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIFOELSRGLP 11
DB 4 KLSQELHKGTP 14

RESULT 13
US-09-120-365-87
Sequence 87, Application US/09120365
Patent No. 6103514
GENERAL INFORMATION:
APPLICANT: Natori, Shunji
TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
CURRENT APPLICATION NUMBER: US/09/120,365
CURRENT FILING DATE: 1998-07-22

EARLIER APPLICATION NUMBER: JP 9-333 474
EARLIER FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 87
LENGTH: 14
TYPE: PRT
ORGANISM: Nicotiana
US-09-120-365-87

Query Match 27.0%; Score 27; DB 3; Length 14;
Best Local Similarity 50.0%; Pred. No. 80;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIFOELSRGLP 12
DB 3 EIFDEVAGLPS 14

RESULT 14
US-08-463-862-7
Sequence 7, Application US/08463862
Patent No. 5776751
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G. et al.
TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,862
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/701,544
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-463-862-7

Query Match 27.0%; Score 27; DB 1; Length 16;
Best Local Similarity 60.0%; Pred. No. 94;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IFOELSRGLP 11
DB 1 IFOETARFOP 10

FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-075 (IMI-040cp)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
FAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-440-861-16

Query Match 29.0%; Score 29; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 54;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 10 LPTGQAV 17
:||||:1:
Db 12 IPTGELQI 19

RESULT 10
US-08-440-861-17
Sequence 17, Application US/08440861
Patent No. 5710126
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.
APPLICANT: Kuo, Mei-Chang
APPLICANT: Lugman, Mohammad
TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
TITLE OF INVENTION: ALLERGEN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-075 (IMI-040cp)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
FAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-440-861-17

Query Match 29.0%; Score 29; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 54;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 10 LPTGQAV 17
:||||:1:
Db 2 IPTGELQI 9

RESULT 11
US-08-726-306A-31
Sequence 31, Application US/08726306A
Patent No. 5958684
GENERAL INFORMATION:
APPLICANT: van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
FAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-726-306A-31

Query Match 29.0%; Score 29; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PTGQAV 16
:||||:1:
Db 12 PTGQSO 17

RESULT 12
US-07-794-288D-100

DB 6 IPGELQ1 13

RESULT 7

US-08-488-551B-635
; Sequence 635, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 96062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 635:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-551B-635

Query Match

Best Local Similarity 29.0%; Score 29; DB 3; Length 14;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 SRCLPTG 13

DB 5 SRCLPTG 11

RESULT 8

US-08-634-060-42
; Sequence 42, Application US/08634060
; Patent No. 5712136
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Kovesdi, Imre
; APPLICANT: Roelivink, Petrus W.
; TITLE OF INVENTION: ADENO VIRAL-MEDIATED CELL TARGETING COMMANDED BY

TITLE OF INVENTION: THE ADENOVIRUS PENTON BASE PROTEIN

NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,060
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,162
; FILING DATE: 08-SEP-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk, John Jr.
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71602
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-634-060-42

Query Match

Best Local Similarity 29.0%; Score 29; DB 1; Length 19;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 ELRGVPRG 13

DB 2 KLGKGVPRG 10

RESULT 9

US-08-440-861-16
; Sequence 16, Application US/08440861
; Patent No. 5710126
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.
; APPLICANT: Luo, Mei-Chang
; APPLICANT: Lugman, Mohammad
; TITLE OF INVENTION: T CELL EPIPTOPES OF RYEGRASS POLLEN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,861

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,947
; FILING DATE: 14-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-195-947-30

Query Match          29.0%; Score 29; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 LPTGQAV 17
Db 6 IPTGELQI 13

RESULT 5
US-08-433-885-30
; Sequence 30, Application US/08433885
; Patent No. 5869333
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjiloglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terry
; APPLICANT: Suphloglu, Cenik
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,885
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-039C2D2
; TELECOMMUNICATION INFORMATION:

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;
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-433-885-30

Query Match          29.0%; Score 29; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 LPTGQAV 17
Db 6 IPTGELQI 13

RESULT 6
US-08-433-908B-30
; Sequence 30, Application US/08433908B
; Patent No. 5965455
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjiloglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terry
; APPLICANT: Suphloglu, Cenik
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,908B
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-039C2D4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-433-908B-30

Query Match          29.0%; Score 29; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 LPTGQAV 17
Db 6 IPTGQAV 17

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OY 7 SRGLPTGOA 15
111111:
Db 5 SRGSPGOS 13

RESULT 2

US-08-433-854-30
; Sequence 30, Application US/08433854
; Patent No. 5721119
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjloglu, Asil
; APPLICANT: Theerakulpisut, Piyaeda
; APPLICANT: Hough, Terry
; APPLICANT: Suphloglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5721119rls
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-433-854-30

Query Match 29.0%; Score 29; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 10 LPTGOA0V 17
111111:
Db 6 IPTGELDI 13

RESULT 3

US-08-174-745A-30
; Sequence 30, Application US/08174745A
; Patent No. 5736362
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope

; APPLICANT: Avjloglu, Asil
; APPLICANT: Theerakulpisut, Piyaeda
; APPLICANT: Hough, Terry
; APPLICANT: Suphloglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362rls
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,745A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-174-745A-30

Query Match 29.0%; Score 29; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 10 LPTGOA0V 17
111111:
Db 6 IPTGELDI 13

RESULT 4

US-08-195-947-30
; Sequence 30, Application US/08195947
; Patent No. 5840316
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjloglu, Asil
; APPLICANT: Theerakulpisut, Piyaeda
; APPLICANT: Hough, Terry
; APPLICANT: Suphloglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5840316rls
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:25:37 ; Search time 99.91 Seconds
(without alignments)
3.355 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 1676186 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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2	29.0	29.0	13	1 US-08-433-854-30	Sequence 30, Appli
3	29.0	29.0	13	1 US-08-174-745A-30	Sequence 30, Appli
4	29.0	29.0	13	2 US-08-195-947-30	Sequence 30, Appli
5	29.0	29.0	13	2 US-08-433-885-30	Sequence 30, Appli
6	29.0	29.0	13	2 US-08-433-908B-30	Sequence 30, Appli
7	29.0	29.0	14	3 US-08-488-551B-635	Sequence 635, App
8	29.0	29.0	19	1 US-08-634-060-42	Sequence 42, Appli
9	29.0	29.0	20	1 US-08-440-861-16	Sequence 16, Appli
10	29.0	29.0	20	1 US-08-440-861-17	Sequence 17, Appli
11	29.0	29.0	20	1 US-08-726-306A-31	Sequence 100, App
12	28.0	28.0	14	1 US-07-794-288D-100	Sequence 87, Appli
13	27.0	27.0	14	1 US-09-120-365-87	Sequence 7, Appli
14	27.0	27.0	16	1 US-08-463-862-7	Sequence 7, Appli
15	27.0	27.0	16	2 US-08-458-867-7	Sequence 7, Appli
16	27.0	27.0	16	3 US-08-622-277A-7	Sequence 12, Appli
17	27.0	27.0	16	3 US-08-622-277A-12	Sequence 12, Appli
18	27.0	27.0	17	3 US-08-622-277A-3	Sequence 2, Appli
19	27.0	27.0	19	1 US-07-640-473-2	Sequence 21, Appli
20	27.0	27.0	19	1 US-07-908-317-21	Sequence 21, Appli
21	27.0	27.0	19	4 PCT-US93-06171-21	Sequence 21, Appli
22	27.0	27.0	20	1 US-07-678-974D-9	Sequence 9, Appli
23	27.0	27.0	20	2 US-08-945-168-14	Sequence 14, Appli
24	26.5	26.5	19	1 US-08-244-116B-2	Sequence 2, Appli
25	26.0	26.0	15	1 US-07-859-291C-10	Sequence 10, Appli
26	26.0	26.0	17	4 PCT-US95-04617-3	Sequence 3, Appli
27	25.0	25.0	9	3 US-08-159-339A-1006	Sequence 1006, Ap
28	25.0	25.0	10	3 US-08-159-339A-1024	Sequence 1024, Ap

29	25.0	11	5	5200183-7	Patent No. 5200183
30	25.0	11	5	5200183-10	Patent No. 5200183
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32	25.0	12	1	US-08-433-854-21	Sequence 21, Appli
33	25.0	12	1	US-08-174-745A-21	Sequence 21, Appli
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35	25.0	12	2	US-08-433-885-21	Sequence 21, Appli
36	25.0	12	2	US-08-433-908B-21	Sequence 21, Appli
37	25.0	12	4	PCT-US93-11703-3	Sequence 13, Appli
38	25.0	12	4	PCT-US93-11703-13	Sequence 13, Appli
39	25.0	12	4	PCT-US93-11703-14	Sequence 14, Appli
40	25.0	12	4	PCT-US93-11703-15	Sequence 15, Appli
41	25.0	12	4	PCT-US93-11703-16	Sequence 16, Appli
42	25.0	13	1	PCT-US93-11703-17	Sequence 17, Appli
43	25.0	14	1	US-08-291-601-2	Sequence 2, Appli
44	25.0	14	1	US-08-320-373-87	Sequence 87, Appli
45	25.0	15	1	US-08-625-691-7	Sequence 7, Appli

ALIGNMENTS

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RESULT 1
US-08-418-444A-9
; Sequence 9, Application US/08418444A
; Patent No. 5773688
; GENERAL INFORMATION:
; APPLICANT: KUROTA, HISAO
; APPLICANT: HIROTA, NAOTO
; APPLICANT: ITO, KAZUTOSHI
; TITLE OF INVENTION: GENE EXPRESSION VECTOR USING THE GENE
; TITLE OF INVENTION: EXPRESSION REGULATING REGION OF THE ADP RIBOSYLATION
; TITLE OF INVENTION: FACTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,444A
; FILING DATE: 07-APR-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP HEI 6-71048
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5773688man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 2589-024-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELETYPE: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-418-444A-9
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Query Match 30.0%; Score 30; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 2; Gaps 0;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRE73; TISSUE-HYPOCOTYL;
RX MEDLINE; 95140641.
RA Thomson M.C., MacFarlane J.L., Beagley C.T., Wolstenholme D.R.;
RT "RNA editing of mat-r transcripts in maize and soybean increases
RT similarity of the encoded protein to fungal and bryophyte group II
RT intron maturases: evidence that mat-r encodes a functional protein.";
RL Nucleic Acids Res. 22:5745-5752(1994).
DR EMBL: U09986; AAA6712.1; .
DR INTERPRO: IPR001694; .
DR PFAM; PF00146; NADHdh; 1.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2082 MW; C2DA548846188D3 CRC64;

Query Match 21.2%; Score 22; DB 8; Length 19;
Best Local Similarity 62.5%; Pred. No. 4e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 GEXAMML 11
||| |:
Db 11 GEYANMIL 18

Search completed: December 21, 2000, 08:35:40
Job time: 603 sec

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 GQVYGL 18
11:11
DB 14 GQIGYAL 20

RESULT 11

O9TRQ4 PRELIMINARY; PRT; 20 AA.
AC O9TRQ4:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CALCULIN-ASSOCIATED PROTEIN PEPTIDE L-9, CAP-50=ANNEXIN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN (1)
RP SEQUENCE:
RX MEDLINE: 92317074.
RA Mizutani A., Usuda N., Tokumitsu H., Minami H., Yasui K.,
RA Kobayashi R., Hidaka H.,
RT "CAP-50, a newly identified annexin, localizes in nuclei of cultured
RT fibroblast 3Y1 cells.";
RL J. Biol. Chem. 267:13498-13504(1992).
SQ SEQUENCE 20 AA; 2296 MW; 89492C83166F4523 CRC64;

Query Match 22.1%; Score 23; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DINGE 5
1111:
DB 5 DINGD 9

RESULT 12

O05403 PRELIMINARY; PRT; 8 AA.
AC O05403:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE DNA FOR ORF'S FROM CHROMOSOME XV (FRAGMENT).
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-FY1679;
RA MEDLINE: 96021609.
RA Zumetstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RT more than twice as many unknown as known open reading frames.";
RL Yeast 11:975-986(1995).
DR EMBL: X83121; CAA58183.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 21.2%; Score 22; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 17 GLHN 20
1:11
DB 1 GHN 4

RESULT 13

O9T2S1 PRELIMINARY; PRT; 17 AA.
ID O9T2S1:
AC O9T2S1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CYTOCHROME-C REDUCTASE 55 KDA SUBUNIT (EC 1.10.2.2) (FRAGMENT).
OS Solanum tuberosum (Potato).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
OC Solanaceae; Solanum.
RN (1)
RP SEQUENCE:
RA Braun H.P., Kruff V., Schmitz U.K.;
RL Planta 193:99-106(1994).
SQ SEQUENCE 17 AA; 1870 MW; 207804E213CD4009 CRC64;

Query Match 21.2%; Score 22; DB 8; Length 17;
Best Local Similarity 44.4%; Pred. No. 3.6e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 6 KAMMLGOV 14
11:11:
DB 1 KAVDILGDI 9

RESULT 14

O9S8U7 PRELIMINARY; PRT; 17 AA.
ID O9S8U7:
AC O9S8U7:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE SOLANIDINE UDP-GLUCOSE GLUCOSYLTRANSFERASE, SGT-19 KDA CNBR CLEAVED
DE FRAGMENT.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
OC Solanaceae; Solanum.
RN (1)
RP SEQUENCE:
RX MEDLINE: 93044546.
RA Stapleton A., Allen P.V., Tao H.P., Belknap W.R., Friedman M.;
RT "Partial amino acid sequence of potato solanidine UDP-glucose
RT glucosyltransferase purified by new anion-exchange and size exclusion
RT media.";
RL Protein Expr. Purif. 3:85-92(1992).
SQ SEQUENCE 17 AA; 1783 MW; 75BADC80077E593C CRC64;

Query Match 21.2%; Score 22; DB 10; Length 17;
Best Local Similarity 66.7%; Pred. No. 3.6e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DINGEK 6
1:1111
DB 8 NISGEK 13

RESULT 15

O36277 PRELIMINARY; PRT; 19 AA.
ID O36277:
AC O36277:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE NADH DEHYDROGENASE SUBUNIT I (FRAGMENT).
OS Zea mays (Maize).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

DR EMBL: AF108100; AAD16884.1; -
 DR INTERPRO: IPR002040; -
 DR PROSITE: PS00267; TACHYKININ; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1203 MW; 8BADC77C6B59C33A CRC64;

Query Match 23.1%; Score 24; DB 5; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 TGERKAMMLG 12
 ||:| |:
 DB 2 TGDKFYGLMG 11

RESULT 7
 O9S739 PRELIMINARY; PRT; 20 AA.
 AC O9S739;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE CALMODULIN-1 (FRAGMENT).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
 OC Brassicaceae; Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ECOTYPE BE-0, ECOTYPE C24, ECOTYPE IER-0, AND ECOTYPE COL-4;
 RA Lordon K., Cournoyer B., Goubely C., Delpechs A., Picard G.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF027616; AAD01853.1; -
 DR EMBL: AF027613; AAD01850.1; -
 DR EMBL: AF027614; AAD01851.1; -
 DR EMBL: AF027615; AAD01852.1; -
 DR INTERPRO: IPR002048; -
 DR PFM: PFO0036; efnand; 1.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 20 AA; 2303 MW; DA1407B6ADF82006 CRC64;

Query Match 23.1%; Score 24; DB 10; Length 20;
 Best Local Similarity 31.2%; Pred. No. 2e+03; 2; Indels 6; Gaps 1;
 Matches 5; Conservative 3; Mismatches 2;

OY 1 DITGKAMMLGQVYK 16
 ||:| |:
 DB 1 DVDGD-----GQINY 10

RESULT 8
 O9TQZ5 PRELIMINARY; PRT; 17 AA.
 AC O9TQZ5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (FRAGMENT).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 96273610.
 RA Nicolas M.G., Fujiki K., Murayama K., Suzuki M.T., Mineki R.,
 RA Hayakawa M., Yoshikawa Y., Cho F., Kanai A.;
 RT "Studies on the mechanism of early onset macular degeneration in
 RT cynomolgus (Macaca fascicularis) monkeys. I. Abnormal concentrations
 RT of two proteins in the retina.";

RL Exp. Eye Res. 62:211-219(1996).
 SQ SEQUENCE 17 AA; 1671 MW; 52CCDD01A98B3DAF CRC64;

Query Match 22.1%; Score 23; DB 6; Length 17;
 Best Local Similarity 50.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 12 GQVYGLH 19
 ||:| |:
 DB 1 GKVKGVN 8

RESULT 9
 O34197 PRELIMINARY; PRT; 20 AA.
 AC O34197;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE GROES (FRAGMENT).
 CN GROES.
 OS Rickettsia rickettsii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R;
 RX MEDLINE: 97373904.
 RA Sumner J.W., Nicholson W.L., Massung R.F.;
 RT "PCR amplification and comparison of nucleotide sequences from the
 RT groESL heat shock operon of Ehrlichia species.";
 RL J. Clin. Microbiol. 35:2087-2092(1997).
 DR EMBL: U96733; AAB65634.1; -
 DR INTERPRO: IPR001476; -
 DR PFM: PFO0166; cpn10; 1.
 FT NON_TER 1
 SQ SEQUENCE 20 AA; 2235 MW; EB6FEB9F3711E52 CRC64;

Query Match 22.1%; Score 23; DB 2; Length 20;
 Best Local Similarity 25.0%; Pred. No. 2.9e+03;
 Matches 5; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 1 DITGKAMMLGQVYGLHN 20
 ||:| |:
 DB 1 EIKGTRLYMKESDVFGIIN 20

RESULT 10
 O9R5L1 PRELIMINARY; PRT; 20 AA.
 AC O9R5L1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE THYMIDINE 5'-DIPHOSPHATE D-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
 DE (FRAGMENT).
 OS Streptomyces peucetius.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 92268857.
 RA Thompson M.W., Strohl W.R., Floss H.G.;
 RT "Purification and characterization of TDP-D-glucose 4,6-dehydratase
 RT from anthracycline-producing streptomycetes.";
 RL J. Gen. Microbiol. 138:779-786(1992).
 SQ SEQUENCE 20 AA; 1943 MW; 7958730238C00AC9 CRC64;

Query Match 22.1%; Score 23; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 2.9e+03;

OS Chlorogonium elongatum.
OC Mitochondrion.
OC Eukaryota: Vitellipiantae: Chlorophyta: Chlorophyceae: Volvocales:
OC Haematococcaceae: Chlorogonium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-2E;
RX MEDLINE: 97306270.
RA Kroymann J., Zetsche K.:
RT "The apocytochrome-b gene in Chlorogonium elongatum
(Chlamydomonadaceae): an intronic GY-YIG ORF in green algal
mitochondria.";
RT Curr. Genet. 31:414-418(1997).
CC -1- CATALYTIC ACTIVITY: NADH + ACCEPTOR -> NAD(+) + REDUCED ACCEPTOR.
CC -1- COFACTOR: FLAVOPROTEIN; IRON-SULFUR.
DR EMBL: Y07814; CAA69147.1; -.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 1844 MW; BC88B2EBE529A229 CRC64;

Query Match 26.0%; Score 27; DB 8; Length 17;
Best Local Similarity 31.2%; Pred. No. 5.3e+02;
Matches 5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 3 TCEKAMMLGQVYKYL 18
DB 2 TSGKGLFVHDQVSL 17

RESULT 3
ID 031045 PRELIMINARY; PRT; 19 AA.
AC 031045:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE LEUA LEADER PEPTIDE.
GN LEUA.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes: Actinobacteria: Actinobacteridae:
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-D132;
RA Potter C.A., Baumberg S.:
RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF026444; AAB82585.1; -.
SQ SEQUENCE 19 AA; 2080 MW; 1A591DC299760D4 CRC64;

Query Match 24.0%; Score 25; DB 2; Length 19;
Best Local Similarity 44.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 10 LUGOVYKYL 18
DB 1 MGLIMRFL 9

RESULT 4
ID 09TWD0 PRELIMINARY; PRT; 19 AA.
AC 09TWD0:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE SIALOPROTEIN I (FRAGMENT).
OS Sphaerichnus granularis (Purple sea urchin).
OC Eukaryota: Metazoa: Echinodermata: Echinozoa: Echinoidea:
OC Euechinozoa: Echinozoa: Echinozoa: Echinozoa: Echinozoa:
OC Sphaerichnus.
RN [1]

RP SEQUENCE.
RX MEDLINE: 96428846.
RA Karanamos N.K., Manouras A., Anagnostides S., Makatsori E.,
RA Tseganidis T., Antonopoulos C.A.:
RT "Isolation, biochemical and immunological characterisation of two sea
urchin glycoproteins bearing sulphated poly(sialic acid)
RT polysaccharides rich in N-glycolyl neuraminic acid.";
RL Biochimie 78:171-182(1996).
SQ SEQUENCE 19 AA; 2265 MW; 38FFDEB1A033EB50 CRC64;

Query Match 24.0%; Score 25; DB 5; Length 19;
Best Local Similarity 27.3%; Pred. No. 1.3e+03;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 6 KAMMLGQVYKYL 16
DB 8 QXMLTXGEIEY 18

RESULT 5
ID 053545 PRELIMINARY; PRT; 19 AA.
AC 053545:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE VIRF (FRAGMENT).
GN VIRF.
OS Shigella sonnei.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae:
OC Shigella.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95394812.
RA Nakayama S., Watanabe H.:
RT "Involvement of cpxA, a sensor of a two-component regulatory system,
RT in the pH-dependent regulation of expression of Shigella sonnei virF
RT gene.";
RL J. Bacteriol. 177:5062-5069(1995).
DR EMBL: S79443; AAB35192.1; -.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2344 MW; 52A53B9DAAEFCFA CRC64;

Query Match 23.6%; Score 24.5; DB 2; Length 19;
Best Local Similarity 38.9%; Pred. No. 1.6e+03;
Matches 7; Conservative 2; Mismatches 4; Indels 5; Gaps 1;

OY 8 MMLG-----QVYKGLHN 20
DB 1 MMDGKHKRIDIVRLHN 18

RESULT 6
ID 09UAR8 PRELIMINARY; PRT; 11 AA.
AC 09UAR8:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE SIALOKININ I PREPROTEIN (FRAGMENT).
OS Aedes aegypti (yellow fever mosquito).
OC Eukaryota; Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae:
OC Culicidae; Aedes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ROCKEFELLER/RED: TISSUE-SALIVARY GLAND;
RA Beerntsen B.T., Champagne D.E., Coleman J.L., Campos Y.A., James A.A.:
RT "Characterization of the sialokinin I gene encoding the salivary
RT vasodilator of the yellow fever mosquito, Aedes aegypti.";
RT Insect Mol. Biol. 0:0-0(1999).

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:35:39 ; Search time 157.2 Seconds
(without alignments)
11.880 Million cell updates/sec

Title: US-08-934-367-13
Perfect score: 104
Sequence: 1 DITGEKAMMLGOVKYGLHN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	27.9	19	10	0958G6
2	27	26.0	17	8	003888
3	25	24.0	19	2	031045
4	25	24.0	19	5	09TMD0
5	24.5	23.6	19	2	053545
6	24	23.1	11	5	09UAR8
7	24	23.1	20	10	09S739
8	23	22.1	17	6	09TQZ5
9	23	22.1	20	2	034197
10	23	22.1	20	6	09R5L1
11	23	22.1	20	6	09R5L1
12	23	22.1	8	3	005403
13	22	21.2	17	8	09T2S1
14	22	21.2	17	10	09S807
15	22	21.2	19	8	036277
16	22	21.2	19	10	09S901
17	22	21.2	20	4	09UCP6
18	22	21.2	20	6	028734
19	22	21.2	20	13	09PRM4

20	21	20.2	15	6	09TRM0	09Lrw0 oryctolagus
21	21	20.2	17	4	09UCF0	09ucf0 homo sapien
22	21	20.2	17	11	09OX07	09qy07 mus musculu
23	21	20.2	18	4	09UCH2	09ubc2 homo sapien
24	21	20.2	19	5	057012	057012 staphylococ
25	21	20.2	19	5	09TWK7	09twk7 trypanosoma
26	21	20.2	19	11	064132	064132 rattus norv
27	21	20.2	19	11	09QXP9	09qxp9 mus musculu
28	21	20.2	20	13	09PSH5	09psh5 gallus gall
29	21	20.2	20	3	09UWM2	09uvw2 schizophy11
30	20	19.2	10	5	025355	025355 locusta mig
31	20	19.2	11	12	084247	084247 polyomaviru
32	20	19.2	14	2	053326	053326 synechococc
33	20	19.2	15	5	09TXC8	09txc8 locusta mig
34	20	19.2	15	12	084332	084332 simian viru
35	20	19.2	16	4	09UCI8	09uci8 homo sapien
36	20	19.2	17	2	084353	084353 simian viru
37	20	19.2	17	2	052748	052748 anabaena sp.
38	20	19.2	18	11	09QVBO	09qvbo rattus sp.
39	20	19.2	19	2	06140	06140 neisseria m
40	20	19.2	19	2	09K4X3	09k4x3 bacillus ce
41	20	19.2	19	12	084863	084863 unidentified
42	20	19.2	20	2	09R9A5	09r9a5 nitrosospir
43	20	19.2	20	2	09R9A5	09r9a5 nitrosospir
44	20	19.2	20	2	09R5T8	09r5t8 campylobact
45	20	19.2	20	3	013594	013594 saccharomyc

ALIGNMENTS

RESULT 1
ID 09S8G6 PRELIMINARY; PRT; 19 AA.
AC 09S8G6;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE TYPE 2 LECTIN (FRAGMENT).
OS Colocasia esculenta (Elephant's ear) (Taro).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
CC Magnoliophyta; Liliopsida; Araceae; Colocasia.
[1]
RP SEQUENCE.
RX MEDLINE; 95288362.
RA Van Damme E.J., Goossens K., Smeets K., van Leuven F., Verhaert P.,
RT Peumans W.J.;
RT "The major tuber storage protein of araceae species is a lectin.
RT Characterization and molecular cloning of the lectin from Arum
maculatum L.";
RL Plant Physiol. 107:1147-1158(1995).
SQ SEQUENCE 19 AA; 2066 MW; F9C1865CA58608A CRC64;

Query Match 27.9%; Score 29; DB 10; Length 19;
Best Local Similarity 50.0%; Pred. NO. 2.8e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 8 MMLGQVKG 17
DB 8 LFGSGVXKG 17
RESULT 2
ID 003888 PRELIMINARY; PRT; 17 AA.
AC 003888;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE)
DE (TYPE I DEHYDROGENASE) (FRAGMENT).
GN NAD5.


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RP SEQUENCE.
RC STRAIN-OM5;
RX MEDLINE: 90055678.
RA "Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RL carboxydotrophic bacteria.";
RU Arch. Microbiol. 152:335-341(1989).
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + FERROCYTOCHROME B-561 = CO(2) +
CC 2 H(+)+ + FERRICYTOCHROME B-561.
CC -1- COFACTOR: MOLYBDENUM.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR: P10141; P10141.
KW Oxidoreductase; Molybdenum.
FT NON_TER 15
SQ SEQUENCE 15 AA: 1779 MW; 82DD3BF93E739D63 CRC64;

Query Match 19.2%; Score 20; DB 1; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 MMLIGQVKY 16
DB 1 MMITPESFDY 9

RESULT 14
DCNM_PSECH STANDARD; PRT; 15 AA.
AC P19917;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARBON MONOXIDE DEHYDROGENASE MEDIUM CHAIN (EC 1.2.99.2) (FRAGMENT).
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria.
RN [1]
RP SEQUENCE.
RX MEDLINE: 90055678.
RA "Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RL carboxydotrophic bacteria.";
RU Arch. Microbiol. 152:335-341(1989).
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
CC ACCEPTOR.
CC -1- COFACTOR: MOLYBDENUM.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR: P10143; P10143.
KW Oxidoreductase; Molybdenum.
FT NON_TER 15
SQ SEQUENCE 15 AA: 1815 MW; 90508CF93E739D63 CRC64;

Query Match 19.2%; Score 20; DB 1; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 MMLIGQVKY 16
DB 1 MMITPGRHFDY 9

RESULT 15
ARCD_PSEPU STANDARD; PRT; 16 AA.
ID ARCD_PSEPU
AC P41147;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ARGININE/ORNITHINE ANTIPORTER (FRAGMENT).
GN ARCD.

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```

OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 4359;
RA Wilson S.D., Wang M., Filipula D.;
RU Submitted (FEB-1994) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CATALYZES AN ELECTRONEUTRAL EXCHANGE BETWEEN ARGININE
CC AND ORNITHINE TO ALLOW HIGH-EFFICIENCY ENERGY CONVERSION IN THE
CC ARGININE DETERMINASE PATHWAY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
CC PERMASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
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CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.slb.ch).
CC -----
CC EMBL: U07185; AAA16963.1; -.
DR Transport; Amino-acid transport; Transmembrane; Inner membrane.
KW NON_TER 1
FT SEQUENCE 16 AA: 1644 MW; 90B48A7C8F9A9705 CRC64;

Query Match 19.2%; Score 20; DB 1; Length 16;
Best Local Similarity 60.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 16 YGLIN 20
DB 7 YGLYD 11

```

Search completed: December 21, 2000, 08:32:59
Job time: 442 sec

RESULT 10
 ID TEME_RANTE STANDARD: PRT: 14 AA.
 AC P56917;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE TEMPORIN A.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 RP [1]
 SEQUENCE, AND SYNTHESIS.
 RC TISSUE-SKIN;
 RX MEDLINE: 97175050.
 RA Slimaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barra D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
 BACTERIA.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 FAMILY.
 CC Amphibian skin: Antibiotic: Amidation: Multigene family.
 KW MOD_RES 14
 FT SEQUENCE 14 AA: 1469 MW: 601653612B9DECD4 CRC64;

Query Match 20.2%; Score 21; DB 1; Length 14;
 Best Local Similarity 44.4%; Pred. No. 1.3e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 10 LIGQVKYGL 18
 I : I : I :
 Db 4 LIGKVLSCI 12

RESULT 11
 ID TEME_RANTE STANDARD: PRT: 14 AA.
 AC P56921;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE TEMPORIN F.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 RP [1]
 SEQUENCE.
 RC TISSUE-SKIN;
 RX MEDLINE: 97175050.
 RA Slimaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barra D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
 GRAM-POSITIVE BACTERIA.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 FAMILY.
 CC Amphibian skin: Antibiotic: Amidation: Multigene family.
 KW MOD_RES 14
 FT SEQUENCE 14 AA: 1441 MW: 4D1653612B9DECC3 CRC64;

Query Match 20.2%; Score 21; DB 1; Length 14;
 Best Local Similarity 44.4%; Pred. No. 1.3e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 10 LIGQVKYGL 18
 I : I : I :
 Db 4 LIGKVLSCI 12

RESULT 12
 ID IDHC_PIG STANDARD: PRT: 13 AA.
 AC P20304;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE ISOCITRATE DEHYDROGENASE [NADP] CYTOSOLIC (EC 1.1.1.42)
 DE (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC IDH) (IDP
 DE (FRAGMENT).
 GN IDH1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 RP [1]
 SEQUENCE.
 RX MEDLINE: 87308293.
 RA Bailey J.M., Colman R.F.;
 RT "Isolation of the glutamyl peptide labeled by the nucleotide analogue
 2-(4-bromo-2,3-dioxobutylthio)-1,N(6)-ethenoadenosine
 2',5'-biphosphate in the active site of NADP+-specific isocitrate
 dehydrogenase.";
 RL J. Biol. Chem. 262:12620-12626(1987).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE: 87308292.
 RA Ehrlich R.S., Colman R.F.;
 RT "Characterization of an active site peptide modified by the substrate
 analogue 3-bromo-2-ketoglutarate on a single chain of dimeric NADP+-
 RT dependent isocitrate dehydrogenase.";
 RL J. Biol. Chem. 262:12614-12619(1987).
 CC -1- CATALYTIC ACTIVITY: ISOCITRATE + NADP(+) -> 2-OXOGlutarate +
 CO(2) + NADPH.
 CC -1- SUBUNIT: HOMODIMER.
 CC PIR: A27371; A27371.
 DR PIR: A27372; A27372.
 DR INTERPRO: IPR001804; .
 DR PROSITE: PS00470; IDH_IMDH, PARTIAL.
 KW Oxidoreductase; NADP; Tricarboxylic acid cycle.
 FT NON_TER 1
 FT ACT_SITE 5
 FT NON_TER 13
 FT SEQUENCE 13 AA: 1353 MW: 1B640F0E9F7C71E0 CRC64;

Query Match 19.7%; Score 20.5; DB 1; Length 13;
 Best Local Similarity 45.5%; Pred. No. 1.5e+03;
 Matches 5; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

OY 10 LIGQVKYGLHN 20
 I : I : I : I :
 Db 2 LAGEI-HGLSN 11

RESULT 13
 ID DCM_PSECA STANDARD: PRT: 15 AA.
 AC P19920;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE CARBON MONOXIDE OXYGENASE (CYTOCHROME B-561) MEDIUM CHAIN (EC 1.2.2.4)
 DE (FRAGMENT).
 OS Pseudomonas carboxydovorans.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 RN Bradyrhizobium group; Oligotrophia.
 RN [1]

CRBL_VESOR
ID CRBL_VESOR STANDARD; PRT; 14 AA.
AC P17231;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE HISTAMINE-RELEASING PEPTIDE II (HR-II).
OS Vespa orientalis (Oriental hornet).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vespoidea; Vespidae; Vespinae; Vespa.
RN [1]
RP SEQUENCE.
RC TISSUE=VENOM;
RA Miroshnikov A.I., Suezhkova L.G., Nazimov I.V., Reshetova O.I.,
Rozyanov B.V., Gushchin I.S.;
RT "Structure and properties of histamine releasing peptides from the
venom of Vespa orientalis hornet."
RL Bioorg. Khim. 7:1467-1477(1981).
CC -I- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
OF NEUTROPHILS.
DR PIR: JN0390; JN0390.
KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
FT MOD.RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA; 1524 MW; 22015BA46CEDFD38 CRC64;

Query Match 21.2%; Score 22; DB 1; Length 14;
Best Local Similarity 40.0%; Pred. No. 9e+02; Indels 0; Gaps 0;
Matches 4; Conservative 4; Mismatches 2; Indels 0;

OY 9 MLGQVXYGL 18
Db 4 LILGKLVKGL 13

RESULT 7
LECH_IRIHO
ID LECH_IRIHO STANDARD; PRT; 20 AA.
AC P36231;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE N-ACETYL-D-GALACTOSAMINE-BINDING LECTIN SUBUNIT B (A-DISACCHARIDE-
BINDING LECTIN SUBUNIT B) (FRAGMENT).
OS Iris hollandica (Dutch iris).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Asparagales; Iridaceae; Iris.
RN [1]
RP SEQUENCE.
RC STRAIN=CV. GOLDEN HARVEST, AND CV. PROF. BLANUV; TISSUE=BOULB;
RX MEDLINE: 94171801.
RA Mo H., van Damme E.J.M., Peumans W.J., Goldstein I.J.;
RT "Isolation and characterization of an
N-acetyl-D-galactosamine-binding lectin from Dutch iris bulbs which
recognizes the blood group A disaccharide (GalNAc alpha 1-3gal)."
RL J. Biol. Chem. 269:7666-7673(1994).
CC -I- FUNCTION: GAL / GALNAc-SPECIFIC LECTIN. AGGLUTINATES BOTH NATIVE
AND TRYPSIN-TREATED RABBIT ERYTHROCYTES BUT NOT HUMAN ERYTHROCYTES
IRRESPECTIVE OF BLOOD GROUP TYPE.
KW LECTIN.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2246 MW; DE08DA025FD17D56 CRC64;

Query Match 21.2%; Score 22; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.3e+03; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 2; Indels 0;

OY 5 EKAMMLIG 12
Db 9 EETMMRIG 16

RESULT 8
AL16_CARMA
ID AL16_CARMA STANDARD; PRT; 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINOSTATIN 16.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
RN [1]
RP SEQUENCE.
RC TISSUE=CEREBRAL GANGLION, AND THORACIC GANGLION;
RX MEDLINE: 98121193.
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -I- FUNCTION: MAY ACT AS A NEUROTROPHIC FACTOR OR NEUROMODULATOR.
CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD.RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match 20.2%; Score 21; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 8.8e+04; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 3; Indels 0;

OY 12 GQVXYGL 18
Db 2 GPYSTGL 8

RESULT 9
CRBL_VESOR
ID CRBL_VESOR STANDARD; PRT; 13 AA.
AC P17231;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE VESPID CHEMOTACTIC PEPTIDE T (VSCP-T).
OS Vespa tropica (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vespoidea; Vespidae; Vespinae; Vespa.
RN [1]
RP SEQUENCE.
RC TISSUE=VENOM;
RA Yasuhara T., Nakajima T., Erspaer V.;
RL (in) Sakakibara S. (eds.);
RT Peptide chemistry 1982, pp.213-218, Protein Research Foundation,
Osaka (1983).
CC -I- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
OF NEUTROPHILS.
KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
FT MOD.RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1354 MW; 220140365DFE5338 CRC64;

Query Match 20.2%; Score 21; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 2; Indels 0;

OY 10 LIGQVXYGL 18
Db 4 TLGKILGGL 12

CC METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
 CC -1- CATALYTIC ACTIVITY: SEDOHEPTULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE
 CC 3-PHOSPHATE -> D-ERYTHROSE 4-PHOSPHATE + D-FRUCTOSE 5-PHOSPHATE.
 CC -1- PATHWAY: NONOXIDATIVE PART OF THE PENTOSE-PHOSPHATE PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY.
 DR PIR: A11497; A11497.
 DR INTERPRO: IPR001585; -.
 DR PROSITE: PS00958; TRANSALDOLASE_2; PARTIAL.
 DR PROSITE: PS01054; TRANSALDOLASE_1; PARTIAL.
 KM TRANSFERASE: Pentose shunt.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1033 MW; 325A31A44EB1E058 CRC64;

Query Match
 Best Local Similarity 22.1%; Score 23; DB 1; Length 9;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 16 YGLH 19
 ||:|
 Db 1 YGTH 4

RESULT 3
 MDH_KIBAR
 ID MDH_KIBAR STANDARD; PRT; 20 AA.
 AC P19978;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE MALATE DEHYDROGENASE (EC 1.1.1.37) (FRAGMENT).
 GN MDH.
 OS Kibdelosporangium aridum.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Pseudonocardineae; Pseudonocardaceae;
 OC Kibdelosporangium.
 RP SEQUENCE.
 RN MEDLINE: 89374824.
 RA Rommel T.O., Hund H.-K., Speth A.R., Lingsens F.;
 RT "Purification and N-terminal amino-acid sequences of bacterial malate
 RT dehydrogenases from six actinomycetales strains and from
 RT phenyllobacterium immobile, strain E.";
 RL Biol. Chem. Hoppe-Seyler 370:763-768(1989).
 CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) -> OXALOACETATE + NADH.
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
 DR PIR: S04961; S04961.
 DR HSSP: P10584; 1BDM.
 DR INTERPRO: IPR001252; -.
 DR PROSITE: PS00068; MDH; PARTIAL.
 KM Oxidoreductase; Tricarboxylic acid cycle; NAD.
 FT NON_TER 20
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 1989 MW; 79587B6F8C00AC9 CRC64;

Query Match
 Best Local Similarity 22.1%; Score 23; DB 1; Length 20;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 GOVKYGL 18
 ||:|
 Db 14 GOIGVAL 20

RESULT 4
 MDH_MICGL
 ID MDH_MICGL STANDARD; PRT; 20 AA.
 AC P19979;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE MALATE DEHYDROGENASE (EC 1.1.1.37) (FRAGMENT).

GN MDH.
 OS Microtetraspora glauca.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptosporangineae; Streptosporangiaceae;
 OC Microtetraspora.
 RN SEQUENCE.
 RP MEDLINE: 89374824.
 RA Rommel T.O., Hund H.-K., Speth A.R., Lingsens F.;
 RT "Purification and N-terminal amino-acid sequences of bacterial malate
 RT dehydrogenases from six actinomycetales strains and from
 RT phenyllobacterium immobile, strain E.";
 RL Biol. Chem. Hoppe-Seyler 370:763-768(1989).
 CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) -> OXALOACETATE + NADH.
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
 DR PIR: S04958; S04958.
 DR HSSP: P10584; 1BDM.
 DR INTERPRO: IPR001236; -.
 DR INTERPRO: IPR001252; -.
 DR PFAM: PF00056; ldh; 1.
 DR PROSITE: PS00068; MDH; PARTIAL.
 KM Oxidoreductase; Tricarboxylic acid cycle; NAD.
 FT NON_TER 20
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2065 MW; 740129B859D01EBE CRC64;

Query Match
 Best Local Similarity 22.1%; Score 23; DB 1; Length 20;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 GOVKYGL 18
 ||:|
 Db 11 GOIGVAL 17

RESULT 5
 AL11_CARMA
 ID AL11_CARMA STANDARD; PRT; 9 AA.
 AC P81814;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CARCINOSTATIN 11.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoida; Portunidae; Carcinus.
 RN SEQUENCE.
 RP TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
 RX MEDLINE: 98121193.
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: MAY ACT AS A NEUROTANSMITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KM Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 9
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 927 MW; 832D79CDBA6D861 CRC64;

Query Match
 Best Local Similarity 21.2%; Score 22; DB 1; Length 9;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 GOVKYGL 18
 ||:|
 Db 3 GOYAFGL 9

RESULT 6

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:32:59 ; Search time 62.7 Seconds
(without alignments)
10.191 Million cell updates/sec

Title: US-08-934-367-13

Perfect score: 104
Sequence: 1 DITGEKAMMLIGVKYGLHN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 segs, 31947931 residues
Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	23	22.1	8	1 AL17_CARMA	P81820 carclinus ma
2	23	22.1	9	1 TAL3_PICJA	P17441 pichia jadi
3	23	22.1	20	1 MDH_KIBAR	P19978 kibdelospor
4	23	22.1	20	1 MDH_MIGGL	P19979 microtetras
5	22	21.2	9	1 AL11_CARMA	P81814 carclinus ma
6	22	21.2	14	1 CRBL_VESOR	P17236 vespa orien
7	22	21.2	20	1 LECB_IRIHO	P36231 irils holian
8	21	20.2	8	1 AL16_CARMA	P81819 carclinus ma
9	21	20.2	13	1 CRBL_VESTR	P17231 vespa tropl
10	21	20.2	14	1 TEMA_RANTE	P56917 rana tempor
11	21	20.2	14	1 TEMA_RANTE	P56921 rana tempor
12	20.5	19.7	13	1 IDHC_PIG	P20304 sus scrofa
13	20	19.2	15	1 DCMW_PSECA	P19920 pseudomonas
14	20	19.2	15	1 DCMW_PSECA	P19917 pseudomonas
15	20	19.2	16	1 ARCD_PSEPU	P41147 pseudomonas
16	20	19.2	19	1 PHLG_STAIN	P80924 staphylococ
17	20	19.2	19	1 UP25_UPEIN	P82031 upercoleia i
18	20	19.2	20	1 PGK_CLOPA	P81346 clostridium
19	20	19.2	20	1 UCRQ_EQUAR	P81247 equisetum a
20	19	18.3	10	1 TRKS1_AEDAE	P42614 aedes aegypt
21	19	18.3	10	1 TRKS2_AEDAE	P42615 aedes aegypt
22	19	18.3	14	1 TEMC_RANTE	P80618 rana tempor
23	19	18.3	14	1 UC18_MAIZE	P80624 zea mays (m
24	19	18.3	15	1 RRS_PHYPA	P80657 physcomitlre
25	19	18.3	17	1 BOLA_MEGPE	P07495 megacomblre
26	19	18.3	18	1 LOXB_KRYAS	P18300 kryptophana
27	19	18.3	18	1 RL23_HALCU	P05975 halobacteri
28	19	18.3	19	1 MDH_COMAC	P80539 comamonas a
29	19	18.3	20	1 COG2_CHIOP	P34154 chionoecete
30	19	18.3	20	1 COG3_CHIOP	P34155 chionoecete
31	19	18.3	20	1 COGA_PARCM	P20732 parallthode
32	19	18.3	20	1 COGB_PARCM	P20733 parallthode
33	18	17.3	9	1 TAL1_PICJA	P17440 pichia jadi

34	18	17.3	12	1 PAZB_VIPHO	P31859 vipera beru
35	18	17.3	13	1 CRBL_VESMA	P17232 vespa manda
36	18	17.3	14	1 TAT_HY1W2	P12509 human immun
37	18	17.3	14	1 TAT_HY1Z8	P12511 human immun
38	18	17.3	15	1 CDNS_LITCE	P82077 littoria cae
39	18	17.3	17	1 FLA2_BARBA	P36634 bartonella
40	18	17.3	17	1 FLA2_BARBA	O36834 trichophyto
41	18	17.3	19	1 NS19_SPICI	O31159 spiriplasma
42	18	17.3	20	1 NS19_SPICI	P80335 oncorhynchu
43	18	17.3	20	1 COXO_ONCMY	P80983 thunnus obe
44	18	17.3	20	1 COXO_THUOB	P81818 carclinus ma
45	17	16.3	9	1 AL15_CARMA	P01158 oryctolagus
			1	1 DSIP_RABIT	

ALIGNMENTS

RESULT 1
AL17_CARMA STANDARD; PRT; 8 AA.
ID AL17_CARMA
AC P81820:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINUSMAENAS 17.
OS Carclinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carclinus.
RN [1]
RP TISSUE=CEREBRAL GANGLION, AND THORACIC GANGLION;
RC MEDLINE: 98121193.
RX DUE H., JOHNSON A.H., MAESTRO J.-L., SCOTT A.G., JAROS P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carclinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
KW MOD.RES 8
KW SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;

Query Match 22.1%; Score 23; DB 1; Length 8;
Best local similarity 57.1%; Pred. No. 8.8e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 GOVKYGL 18
DB 2 GOVSFGL 8
RESULT 2
TAL3_PICJA STANDARD; PRT; 9 AA.
ID TAL3_PICJA
AC P17441:
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE TRANSALDOLASE III (EC 2.2.1.2) (PRAGMENT).
OS Pichia jadinii (Yeast) (Candida utilis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Pichia.
RN [1]
RP SEQUENCE.
RX MEDLINE: 75145197.
RX TSOLOS O., SUN S.C.;
RT "Isolation of a peptide containing a histidiny1-cysteiny1 sequence
RT from the active center of transaldolase.";
RL Arch. Biochem. Biophys. 167:525-533(1975).
CC -1- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF

Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 ITGERAMMLG 12

DB 5 ITGNTKRLIFG 15

RESULT 14

A49887 transcription factor HNF-3 beta - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 07-May-1999

C:Accession: A49887

R:Sasaki, H.; Hogan, B.L.M.

Cell 76, 103-115, 1994

A:Title: HNF-3beta as a regulator of floor plate development.

A:Reference number: A49887; MUID:94116056

A:Accession: A49887

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-15 <SAS>

C:Keywords: alternative initiators; alternative splicing; transcription factor

Query Match

21.2%; Score 22; DB 2; Length 15;

Best Local Similarity 55.6%; Pred. No. 2e+03;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 AMMLGOVK 15

DB 4 ASSMLGAVK 12

RESULT 15

S02455 DNA-Invertase - phage Mu (fragment)

C:Species: phage Mu

C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 16-Feb-1997

C:Accession: S02455

R:Klippel, A.; Mertens, G.; Patschinsky, T.; Kahmann, R.

EMBO J. 7, 1229-1237, 1988

A:Title: The DNA Invertase Gln of phage Mu: formation of a covalent complex with DNA via

A:Reference number: S02455; MUID:88296429

A:Accession: S02455

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-16 <KLI>

C:Genetics:

A:Gene: qin

C:Keywords: DNA binding

Query Match

21.2%; Score 22; DB 2; Length 16;

Best Local Similarity 57.1%; Pred. No. 2.1e+03;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 9 MLGOVK 15

DB 1 MLIGYVR 7

Search completed: December 21, 2000, 08:30:07
Job time: 271 sec

C:Keywords: oxidoreductase; tricarboxylic acid cycle

Query Match 22.1%; Score 23; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 GQVRYGL 18
||:|:|
Db 11 GQIGYAL 17

RESULT 9

B44835

dTDPglucose 4,6-dehydratase (EC 4.2.1.46) - Streptomyces peucetius (fragment)

C:Species: Streptomyces peucetius

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: B44835

R:Thompson, M.W.; Strohl, W.R.; Floss, H.G.

J. Gen. Microbiol. 138, 779-786, 1992

A:Title: Purification and characterization of TDP-D-glucose 4,6-dehydratase from anthrac

A:Reference number: A44835; MUID:92268857

A:Accession: B44835

A:Molecule type: protein

A:Residues: 1-20 <THO>

A:Cross-references: PIDN:AAB22196.1; PID:g249564

A:Experimental source: AMCC 29050

A>Note: sequence extracted from NCBI backbone (NCBIRP:103673)

C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 22.1%; Score 23; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 GQVRYGL 18
||:|:|
Db 14 GQIGYAL 20

RESULT 10

PH1338

Ig heavy chain DJ region (clone C372-115) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: PH1338

R:Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A:Reference number: PH1302; MUID:93094761

A:Accession: PH1338

A:Molecule type: DNA

A:Residues: 1-20 <MAS>

C:Keywords: heterodimer; immunoglobulin

Query Match 22.1%; Score 23; DB 2; Length 20;
Best Local Similarity 30.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 8 MMLGQVRYG 17
::|:|:|
Db 4 ILRIGLRYG 13

RESULT 11

JN0390

histamine-releasing peptide II - oriental hornet

N:Alternate names: venom protein HR-2

C:Species: Vespa orientalis (oriental hornet)

C>Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 23-Aug-1997

C:Accession: JN0390; S10919

R:Mirosnikov, A.I.; Snezhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozhnov, B.V.; Gus

Bioorg. Khim. 7, 1467-1477, 1981

A:Title: Structure and properties of histamine releasing peptides from the venom of V

A:Reference number: JN0389

A:Accession: JN0390

A:Molecule type: protein

A:Residues: 1-14 <MIR>

R:Tutubidav, M.U.; Akmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.

Biochemistry (N.Y.) 53, 183-190, 1988

A:Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis.

A:Reference number: S06445

A:Accession: S10919

A:Molecule type: protein

A:Residues: 1-14 <TVI>

C:Superfamily: crabrolin

C:Keywords: amidated carboxyl end; venom

F14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 21.2%; Score 22; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;

Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 9 MMLGQVRYGL 18
::|:|:|
Db 4 ILRIGLRYGL 13

RESULT 12

S72217

D-arabinose 1-dehydrogenase (NAD(P)+) (EC 1.1.1.117) - yeast (Candida albicans) (frag

C:Species: Candida albicans

C>Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 13-Mar-1998

C:Accession: S72217

R:Kim, S.T.; Huh, W.K.; Kim, J.Y.; Hwang, S.W.; Kang, S.O.

Biochim. Biophys. Acta 1297, 1-8, 1996

A:Title: D-arabinose dehydrogenase and biosynthesis of erythroascorbic acid in Candida

A:Reference number: S72217; MUID:96439039

A:Accession: S72217

A:Molecule type: protein

A:Residues: 1-14 <KIM>

C:Keywords: oxidoreductase

Query Match 21.2%; Score 22; DB 2; Length 14;
Best Local Similarity 30.8%; Pred. No. 1.8e+03;

Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 MMLGQVRYGLHN 20
||:|:|:|
Db 1 MKLATEIDFXLNN 13

RESULT 13

PH0797

T-cell receptor alpha chain (PR2.10.1 V-alpha-3.AR5) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PH0797

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility comple

allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846

A:Accession: PH0797

A:Molecule type: mRNA

A:Residues: 1-15 <CAS>

A:Cross-references: EMBL:X60903

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 21.2%; Score 22; DB 2; Length 15;
Best Local Similarity 36.4%; Pred. No. 2e+03;

RESULT 3
PC4213
bphB protein - Comamonas testosteroni (fragment)
C:Species: Comamonas testosteroni
C:Date: 17-Dec-1996 #sequence_revision 21-Jan-1997 #text_change 08-Oct-1999
C:Accession: PC4213
R: Sylvestre, M.; Strols, M.; Hurtubise, Y.; Bergeron, J.; Ahmad, D.; Shareck, F.; Barria
Gene 174, 195-202, 1996
A:Title: Sequencing of Comamonas testosteroni strain B-356-diphenyl/chlorobiphenyl dioxy
A:Reference number: JG4993; MUID:97043812
A:Accession: PC4213
A:Molecule type: DNA
A:Residues: 1-15 <STYL>
A:Cross-references: GB:U47637; NID:91245151; PIDN:ACC44530.1; PID:91245156
A:Experimental source: strain B-356
C:Genetics:
A:Gene: bphB

Query Match 23.1% Score 24; DB 2; Length 15;
Best Local Similarity 45.5% Pred. No. 9.1e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGEKAMMLG 12
||| |:
DB 3 LTGEVALLITGG 13

RESULT 4
PH1475
T-cell receptor beta chain (clone 223/5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1475
R: Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatih
A:Reference number: PH1430; MUID:93171821
A:Accession: PH1475
A:Molecule type: mRNA
A:Residues: 1-16 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Superfamily: Immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 23.1% Score 24; DB 2; Length 16;
Best Local Similarity 40.0% Pred. No. 9.8e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGEKAMMLG 12
||| |:
DB 7 TGERERLFRG 16

RESULT 5
A11497
transaldolase (EC 2.2.1.2) III - yeast (Pichia jadinii) (fragment)
C:Species: Pichia jadinii, Candida utilis
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 30-Sep-1993
C:Accession: A11497
R: Tsolas, O.; Sun, S.C.
Arch. Biochem. Biophys. 167, 525-533, 1975
A:Title: Isolation of a peptide containing a histidinyl-cysteiny sequence from the acti
A:Reference number: A11497; MUID:75145197
A:Accession: A11497
A:Molecule type: protein
A:Residues: 1-9 <TSC>
C:Keywords: transferase

Query Match 22.1% Score 23; DB 2; Length 9;
Best Local Similarity 75.0% Pred. No. 1.8e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 16 YGLH 19
||:|
DB 1 YGIIH 4

RESULT 6
S74147
glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C:Accession: S74147
R: Fukuda, A.; Osawa, T.; Mitomi, K.; Uchida, K.
Arch. Biochem. Biophys. 333, 419-426, 1996
A:Title: 4-Hydroxy-2-nonenal cytotoxicity in renal proximal tubular cells: protein mo
A:Reference number: S74147; MUID:96404942
A:Accession: S74147
A:Molecule type: protein
A:Residues: 1-10 <FRK>
A:Experimental source: LLC-PK1 cells (renal tubular epithelial cells)
C:Keywords: NAD; oxidoreductase

Query Match 22.1% Score 23; DB 2; Length 10;
Best Local Similarity 50.0% Pred. No. 8.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 GQVKYGLH 19
|:| |:
DB 1 GKVKGVGN 8

RESULT 7
S04961
malate dehydrogenase (EC 1.1.1.37) - Kladosporangium aridum (fragment)
C:Species: Kladosporangium aridum
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Aug-1994
C:Accession: S04961
R: Rommel, T.O.; Hund, H.K.; Speith, A.R.; Lingens, F.
Biol. Chem. Hoppe-Seyler 370, 763-768, 1989
A:Title: Purification and N-terminal amino-acid sequences of bacterial malate dehydro
A:Reference number: S04956; MUID:89374824
A:Accession: S04961
A:Molecule type: protein
A:Residues: 1-20 <ROM>
C:Superfamily: L-lactate dehydrogenase
C:Keywords: oxidoreductase; tricarboxylic acid cycle

Query Match 22.1% Score 23; DB 2; Length 20;
Best Local Similarity 57.1% Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 GQVKYGL 18
||:| |
DB 14 GQICVAL 20

RESULT 8
S04958
malate dehydrogenase (EC 1.1.1.37) - Microtetrastpora glauca (fragment)
C:Species: Microtetrastpora glauca
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Aug-1994
C:Accession: S04958
R: Rommel, T.O.; Hund, H.K.; Speith, A.R.; Lingens, F.
Biol. Chem. Hoppe-Seyler 370, 763-768, 1989
A:Title: Purification and N-terminal amino-acid sequences of bacterial malate dehydro
A:Reference number: S04956; MUID:89374824
A:Accession: S04958
A:Molecule type: protein
A:Residues: 1-20 <ROM>
C:Superfamily: L-lactate dehydrogenase

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:30:07 ; Search time 112.59 Seconds

(without alignments)
11.273 Million cell updates/sec

Title: US-08-934-367-13

Perfect score: 104

Sequence: 1 DITGEKAMMLGQVKYGLHN 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	25.0	18	2	152623
2	24	23.1	15	2	PA0091
3	24	23.1	15	2	PC4213
4	24	23.1	16	2	PH1475
5	23	22.1	9	2	PH1497
6	23	22.1	10	2	glucosyltransferase (EC
7	23	22.1	20	2	malate dehydrogenase
8	23	22.1	20	2	malate dehydrogenase
9	23	22.1	20	2	malate dehydrogenase
10	23	22.1	20	2	malate dehydrogenase
11	22	21.2	14	2	PH1338
12	22	21.2	14	2	PH1338
13	22	21.2	15	2	PH0797
14	22	21.2	15	2	PH0797
15	22	21.2	16	2	PH0797
16	22	21.2	16	2	PH0797
17	22	21.2	16	2	PH0797
18	22	21.2	16	2	PH0797
19	22	21.2	16	2	PH0797
20	22	21.2	16	2	PH0797
21	22	21.2	16	2	PH0797
22	22	21.2	16	2	PH0797
23	22	21.2	16	2	PH0797
24	22	21.2	16	2	PH0797
25	22	21.2	16	2	PH0797
26	22	21.2	16	2	PH0797
27	22	21.2	16	2	PH0797
28	22	21.2	16	2	PH0797
29	22	21.2	16	2	PH0797

30	20	19.2	13	2	PS0325	tetrahydroberberin
31	20	19.2	13	2	PH1772	T cell receptor al
32	20	19.2	14	2	PS0371	hypothetical prote
33	20	19.2	14	2	PH1332	Ig heavy chain DJ
34	20	19.2	15	2	S26791	Ig heavy chain V r
35	20	19.2	15	2	PI0143	carbon-monoxide de
36	20	19.2	15	2	A30330	neuropeptide pep -
37	20	19.2	15	2	PH1619	Ig H chain V-D-J r
38	20	19.2	15	2	PH0775	T-cell receptor al
39	20	19.2	15	2	PH0779	T-cell receptor al
40	20	19.2	15	2	PH1455	T-cell receptor al
41	20	19.2	18	2	A39997	group III allergen
42	20	19.2	19	2	S43637	hsp90 protein homo
43	20	19.2	20	2	S11416	ribosomal protein
44	19.5	18.8	15	2	PA0106	protein CP20076 -
45	19.5	18.8	19	2	A39504	octamer-binding pr

ALIGNMENTS

RESULT 1
152623
hypothetical protein TCR delta [imported] - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 20-Jun-2000
C:Accession: 152623
R:Przybylski, G.; Oettle, H.; Ludwig, W.D.; Siegfert, W.; Schmidt, C.A.
Br. J. Haematol. 87, 301-307, 1994
A:Title: Molecular characterization of illegitimate TCR delta gene rearrangements in
A:Reference number: 152623; MUID:95034253
A:Accession: 152623
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18 <RES>
A:Cross-references: GB:S73537; MID:9688155
A:Genetics:
A:Gene: TCRdelta

Query Match 25.0%; Score 26; DB 2; Length 18;
Best Local Similarity 41.2%; Pred. No. 5.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 8; Gaps 1;
OY 11 LGQVKY-----GLH 19
DB 1 LGQKKYSSYLWGTSVH 17
RESULT 2
PA0091
methionine adenosyltransferase (EC 2.5.1.6) 2 - fungus (Fusarium sporotrichoides) (f
C:Species: Fusarium sporotrichoides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-May-2000
R:Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Reference number: PA0051
A:Accession: PA0091
A:Molecule type: protein
A:Residues: 1-15 <CHO>
C:Keywords: S-adenosylmethionine; transferase
Query Match 23.1%; Score 24; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 9.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 3 TGEKAMMLG 12
DB 1 TTEKALEQLG 10

CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,
 CC which forms an amphipathic alpha-helix in presence of lipids. (A),
 CC optionally as a complex with lipids, and host cells that contain (A),
 CC are useful for gene therapy, or prevention, of diseases associated with
 CC dyslipidemia, specifically hypercholesterolemia, cardiovascular disease,
 CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I
 CC deficiency, hypertriglyceridemia and metabolic syndrome. also to treat
 CC endotoxemia (septic shock). Host cells containing (A) can also be used
 CC to study the role of apoA-I in lipid metabolism. (B) can be used
 CC diagnostically, e.g. to measure serum HDL (particularly its
 CC subpopulation involved in retrograde cholesterol transport) and for
 CC imaging the circulatory system or HDL accumulations at fatty streaks.
 CC The present sequence represents a peptide from the present invention.
 CC
 XX Sequence 22 AA:
 SO

Query Match 28.8%; Score 32; DB 20; Length 22;
 Best Local Similarity 58.3%; Pred. No. 94;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 11 EHLVDFLQSLG 22
 I I I I I I I I
 Db 7 erlleclllqaln 18

RESULT 14
 Y19320 standard; Peptide: 22 AA.
 Y19320:
 14-JUL-1999 (first entry)
 Lectin:cholesterol acyltransferase activation exhibiting peptide #133.
 Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
 human; lectin:cholesterol acyltransferase; LCAT; hypercholesterolemia;
 cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
 high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
 septic shock.
 OS Synthetic.
 OS Homo sapiens.
 PN MO9916459-A1.
 PD 08-APR-1999.
 PF 28-SEP-1998; 98MO-US20327.
 PR 29-SEP-1997; 97US-0940095.
 PA (BUTT/) BUTTNER K.
 PA (CORN/) CORNUT I.
 PA (DASS/) DASSEUX J.
 PA (DUFO/) DUFOURCO J.
 PA (METZ/) METZ G.
 PA (SEKU/) SEKUL R.
 PI Butner K, Cornut I, Dasseux J, Dufourcq J, Metz G;
 PI Sekul R;
 DR WPI: 1999-277035/23.
 XX Peptide agonists of apolipoprotein A-I
 PT
 PS Claim 19; Page 157; 280pp; English.
 XX The present invention describes an agonist (A) of apolipoprotein A-I
 CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
 CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
 CC complexes, are used to treat or prevent diseases associated with

CC dyslipidemia, specifically hypercholesterolemia, cardiovascular disease,
 CC atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
 CC deficiency; hypertriglyceridemia and metabolic syndrome, also for
 CC treating septic shock. When labeled, (A) can also be used diagnostically
 CC to measure serum levels of HDL, in particular the HDL subpopulation that
 CC is involved in retrograde cholesterol transport. also to image HDL at
 CC e.g. atherosclerotic streaks, and to raise antibodies. Y19188 to Y19441
 CC represent lectin:cholesterol acyltransferase (LCAT) activity
 CC exhibiting core peptides, which are apoA-I agonists.
 CC
 XX Sequence 22 AA:
 SO

Query Match 28.8%; Score 32; DB 20; Length 22;
 Best Local Similarity 58.3%; Pred. No. 94;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 11 EHLVDFLQSLG 22
 I I I I I I I I
 Db 7 erlleclllqaln 18

RESULT 15
 Y32796 standard; peptide: 12 AA.
 Y32796:
 09-NOV-1999 (first entry)
 Mammalian prolactin receptor derived polypeptide.
 Signal transduction; proteolytic cleavage; prolactin receptor;
 protein kinase binding site; muscle wasting; renal tubular defect; uraemia;
 diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin;
 growth hormone deficiency; inhibitor.
 OS Orcyolagus cuniculus.
 OS Rattus sp.
 OS Mus sp.
 PN EP943624-A1.
 PD 22-SEP-1999.
 PF 12-MAR-1998; 98EP-0200799.
 PR 12-MAR-1998; 98EP-0200799.
 PA (UYUT-) RIJKSUNIV UTRECHT.
 DR WPI: 1999-510568/43.
 XX Controlling the availability and/or signal transduction capability
 PT of a cell surface receptor, useful for treating growth hormone
 PT deficiencies
 PS Disclosure: Page 9; 36pp; English.
 XX This sequence is a polypeptide from the mammalian prolactin receptor.
 CC Sequences (Y32794-Y32823) are examples of polypeptide sequences found at
 CC or near the ubiquitin/proteasome complex binding site located on the
 CC intracellular part of a cell surface receptor. These sequences are used
 CC in a method for controlling the availability and signal transduction
 CC capability of a cell surface receptor by administering an inhibitor that
 CC is capable of inhibiting proteolytic cleavage of the receptor. Inhibition
 CC of this proteolytic cleavage results in the receptors being present on
 CC the surface for longer and therefore signalling for longer to the
 CC interior of the cell. This increases the sensitivity of cells to any
 CC hormones which might be present. The inhibitor is either derived from,
 CC competes with or binds to a polypeptide sequence of which sequences
 CC Y32794-Y32823 are examples. The inhibitor may be used to treat muscle
 CC wasting, associated with disorders such as renal tubular defects,

PA	(METZ/) METZ G.
PA	(SERU/) SERUL R.
XX	
XX	Buttner K, Cornut I, Dasseux J, Metz G, Sekul R;
PI	
XX	
XX	WPI: 1999-277034/23.
DR	
XX	
PT	Peptide agonists of apolipoprotein A-I
XX	
PS	Example: Page 114: 254pp: English.
XX	
CC	The present invention describes an agonist (A) of apolipoprotein A-I
CC	(apoA-I) which is a 15-29 residue peptide, or analog, that forms an
CC	amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC	complexes, are used to treat or prevent diseases associated with
CC	hyperlipidaemia, specifically hypercholesterolaemia, cardiovascular disease,
CC	atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
CC	deficiency: hypertriglyceridaemia and metabolic syndrome, also for
CC	treating septic shock. When labeled, (A) can also be used diagnostically
CC	to measure serum levels of HDL, in particular the HDL subpopulation that
CC	is involved in retrograde cholesterol transport, also to image HDL at
CC	e.g. atherosclerotic streaks, and to raise antibodies. Y18934 to Y19187
CC	represent lectin:cholesterol acyltransferase (LCAT) activity
CC	exhibiting core peptides, which are apoA-I agonists.
XX	
XX	
XX	Sequence 22 AA:

Query Match	28.8%	Score 32	DB 20	Length 22
Best Local Similarity	58.3%	Pred. No. 94		
Matches 7	Conservative 2	Mismatches 3	Indels 0	Gaps 0
QY	11 EHLTVDFLOSLS 22			
Db	7 erllledllqaln 18			
RESULT 12				
Y18812	Y18812 standard; Peptide; 22 AA.			
XX	Y18812:			
AC				
XX				
DT	09-JUL-1999 (first entry)			
XX				
DE	lecithin:cholesterol acyltransferase activation exhibiting peptide #133.			
XX				
KM	Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;			
KM	human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;			
KM	cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;			
KM	high density lipoprotein; hypertriglyceridemia; metabolic syndrome;			
KM	septic shock.			
XX				
XX	Synthetic.			
OS	Homo sapiens.			
XX				
PN	M09916408-A2.			
XX				
PD	08-APR-1999.			
XX				
PF	28-SEP-1998; 98WO-US20328.			
XX				
PR	29-SEP-1997; 97US-0940093.			
XX				
PA	(BUTY/) BUTNER K.			
PA	(CORN/) CORNUT I.			
PA	(DASS/) DASSEUX J.			
PA	(METZ/) METZ G.			
PA	(SEKU/) SEKUL R.			
XX				
PI	Butner K, Cornut I, Dasseux J, Metz G, Sekul R;			
XX				
WR	WPI: 1999-277031/23.			

XX	Peptide agonists of apolipoprotein A-I
PT	
XX	
PS	Example; Page 111, 152pp; English.
XX	
CC	The present invention describes an agonist (A) of apolipoprotein A-I
CC	(apoA-I) which is a 14-22 residue peptide, or analog, that forms an
CC	amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC	complexes, are used to treat or prevent diseases associated with
CC	dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC	atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
CC	deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC	treating septic shock. When labeled, (A) can also be used diagnostically
CC	to measure serum levels of HDL, in particular the HDL subpopulation that
CC	is involved in retrograde cholesterol transport, also to image HDL at
CC	e.g. atherosclerotic streaks, and to raise antibodies Y18660 to Y18933
CC	represent lectin:cholesterol acyltransferase (LCAT) activity
CC	exhibiting core peptides, which are apoA-I agonists.
XX	
XX	Sequence 22 AA:

Query Match	28.8%;	Score 32;	DB 20;	Length 22;
Best Local Similarity	58.3%;	Pred. No. 94;		
Matches 7;	Conservative	2;	Mismatches	3;
			Indels	0;
			Gaps	0;
QY	11 EHLTVDFLOSL	22		
Db	7 erllledllqain	18		
RESULT	13			
ID	Y18549			
XX	Y18549 standard; Peptide; 22 AA.			
AC	Y18549;			
DT	09-JUL-1999 (first entry)			
DE	lecithin:cholesterol acyltransferase activation exhibiting peptide #133.			
KM	Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder;			
KW	ApA-I; cardiovascular disease; atherosclerosis; restenosis; LCAT;			
XX	hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.			
OS	Synthetic.			
OS	Homo sapiens.			
PN	W09916409-A2.			
PD	08-APR-1999.			
PF	28-SEP-1998; 98WO-US20329.			
PR	29-SEP-1997; 97US-0940136.			
PA	(BUTT/) BUTTNER K.			
PA	(CORN/) CORNUT I.			
PA	(DASS/) DASSEUX J.			
PA	(DUFO/) DUFOURCO J.			
PA	(METZ/) METZ G.			
PA	(SEKU/) SEKUL R.			
PI	Burtner K, Cornut I, Dasseux J, Dufourcq J, Metz G;			
PI	Sekul R;			
XX				
DR	WPI; 1999-254921/21.			
PT	Nucleic acid encoding apolipoprotein A-I agonist peptides			
PS	Claim 18; Page 166; 232pp; English.			
CC	The present invention describes a nucleic acid (A) encoding an			

PR 17-NOV-1997; 97US-0066090.
 PR 17-NOV-1997; 97US-0066094.
 PR 17-NOV-1997; 97US-0066095.
 PR 17-NOV-1997; 97US-0066089.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Carter KC, Ebner R, Endress GA, Feng P, Janat F;
 PI Kyaw H, Lafleur DW, Moore PA, Ni J, Olsen HS, Rosen CA;
 PI Ruben SM, Shi Y, Soppet DR, Wei Y;
 XX
 DR WPI: 1999-337740/28.
 DR N-PSDB: X85016.
 XX
 PT New human secreted proteins and coding sequences useful for treating
 PT disorders of the immune system and hyperproliferative disorders
 PS
 PS Disclosure: Page 119; 507pp; English.
 XX
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. X84924) for increasing the stability of the fused protein
 CC as compared to the human protein only.
 CC The invention relates to 125 novel genes and their fragments (nucleic
 CC acid sequences: X84933-X85057; amino acid sequences Y27567-Y27933) which
 CC are useful for preventing, treating or ameliorating medical conditions
 CC e.g. by protein or gene therapy. Also, pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the 125 polynucleotides, based on
 CC which tissues they are most highly expressed in (see X84933 for described
 CC uses).
 XX
 SO Sequence 14 AA;
 XX
 Query Match 29.7%; Score 33; DB 20; Length 14;
 Best Local Similarity 61.5%; Pred. No. 40;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 10 PHLVDFLOSLS 22
 DB 1 phsrsvflqsls 13
 XX
 RESULT 10
 ID W65690 standard: peptide: 21 AA.
 AC W65690;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #34.
 XX
 KW microbial surface components recognising adhesive matrix molecule;
 KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 KW antibiotic; bacterial infection; antibiotic-resistant strain.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN W09831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US01222.
 XX
 PR 21-JAN-1997; 97US-0036139.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX

PI Hoeck M, House-pompeo KL, Joh D, Megavin MJ, Patti JM;
 PI Speziale P;
 XX
 DR WPI: 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial
 PT infection, especially by Staphylococci and Streptococci
 PS
 PS Example 8; Page 101; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding
 CC the isolated peptide of (1). Antibodies, the isolated peptides of
 CC (1) and the nucleic acids are all useful for immunisation (active or
 CC passive) and (by inhibiting binding of bacteria to fibronectin) for
 CC preventing or treating infection in humans or other animals, particularly
 CC by staphylococci or streptococci, e.g. meningitis, otitis media,
 CC pneumonia, endocarditis, mastitis in cattle, abortion in horses and many
 CC others. Since the antibodies block binding of bacteria, they should be
 CC effective against antibiotic-resistant strains, and may replace
 CC antibiotic therapy or increase its effectiveness. Sequences W65670-90
 CC represent a series of synthetic peptides based on the D3 repeat of
 CC S. aureus fibronectin binding protein A. They were synthesised to contain
 CC a proline residue at each position through the sequence (ie a proline
 CC scan).
 XX
 SO Sequence 21 AA;
 XX
 Query Match 28.8%; Score 32; DB 19; Length 21;
 Best Local Similarity 54.5%; Pred. No. 90;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 7 FGPEHLVDF 17
 DB 4 Yqfpphmsvdf 14
 XX
 RESULT 11
 ID Y19066 standard: peptide: 22 AA.
 AC Y19066;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #133.
 XX
 KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
 KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
 KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
 KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
 KW septic shock.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09916458-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 28-SEP-1998; 98WO-US20326.
 XX
 PR 29-SEP-1997; 97US-0940096.
 XX
 PA (BUTN/) BUTTNER K.
 PA (CORN/) CORNUT I.
 PA (DASS/) DASSEUX J.

PI Mark DF, Creasey AA;
 XX WPI: 1983-723186/30.
 DR N-PSDB: N30158.
 XX
 PT Multi-class hybrid interferon poly:peptide(s) - with restricted
 PT antiviral and cell growth regulatory activities
 XX
 XX Example: Fig 17: 61pp; English.
 PS
 CC The inventors claim a multiclass hybrid interferon polypeptide and a
 CC DNA unit having a nucleotide sequence which encodes it. Pref. the
 CC AA sequence consists of alpha and beta interferons. Pref. IF1 is
 CC (1) the 1-73 AA seq. of HuIFN-alpha-1 (and IF2 is the 74-166 AA seq.
 CC of HuIFN-alpha-1) (see N30155, P30222); or (ii) the 1-41 AA seq. of
 CC HuIFN-alpha-61A (and IF2 is the 43-166 AA seq. of HuIFN-beta-1) (see
 CC N30160, P30227). Alternatively IF1 is the amino terminal end of a
 CC beta-IF and IF2 is the carboxy terminal of an alpha-IF (esp. the
 CC 1-73 seq. of HuIFN-beta-1 and the 74-167 seq. of HuIFN-alpha-1
 CC resp.) (see N30156, P30223). In the examples plasmids pGM5 and
 CC pDM101/crip/beta-1 and p-alpha-61A were used (see N30151, N30152,
 CC N30157). Hint1 was used to digest the DNA sequences in the region
 CC of significant handicaps (see N30153, N30154, N30158, N30159), and
 CC the restriction fragments were ligated to form hybrid DNA.
 CC
 SQ Sequence 12 AA:
 XX
 OY 6 DEGPPE 11
 DB 2 dfgrpq 7
 XX
 RESULT 8
 ID P80053 standard; protein; 12 AA.
 AC P80053;
 XX
 DT 17-NOV-1990 (first entry)
 DE Sequence of human interferon (huIFN) alpha-61A gene around AA 40.
 XX
 KM Alpha-beta hybrid interferon: multi-class hybrid interferon:
 KM antitumour; antiviral; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 7 /note="Residue 40"
 XX
 PN US4758428-A.
 PD 19-JUL-1988.
 XX
 PF 15-JUL-1985; 85US-0755265.
 XX
 PR 15-JUL-1985; 85US-0755265.
 PR 19-JAN-1983; 83CA-0419758.
 XX
 PA (CETU) CETUS CORP.
 XX
 PI Mark DF, Creasey AA;
 XX WPI: 1988-219882/31.
 DR N-PSDB: n80050.
 XX
 PT Multi-class hybrid interferon poly:peptide(s) -

PT having sequence from interferon-alpha-1 and sequence from
 PT interferon-beta-1 for restricted activity
 XX
 XX Example: Fig 17: 24pp; English.
 PS
 CC Multi-class hybrid IFN polypeptides having an AA sequence composed
 CC of 2 distinct subsequences are claimed. The plasmids used in the
 CC construction of huIFN-alpha-61A-beta-1 hybrid are plasmids palpa61A and
 CC pDM101/crip/beta-1. Assembly of the palpa61A plasmid involved replacing
 CC the DNA fragment encoding the 23 AA signal polypeptide of preinterferon
 CC with a 120BP EcoRI/Sau3A promoter fragment E. coli trp promoter, operator,
 CC and trp leader ribosome binding site preoperator, encoding an Arg
 CC initiation codon and using HindIII site that was inserted, 59 nucleotides
 CC 3'-end of the TGA translational stop codon, to insert the gene into the
 CC plasmid pBM11 (a deriv of pBR322 having a deletion between the HindIII
 CC and PvuII sites). The complete DNA sequence of the promoter and gene
 CC fragments inserted between the EcoRI and HindIII sites of pBM11 is shown
 CC in n80049. The hybrid gene was constructed by taking advantage of the
 CC homologues between huIFN-alpha-61A & huIFN beta-1 at around AA 40 of both
 CC proteins. The DNA sequence 5'-proximal to the DdeI restriction enzyme
 CC cutting site of the huIFN alpha-61A DNA is ligated to the DNA sequence
 CC 3'-proximal to the site of huIFN beta-1, to create a fusion of the
 CC two genes while preserving the translational reading frame of both.
 CC
 SQ Sequence 12 AA:
 XX
 OY 6 DEGPPE 11
 DB 2 dfgrpq 7
 XX
 RESULT 9
 ID Y27814 standard; protein; 14 AA.
 AC Y27814;
 XX
 DT 30-JUL-1999 (first entry)
 DE Human secreted protein encoded by gene No. 84.
 XX
 DE Human secreted protein encoded by gene No. 84.
 XX
 KM Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KM diagnosis; lissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KM developmental abnormality; foetal deficiency; blood; allergy; renal;
 KM immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KM inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 XX
 PN W09924836-A1.
 PD 20-MAY-1999.
 XX
 PF 04-NOV-1998; 98MO-US23435.
 XX
 PR 17-NOV-1997; 97US-0066100.
 PR 07-NOV-1997; 97US-0064900.
 PR 07-NOV-1997; 97US-0064908.
 PR 07-NOV-1997; 97US-0064911.
 PR 07-NOV-1997; 97US-0064912.
 PR 07-NOV-1997; 97US-0064983.
 PR 07-NOV-1997; 97US-0064984.
 PR 07-NOV-1997; 97US-0064985.
 PR 07-NOV-1997; 97US-0064987.
 PR 07-NOV-1997; 97US-0064988.

CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration); for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target antigen.
 CC Th can replace carrier proteins and pathogen-derived T helper epitopes.
 CC Sequence Y91121 represents a promiscuous T helper epitope from the
 CC measles virus F (MVF) protein and sequences Y91122-Y91142, Y91226 and
 CC Y91245-Y91246 represent synthetic Th epitopes based on the MVF Th
 CC epitope. Sequence Y91143 represents a promiscuous Th epitope from
 CC hepatitis B virus (HBV) surface antigen, and sequences Y91144-Y91155 are
 CC synthetic epitopes derived from this HBV epitope. Y91156-Y91196,
 CC Y91227 and Y91242-Y91244 are antigenic peptides comprising an LHRH
 CC sequence joined to a promiscuous Th epitope. Y91197 is the LHRH target
 CC antigenic peptide used in these LHRH antigenic peptides. Y91200 is
 CC somatostatin, and Y91201-Y91207 are antigenic peptides comprising
 CC somatostatin and a Th epitope. Somatostatin immunogens may be used
 CC to promote growth in livestock. Y91208 is a human CD4 CDR2-like domain
 CC antigenic site, and Y91209-Y90211 are MVH Th epitope/CD4 CDR2
 CC antigenic peptides which may be used to prevent HIV infection of T
 CC cells. Y90212 is a modified version of a human Ige (immunoglobulin
 CC E) CH3 domain, and Y90213-Y90219 are Th epitope/Ige CH3 antigenic
 CC peptides which may be used in the treatment of allergies. Y91220 is
 CC a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid
 CC protein and Y91221-Y91222 comprise this peptide and a Th epitope. Y91223
 CC is a Plasmodium falciparum circumsporozoite (CS) target antigen, and
 CC Y91224-Y91225 comprise the CS antigen and an MVF Th epitope and may be
 CC used in a malaria vaccine. Y91228-Y91231 represent CETP-derived peptides
 CC and Y91332-Y91341 are immunogens comprising a CETP peptide and a Th
 CC epitope which may be used to prevent or treat arteriosclerosis and
 CC cardiovascular disease. Y91247 and Y91252-Y91257 are HIV-1 neutralising
 CC B-cell epitopes, and Y91248-Y91251 and Y91258-Y91273 are antigenic
 CC peptides comprising MVH Th and HIV-1 B-cell epitope which may be used as
 CC a component in an anti-HIV-1 vaccine. Y91198 and Y91199 are respectively
 CC an immunostimulatory invasion protein epitope from *Yersinia* species, and
 CC hinge spacer peptide, both of which may optionally be used in the
 CC antigenic peptides of the invention.

CC Sequence 16 AA:

Query Match 71.2%; Score 79; DB 21; Length 16;
 Best Local Similarity 93.8%; Pred. No. 3.5e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FGPEHLVDFLOSL 22
 |||||:|||||||
 Db 1 fgfpkhlvdflls 16

RESULT 6
 W24294
 ID W24294 standard; peptide: 11 AA.

AC W24294;

DT 17-OCT-1997 (first entry)

DE Human/Rabbit CETP common peptide.

KW Immune response: high density lipoprotein; HDL; cholesterol; human;

KM serum; epitope; cholesterol ester transfer protein; CETP; rabbit.

OS *Oryctolagus cuniculus*.

OS *Homo sapiens*.

XX

PN W09639168-A1.

XX 12-DEC-1996.

PD 05-JUN-1996; 96WO-US09143.

PF 06-JUN-1995; 95US-0482454.

PR (IMMU-) IMMUNE RESPONSE CORP.

PI Brostoff SW, Carlo DJ, Kwoh DY;

XX WPI; 1997-042849/04.

PT Stimulating an immune response to increase high density lipoprotein

PT - avoids repeated administration of toxic drugs to lower cholesterol

PT ester transfer protein levels

XX Claim 5; Page 16; 26pp; English.

CC The sequences given in W24292-94 were used in the method of the

CC invention to stimulate an immune response to increase high density

CC lipoprotein (HDL) cholesterol in a mammal exhibiting low levels of

CC serum HDL. These peptides represent immunogenic epitopes of

CC cholesterol ester transfer protein (CETP). The method utilizes

CC the body's own immune system to lower CETP levels, thereby increasing

CC the level of beneficial HDL cholesterol, preferably in serum. The

CC method avoids the problems associated with the repeated administration

CC of drugs which have undesirable side effects. This peptide represents

CC a region of CETP which is common to both human and rabbit proteins.

SQ Sequence 11 AA:

Query Match 47.7%; Score 53; DB 18; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 HLIVDFLOSL 22
 |||||:|||||
 Db 1 hlivdflls 11

RESULT 7
 P30225
 ID P30225 standard; Protein: 12 AA.

AC P30225;

DT 25-MAY-1992 (first entry)

DE Sequence of Interferon (HuIFN) -alpha-61A around amino acid 40.

KW Hybrid Interferon; antiviral; therapy; cancer; tumour.

OS *Homo sapiens*.

XX Key Location/Qualifiers

FT Misc-difference 7 /label= AA No. 40

XX W08302461-A.

XX 21-JUL-1983.

PD 18-JAN-1983; 83WO-0900607.

PR 19-JAN-1982; 82US-0340782.

PR 03-FEB-1983; 83US-0463574.

PR 15-JUL-1985; 85US-0755265.

PA (CETU-) CETUS CORP.

XX

Y91229
ID Y91229 standard; peptide; 16 AA.
XX
AC Y91229;
XX
DT 22-MAY-2000 (first entry)
XX
DE Human cholesterol transport protein (CERP) peptide, SEQ ID NO:107.
XX
KW Promiscuous T-cell epitope; measles virus F protein; MVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW luteinizing hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
KW cholesterol ester transport protein; anti-arteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US13975.
XX
PR 20-JUN-1998; 98US-0100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI: 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus
XX
PS Claim 10; Page 50; 129pp; English.
XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesterol ester transport
CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinizing hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration; for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target antigen.
CC Th can replace carrier proteins and pathogen-derived T helper epitopes.
CC Sequence Y91121 represents a promiscuous T helper epitope from the
CC measles virus F (MVF) protein and sequences Y91122-Y91142, Y91226 and
CC Y91245-Y91246 represent synthetic Th epitopes based on the MVF Th
CC epitope. Sequence Y91143 represents a promiscuous Th epitope from
CC hepatitis B virus (HBV) surface antigen, and sequences Y91144-Y91155 are
CC synthetic epitopes derived from this HBV epitope. Y91156-Y91196,
CC Y91227 and Y91242-Y91244 are antigenic peptides comprising an LHRH
CC sequence joined to a promiscuous Th epitope. Y91197 is the LHRH target
CC antigenic peptide used in these LHRH antigenic peptides. Y91200 is
CC somatostatin, and Y91201-Y91207 are antigenic peptides comprising
CC somatostatin and a Th epitope. Somatostatin immunogens may be used
CC to promote growth in livestock. Y91208 is a human CD4/CD2-1-like domain
CC antigenic site, and Y91209-Y90211 are MVA Th epitope/CD4 CD2
CC antigenic peptides which may be used to prevent HIV infection of T
CC cells. Y90212 is a modified version of a human IGE (immunoglobulin
CC E) CH3 domain, and Y90213-Y90219 are Th epitope/IgE CH3 antigenic

CC peptides which may be used in the treatment of allergies. Y91220 is
CC a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid
CC protein and Y91221-Y91222 comprise this peptide and a Th epitope. Y91223
CC is a Plasmodium falciparum circumsporozoite (CS) target antigen, and
CC Y91224-Y91225 comprise the CS antigen and an MVA Th epitope and may be
CC used in a malaria vaccine. Y91228-Y91231 represent CERP-derived peptides
CC and Y91232-Y91241 are immunogens comprising a CERP peptide and a Th
CC epitope which may be used to prevent or treat arteriosclerosis and
CC cardiovascular disease. Y91247 and Y91252-Y91257 are HIV-1 neutralising
CC B-cell epitopes, and Y91248-Y91251 and Y91258-Y91273 are antigenic
CC peptides comprising MVA Th and HIV-1 B-cell epitope which may be used as
CC an immunostimulatory invasive protein epitope from Yersinia species, and
CC hinge spacer peptide, both of which may optionally be used in the
CC antigenic peptides of the invention.
XX
SQ Sequence 16 AA:
XX
Query Match 74.8%; Score 83; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 EGFPEHLVDFLOSL 22
Db 1 fgfpehlvdfqls 16
RESULT 5
Y91230
ID Y91230 standard; peptide; 16 AA.
XX
AC Y91230;
XX
DT 22-MAY-2000 (first entry)
XX
DE Human cholesterol transport protein (CERP) peptide, SEQ ID NO:108.
XX
KW Promiscuous T-cell epitope; measles virus F protein; MVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW luteinizing hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
KW cholesterol ester transport protein; anti-arteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US13975.
XX
PR 20-JUN-1998; 98US-0100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI: 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus
XX
PS Claim 10; Page 62; 129pp; English.
XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesterol ester transport

CC This sequence represents an immunogenic fragment of the rabbit
 CC cholesterol ester transferase protein (CETP).
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CETP, which can be used for producing antibodies to lessen the
 CC transfer of cholesterol esters from high density lipoprotein (HDL). The
 CC method can provide an autogenic immunological process for lessening the
 CC transfer of cholesterol esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CETP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.

CC Sequence 22 AA:

Query Match 100.0%; Score 111; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLQMDGFPPEHLVDFLOSLS 22
 Db 1 lllqmdgfppehlvdflosls 22

RESULT 2
 Y13821

ID Y13821 standard; peptide: 22 AA.

AC Y13821;

DT 08-JUL-1999 (first entry)

XX Human CETP immunogenic fragment.

CC CETP: cholesterol-ester transfer protein; recombinant DNA vaccine; HDL;
 CC antibody production; cholesterol ester transfer; therapy;
 CC high density lipoprotein; HDL cholesterol concentration;
 CC pro-atherogenic dyslipoproteinaemia.

XX Homo sapiens.

XX WO915655-A1.

PD 01-APR-1999.

PF 17-SEP-1998; 98WO-US19366.

PR 19-SEP-1997; 97US-0934367.

PA (MONS) MONSANTO CO.

PI Glenn K, Needleman P;

DR WPI, 1999-276984/23.

XX New recombinant DNA vaccines

XX Disclosure: Page 88; 99pp; English.

CC This sequence represents an immunogenic fragment of the human
 CC cholesterol ester transferase protein (CETP).
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CETP, which can be used for producing antibodies to lessen the
 CC transfer of cholesterol esters from high density lipoprotein (HDL). The
 CC method can provide an autogenic immunological process for lessening the
 CC transfer of cholesterol esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CETP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.

SQ Sequence 22 AA:

Query Match 100.0%; Score 111; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLQMDGFPPEHLVDFLOSLS 22
 Db 1 lllqmdgfppehlvdflosls 22

RESULT 3

Y13809

ID Y13809 standard; peptide: 22 AA.

AC Y13809;

DT 08-JUL-1999 (first entry)

XX Rabbit CETP immunogenic fragment.

CC CETP: cholesterol-ester transfer protein; recombinant DNA vaccine; HDL;
 CC antibody production; cholesterol ester transfer; therapy;
 CC high density lipoprotein; HDL cholesterol concentration;
 CC pro-atherogenic dyslipoproteinaemia.

XX Oryctolagus sp.

XX WO915655-A1.

PD 01-APR-1999.

PF 17-SEP-1998; 98WO-US19366.

PR 19-SEP-1997; 97US-0934367.

PA (MONS) MONSANTO CO.

PI Glenn K, Needleman P;

DR WPI, 1999-276984/23.

XX New recombinant DNA vaccines

XX Example 1; Page 73; 99pp; English.

CC This sequence represents an immunogenic fragment of the rabbit
 CC cholesterol ester transferase protein (CETP).
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CETP, which can be used for producing antibodies to lessen the
 CC transfer of cholesterol esters from high density lipoprotein (HDL). The
 CC method can provide an autogenic immunological process for lessening the
 CC transfer of cholesterol esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CETP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.

XX Sequence 22 AA:

Query Match 96.4%; Score 107; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 2.3e-10;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLQMDGFPPEHLVDFLOSLS 22
 Db 1 lllqmdgfppehlvdflosls 22

RESULT 4

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2000, 08:36:12 ; Search time 34.96 Seconds
(without alignments)
21.518 Million cell updates/sec

Title: US-08-934-367-10
Perfect score: 111
Sequence: 1 ILIQMDFGFPEHLVDFLQSLT 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 134459

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:*
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- 11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT:*
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- 18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	111	100.0	22	20	Y13815
2	111	100.0	22	20	Y13821
3	107	96.4	22	20	Y13809
4	83	74.8	16	21	Y91229
5	79	71.2	16	21	Y91230
6	53	47.7	11	18	W24294
7	33	29.7	12	4	P30225
8	33	29.7	12	9	P80053
9	33	29.7	14	20	Y27814
10	32	28.8	21	19	W65690
11	32	28.8	22	20	Y19066
12	32	28.8	22	20	Y18812

13	32	28.8	22	20	Y18549	Lecithin:cholester
14	32	28.8	22	20	Y19320	Lecithin:cholester
15	31	27.9	12	20	Y32796	Mammalian prolacti
16	31	27.9	21	19	W65666	Fibronectin bindin
17	31	27.9	22	19	W65669	Peptide #13. Sync
18	30	27.0	20	15	R61276	Transactivating pr
19	30	27.0	20	19	W41190	Tax protein fragme
20	30	27.0	22	17	R95899	Fragment #4 of 7-a
21	29	26.1	11	20	W99442	Interleukin-2 rece
22	29	26.1	11	21	Y82915	Peptide exhibiting
23	29	26.1	13	18	W10883	MAB anti-HBsAg bin
24	29	26.1	19	16	W13199	Fragment of p53 bl
25	29	26.1	19	19	W57353	Human WBPI immunog
26	29	26.1	20	16	R72269	Glutamic acid deca
27	29	26.1	20	21	Y59570	GAD65 fragment, pe
28	29	26.1	21	21	Y69793	Human interleukin-
29	28	25.2	9	19	W72564	Dengue virus type-
30	28	25.2	10	15	Y38102	Hepatitis B virus-
31	28	25.2	10	20	Y45670	Immunogenic peptid
32	28	25.2	13	19	W62713	Streptococcus pneu
33	28	25.2	14	13	R21617	Sequence encoded b
34	28	25.2	15	19	W45817	Peptide recognised
35	28	25.2	15	19	W45612	Peptide recognised
36	28	25.2	21	18	W38080	PPPY motif contal
37	28	25.2	22	20	Y19067	Lecithin:cholester
38	28	25.2	22	20	Y18813	Lecithin:cholester
39	28	25.2	22	20	Y18550	Lecithin:cholester
40	28	25.2	22	20	Y19321	Lecithin:cholester
41	28	25.2	22	20	W96827	Nucleic acid bindi
42	27.5	24.8	16	17	R98414	Interferon-gamma r
43	27	24.3	9	17	R88341	Adenomatous polypo
44	27	24.3	12	16	R78515	Synthetic HTLV pep
45	27	24.3	12	18	W28864	HTLV-1 derived pep

ALIGNMENTS

RESULT	1
Y13815	Y13815 standard; peptide; 22 AA.
XX	XX
AC	Y13815;
XX	XX
DT	08-JUL-1999 (first entry)
XX	XX
DE	Rabbit CERP immunogenic fragment.
XX	XX
KW	CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
KW	antibody production; cholesteryl ester transfer; therapy;
KW	high density lipoprotein; HDL cholesterol concentration;
KW	pro-atherogenic dyslipoproteinaemia.
XX	XX
OS	Oryctolagus sp.
XX	XX
PN	W09915655-A1.
XX	XX
PD	01-APR-1999.
XX	XX
PF	17-SEP-1998; 98WO-US19366.
XX	XX
PR	19-SEP-1997; 97US-0934367.
XX	XX
PA	(MONS) MONSANTO CO.
XX	XX
PI	Glenn K, Needleman P;
XX	XX
DR	WPI; 1999-276984/23.
XX	XX
PT	New recombinant DNA vaccines
XX	XX
PS	Disclosure; Page 75; 99pp; English.
XX	XX

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 5 EKAMMLGOVK 15
 ||| ||::|
 Db 2 EKAKKLEELK 12

RESULT 15
 5304631-16
 ; Patent No. 5304631
 ; APPLICANT: STEWART, JOHN M.; HAHN, KARL W.; KLIS, WIESLAW A.
 ; TITLE OF INVENTION: SYNTHETIC HELIOTYPE ENZYMES
 ; NUMBER OF SEQUENCES: 16
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/464,932
 ; FILING DATE: 16-JAN-1990
 ; SEQ ID NO:16:
 ; LENGTH: 15
 5304631-16

Query Match 25.0%; Score 26; DB 5; Length 15;
 Best Local Similarity 54.5%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 5 EKAMMLGOVK 15
 ||| ||::|
 Db 2 EKAKKLEELK 12

Search completed: December 21, 2000, 08:31:50
 Job time: 373 sec

Query Match 25.0%: Score 26; DB 4; Length 13;
Best Local Similarity 100.0%: Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DITGE 5
11111
Db 7 DITGE 11

RESULT 12
US-08-484-905-28

; Sequence 28, Application US/08484905
; Patent No. 5976551

; GENERAL INFORMATION:

; APPLICANT: Mottez, Estelle

; APPLICANT: Abastado, Jean-Pierre

; APPLICANT: Kourilsky, Philippe

; TITLE OF INVENTION: An Altered Major Histocompatibility

; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the

; NUMBER OF SEQUENCES: 127

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/484,905

; FILING DATE: 07-JUNE-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/801,818

; FILING DATE: 05-DEC-1991

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/792,473

; FILING DATE: 15-NOV-1991

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Potter, Jane E. R.

; REGISTRATION NUMBER: 33,332

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-484-905-28

; Patent No. 6011146

; GENERAL INFORMATION:

; APPLICANT: Mottez, Estelle

; APPLICANT: Abastado, Jean-Pierre

; APPLICANT: Kourilsky, Philippe

; TITLE OF INVENTION: Altered Major Histocompatibility Complex

; TITLE OF INVENTION:

; NUMBER OF SEQUENCES: 148

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/481,985B

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/801,818

; FILING DATE: 05-DEC-1991

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/792,473

; FILING DATE: 15-NOV-1991

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-481-985B-28

Query Match 25.0%: Score 26; DB 3; Length 15;
Best Local Similarity 38.5%: Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 3 TSEGCROIIGOLQ 15
11111
Db 3 TSEGCROIIGOLQ 15

RESULT 14
5304631-8

; Patent No. 5304631

; APPLICANT: STEWART, JOHN M.; HAHN, KARL W.; KLIS, WIESLAW A.

; TITLE OF INVENTION: SYNTHETIC HELIZYME ENZYMES

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/464,932

; FILING DATE: 16-JAN-1990

; SEQ ID NO: 8;

; LENGTH: 15

Query Match 25.0%: Score 26; DB 5; Length 15;
Best Local Similarity 54.5%: Pred. No. 1.6e+02;

RESULT 13
US-08-481-985B-28
; Sequence 28, Application US/08481985B

OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/920,430
FILING DATE: 19920731
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/796,256
FILING DATE: 20 NOV 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/767,251
FILING DATE: 27 SEPT 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/659,975
FILING DATE: 22 FEB 1991
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 79-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-920-430-3

Query Match 25.0%: Score 26; DB 1; Length 13;
Best Local Similarity 100.0%: Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DITGE 5
Db 7 DITGE 11

RESULT 10
US-08-251-464-3
Sequence 3, Application US/08251464
Patent No. 5723747
GENERAL INFORMATION:
APPLICANT: Lassner, Michael
APPLICANT: Metz, James
TITLE OF INVENTION: WAX ESTERS IN TRANSFORMED PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/251,464
FILING DATE: 01-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler

REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-251-464-3

Query Match 25.0%: Score 26; DB 1; Length 13;
Best Local Similarity 100.0%: Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DITGE 5
Db 7 DITGE 11

RESULT 11
PCT-US92-01364-3
Sequence 3, Application PC/TUS9201364
GENERAL INFORMATION:
APPLICANT: Calgene, Inc.
TITLE OF INVENTION: Fatty Acyl Reductase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/01364
FILING DATE: 19920212
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/659,975
FILING DATE: 22 FEB 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/767,251
FILING DATE: 27 SEPT 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/796,256
FILING DATE: 20 NOV 1991
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE79-2WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-01364-3

MOLECULE TYPE: peptide
US-08-355-888A-25

Query Match 26.0%; Score 27; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVRYGL 18
I:::|
DB 3 QIRYGL 8

RESULT 7
US-08-693-697-25

Sequence 25, Application US/08693697
Patent No. 5869610
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,697
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0037-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-693-697-25

Query Match 26.0%; Score 27; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVRYGL 18
I:::|
DB 3 QIRYGL 8

RESULT 8
US-08-693-696-25
Sequence 25, Application US/08693696
Patent No. 6005080
GENERAL INFORMATION:

APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,696
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/355,888
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-693-696-25

Query Match 26.0%; Score 27; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVRYGL 18
I:::|
DB 3 QIRYGL 8

RESULT 9
US-07-920-430-3
Sequence 3, Application US/07920430
Patent No. 5370996
GENERAL INFORMATION:
APPLICANT: James George Metz
APPLICANT: Michael Roman Pollard
APPLICANT: Michael W. Lassner
TITLE OF INVENTION: Fatty Acyl Reductases
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh

FILING DATE: 06-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/689,807
FILING DATE: 14-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537,400
FILING DATE: 02-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/370,190
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,423
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,759
FILING DATE: 21-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537,397
FILING DATE: 02-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/525,057
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.2800005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-706-706-21

Query Match 26.0%; Score 27; DB 3; Length 10;
Best Local Similarity 62.5%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 ITGERKAM 9
|||:|:
Db 3 ITGDKDML 10

RESULT 5
US-08-306-231-9
Sequence 9, Application US/08306231
Patent No. 5643748
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,231
FILING DATE: 14-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-076
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-306-231-9

Query Match 26.0%; Score 27; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 13 QVRYGL 18
||:||||
Db 3 QIRYGL 8

RESULT 6
US-08-355-888A-25
Sequence 25, Application US/08355888A
Patent No. 5763211
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/355,888A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown

OY 14 VKYGLHN 20
11:11
DB 3 VKHGSJN 9

RESULT 2
US-08-159-340A-17
Sequence 17, Application US/08159340A
Patent No. 5565352

GENERAL INFORMATION:

APPLICANT: Hochstrasser, Mark

APPLICANT: Papa, Feroz

TITLE OF INVENTION: DEUBIQUITINATING ENZYME: COMPOSITIONS

TITLE OF INVENTION: AND METHODS

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/159,340A

FILING DATE: 24-NOV-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: ARCD:112/HYL

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-159-340A-17

Query Match 27.9%; Score 29; DB 1; Length 14;

Best Local Similarity 71.4%; Pred. No. 44;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 14 VKYGLHN 20
11:11
DB 8 VKHGSJN 14

RESULT 3
US-08-706-702-21

Sequence 21, Application US/08706702

Patent No. 5948614

GENERAL INFORMATION:

APPLICANT: Chatterjee, Deb K.

TITLE OF INVENTION: Cloned DNA Polymerases from Thermotoga

TITLE OF INVENTION: maritima and Mutants Thereof

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/706,702

FILING DATE: 06-SEP-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/689,807

FILING DATE: 14-AUG-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/537,400

FILING DATE: 02-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/576,759

FILING DATE: 21-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/537,397

FILING DATE: 02-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/525,057

FILING DATE: 08-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0942.2800006

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2540

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

US-08-706-702-21

Query Match 26.0%; Score 27; DB 2; Length 10;

Best Local Similarity 62.5%; Pred. No. 68;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ITGKXMM 9
11:11
DB 3 ITGDKDML 10

RESULT 4
US-08-706-706-21

Sequence 21, Application US/08706706

Patent No. 6015668

GENERAL INFORMATION:

APPLICANT: Hughes, A. John

TITLE OF INVENTION: Chatterjee, Deb K.

TITLE OF INVENTION: Cloned DNA Polymerases from Thermotoga and

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/706,706

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:31:49 ; Search time 99.91 Seconds

(Without alignments)
3.355 Million cell updates/sec

Title: US-08-934-367-13

Sequence: 1 DTGKAMLLGOVKYGLHN 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 1676186 residues

Total number of hits satisfying chosen parameters: 87906

Minimum DB seq length: 0
Maximum DB seq length: 20Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

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- 2: /cgn2_6/ptodata/2/1aa/5B-COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6-COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/PCrUS-COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	27.9	12	1	US-08-164-618-20
2	27.9	14	1	US-08-159-340A-17
3	27.9	10	2	US-08-706-702-21
4	27.9	10	3	US-08-706-706-21
5	27.9	13	1	US-08-306-231-9
6	27.9	13	1	US-08-355-888A-25
7	27.9	13	2	US-08-693-697-25
8	27.9	13	3	US-08-693-696-25
9	27.9	13	1	US-07-920-430-3
10	27.9	13	1	US-08-251-464-3
11	27.9	13	4	PCT-US92-01364-3
12	27.9	15	2	US-08-484-905-28
13	27.9	15	3	US-08-481-985B-28
14	27.9	15	5	5304631-8
15	27.9	15	5	5304631-16
16	27.9	17	5	US-08-182-067-14
17	27.9	17	5	US-08-465-313-14
18	27.9	17	5	5304631-5
19	27.9	20	2	US-08-466-975A-12
20	27.9	20	2	US-08-466-975A-13
21	27.9	20	2	US-08-391-671A-12
22	27.9	20	2	US-08-391-671A-13
23	27.9	20	2	US-08-475-634D-2
24	27.9	20	3	US-08-467-902A-12
25	27.9	20	3	US-08-467-902A-13
26	27.9	15	2	US-08-480-190-77
27	27.9	15	2	US-08-488-379-77
28	27.9	15	4	PCr-US93-07545-77

29	25	24.0	16	2	US-08-480-190-76	Sequence 76, Appl
30	25	24.0	16	2	US-08-488-379-76	Sequence 76, Appl
31	25	24.0	16	4	PCT-US93-07545-76	Sequence 76, Appl
32	25	24.0	17	1	US-07-884-212A-3	Sequence 3, Appl1
33	25	24.0	18	1	US-07-893-928A-3	Sequence 3, Appl1
34	25	24.0	18	2	US-08-480-190-192	Sequence 192, App
35	25	24.0	18	2	US-08-488-379-192	Sequence 192, App
36	25	24.0	18	4	PCT-US93-07545-192	Sequence 192, App
37	25	24.0	19	2	US-08-480-190-74	Sequence 74, Appl
38	25	24.0	19	2	US-08-480-190-75	Sequence 74, Appl
39	25	24.0	19	2	US-08-488-379-74	Sequence 74, Appl
40	25	24.0	19	2	US-08-488-379-75	Sequence 75, Appl
41	25	24.0	19	2	US-08-696-944-3	Sequence 3, Appl1
42	25	24.0	19	4	PCT-US93-07545-74	Sequence 74, Appl
43	25	24.0	19	4	PCT-US93-07545-75	Sequence 75, Appl
44	25	24.0	20	2	US-08-480-190-191	Sequence 191, App
45	25	24.0	20	2	US-08-749-852-55	Sequence 55, Appl

ALIGNMENTS

RESULT 1
US-08-164-618-20
; Sequence 20, Application US/08164618
; Patent No. 5408036
; GENERAL INFORMATION:
; APPLICANT: Ghadiri, M. Reza
; TITLE OF INVENTION: Isolated Metallopolypeptides:
; TITLE OF INVENTION: Compositions and Synthetic Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 No. 5408036th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,618
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/769,621
; FILING DATE:
; APPLICATION NUMBER: 07/591,988
; FILING DATE: October 2, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamsen, Edward G.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: SCRF 231.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5400
; TELEFAX: (312) 616-5460
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-164-618-20

Query Match 27.9% Score 29; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RT Helicobacter species from humans and animals.*;
 RL Infect. Immun. 60:5259-5266(1992)
 SO SEQUENCE 18 AA; 2060 MW; 29C8E0AB77E21805 CRC64;

Query Match 22.9%; Score 25; DB 2; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LHLHGE 8
 : : : : :
 DB 9 MMLHYGE 16

RESULT 12
 ID 09PRM7 PRELIMINARY; PRT; 18 AA.
 AC 09PRM7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ACID THIO. PROTEASE (FRAGMENT).
 OS Xenopus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 96417001.
 RA Miyata S., Kihara H.K.;
 RT "Cathepsin L-like protease from Xenopus embryos that is stimulated by
 nucleoside phosphates and nucleic acids.*";
 RL Zool. Sci. 12:771-774(1995).
 SO SEQUENCE 18 AA; 2060 MW; AIDC9B106B341504 CRC64;

Query Match 22.9%; Score 25; DB 13; Length 18;
 Best Local Similarity 57.1%; Pred. No. 1.7e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 9 REGWIK 15
 : : : : :
 DB 8 REGWYK 14

RESULT 13
 ID 044850 PRELIMINARY; PRT; 19 AA.
 AC 044850;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
 DE HYPOTHEICAL PROTEIN (FRAGMENT).
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-297;
 RA Atkins D.R., Popova T., Brusca J., Goldberg M.L., Li M., Baker S.C.,
 RL Morgard M.V., Radolf J.D.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L31425; AAA64901.1; -.
 KW Hypothetical protein.
 FT NON_TER 19 19
 SO SEQUENCE 19 AA; 2321 MW; C821BF312DB41512 CRC64;

Query Match 22.9%; Score 25; DB 2; Length 19;
 Best Local Similarity 50.0%; Pred. No. 1.8e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 LHLGEREP 11
 : : : : :
 : : : : :

DB 4 LHLQSTLHP 13

RESULT 14

ID 09UJ18 PRELIMINARY; PRT; 19 AA.

AC 09UJ18;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE DJ33A15.2 (PROSTAGLANDIN E RECEPTOR (EP3E)) (FRAGMENT).
 GN PTGER3.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Frankland J.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031429; CAB52457.1; -.
 KW Receptor.
 FT NON_TER 1 1
 SO SEQUENCE 19 AA; 2245 MW; 142450379B298FEC CRC64;

Query Match 22.9%; Score 25; DB 4; Length 19;
 Best Local Similarity 44.4%; Pred. No. 1.8e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 LHLGEREP 11
 : : : : :
 DB 8 LHLGKXKP 16

RESULT 15
 ID 012088 PRELIMINARY; PRT; 12 AA.
 AC 012088;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE TAT PROTEIN (FRAGMENT).
 GN TAT.
 OS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Turelli P., Guiguen F., Mornex J.F., Vigne R., Querat G.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U81435; AAB60824.1; -.
 FT NON_TER 1 1
 SO SEQUENCE 12 AA; 1279 MW; 4B90BB1E8644EB7 CRC64;

Query Match 22.0%; Score 24; DB 12; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGW 13
 : : : : :
 DB 8 PGW 10

Search completed: December 21, 2000, 08:35:39
 Job time: 602 sec

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OY      13 WIKOLF 18
       11111
Db      1 WIRELY 6

RESULT 7
O9X313 PRELIMINARY; PRT; 17 AA.
AC O9X313:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN PERB.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070176; AAD20791.1; -.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 1953 MW; 630843039ADD51B4 CRC64;

Query Match      23.9%; Score 26; DB 2; Length 17;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY      1 LLLHLOGREP 12
       111111111
Db      1 LLMHFLXDRKG 12

RESULT 8
O9T2R9 PRELIMINARY; PRT; 17 AA.
AC O9T2R9:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CYTOCHROME-C REDUCTASE 55 KDA SUBUNIT (EC 1.10.2.2) (FRAGMENT).
OS Solanum tuberosum (Potato).
OS Mitochondrion.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
OC Solanaceae; Solanum.
RN [1]
RP SEQUENCE.
RA Braun H.P., Schmitz U.K.;
RL Planta 193:99-106(1994).
SQ SEQUENCE 17 AA; 1758 MW; F95F7BF7940F5F21 CRC64;

Query Match      23.9%; Score 26; DB 8; Length 17;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      1 LLLHLOG 7
       1111111
Db      4 LMLHDIG 10

RESULT 9
O9UCG3 PRELIMINARY; PRT; 19 AA.
AC O9UCG3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

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DE ALPHA 2-PLASMIN INHIBITOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 93249387.
RA Bangert K., Johnsen A.H., Christensen U., Thorsen S.;
RT "Different N-terminal forms of alpha 2-plasmin inhibitor in human
RT plasma.";
RL Biochem. J. 291:623-625(1993).
SQ SEQUENCE 19 AA; 2065 MW; 41352BF04DIEBA9 CRC64;

Query Match      23.4%; Score 25.5; DB 4; Length 19;
Best Local Similarity 63.6%; Pred. No. 1.5e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY      2 LHLLOGREP 12
       111111111
Db      10 LKL-GNQEPP 19

RESULT 10
O16045 PRELIMINARY; PRT; 14 AA.
ID O16045:
AC O16045:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE D3 DOPAMINE RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Nagai Y., Ueno S., Saeki Y., Soga F., Yanagihara T.;
RT "Expression of the D3 dopamine receptor gene and a novel variant
RT transcript generated by alternative splicing in human peripheral blood
RT lymphocytes.";
RL Biochem. Biophys. Res. Commun. 194:368-374(1993).
DR EMBL; S63845; CAB32270.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1586 MW; EA310BEFE94CF1B1 CRC64;

Query Match      22.9%; Score 25; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      2 LHLHQ 6
       11111
Db      9 LHLHQ 13

RESULT 11
O9R5F6 PRELIMINARY; PRT; 18 AA.
ID O9R5F6:
AC O9R5F6:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE URASE SMALL SUBUNIT (FRAGMENT).
OS Helicobacter mustelae.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE.
RX MEDLINE; 93084378.
RA Turbett G.R., Hoj P.B., Horne R., Mee B.J.;
RT "Purification and characterization of the urease enzymes of

```

RN [1]
RP SEQUENCE.
RX MEDLINE: 95337087.
RA Thulin C.D., Walsh K.A.;
RT "Identification of the amino terminus of human flaggrin using
RT differential LC/MS techniques: implications for profilaggrin
RT processing.";
RL Biochemistry 34:8687-8692(1995)
SQ SEQUENCE 20 AA: 2199 MW: 0FD0856B199AB332 CRC64;

Query Match 26.6%; Score 29; DB 4; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 4 ILDGEREPGW 13
DB 5 HEQSESHGW 14

RESULT 3
O9PRJ4 PRELIMINARY; PRT; 9 AA.
AC O9PRJ4:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE BRADKININ.
OS Lepisosteus osseus (long-nosed gar), and Amia calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;
RN [1]
RP SEQUENCE.
RX MEDLINE: 95380361.
RA Conlon J.M., Platzack B., Marra L.E., Youson J.H., Olson K.R.;
RT "Isolation and biological activity of [Ttp5]pradylkin from the plasma
RT of the phylogenetically ancient fish, the bowfin and the longnosed
RT gar.";
RL Peptides 16:485-489(1995).
SQ SEQUENCE 9 AA: 1099 MW: 3393D775A3786777 CRC64;

Query Match 25.7%; Score 28; DB 13; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 RPPGW 13
DB 1 RPPGW 5

RESULT 4
O18502 PRELIMINARY; PRT; 14 AA.
AC O18502:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-AUG-1998 (TREMblrel. 07, Last annotation update)
DE LYSOPHOSPHOLIPASE HOMOLOG (FRAGMENT).
GN SMLPLH.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigylidae;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EGYPTIAN;
RA Hamdan F.F., Ribeiro P.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF006679; AAC62255.1; -;
FT NON_TER 14
SQ SEQUENCE 14 AA: 1541 MW: 48B847C2E5D89177 CRC64;

Query Match 25.7%; Score 28; DB 5; Length 14;
Best Local Similarity 38.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 LLLHLOGERPGW 13
DB 2 IFLLHGLDGTGHW 14

RESULT 5
O9R4W5 PRELIMINARY; PRT; 20 AA.
AC O9R4W5:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE 30 KDA MAJOR HEAT SHOCK PROTEIN (FRAGMENT).
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE.
RX MEDLINE: 95020803.
RA Yokota K., Hirai Y., Haque M., Hayashi S., Isogai H., Sugiyama T.,
RA Nagamachi E., Tsukada Y., Fujii N., Oguma K.;
RT "Heat shock protein produced by Helicobacter pylori.";
RL Microbiol. Immunol. 38:403-405(1994).
DR INTERPRO: IPR002026; -;
DR PAM: PF00547; urease_gamma; 1.
SQ SEQUENCE 20 AA: 2302 MW: 29C9DFBFD6D21805 CRC64;

Query Match 24.8%; Score 27; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 9.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LLLHLOGE 8
DB 11 LMLHYAGE 18

RESULT 6
O77893 PRELIMINARY; PRT; 11 AA.
AC O77893:
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE MHC CLASS II B LOCUS 10 (FRAGMENT).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
OC Percomorpha; Perciformes; Labroidae; Cichlidae; Oreochromis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98315113.
RA Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska Z.,
RA Suelmann H., Figueroa F., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid Mhc
RT class II B loci.";
RL Genomics 149:1527-1547(1998).
DR EMBL: AF050003; AAC41342.1; -;
KM MHC.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA: 1296 MW: 68775B73786B572B CRC64;

Query Match 23.9%; Score 26; DB 7; Length 11;
Best Local Similarity 50.0%; Pred. No. 7.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:35:39 ; Search time 157.2 Seconds
(without alignments)
11.880 Million cell updates/sec

Title: US-08-934-367-12
Perfect score: 109
Sequence: 1 LLLHLOGEREPGNIKQLFTN 20

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues
Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_14:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_ricetent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	26.6	10	13 Q9PR21	Q9PR21 oncorhynch
2	29	26.6	20	4 Q9UC71	Q9UC71 homo sapien
3	28	25.7	9	13 Q9PR21	Q9PR21 lepisosteus
4	28	25.7	14	5 Q18502	Q18502 schistosoma
5	27	24.8	20	2 Q9R4W5	Q9R4W5 helicobacte
6	26	23.9	11	7 Q77893	Q77893 oreochromis
7	26	23.9	11	7 Q9X313	Q9X313 prochloroco
8	26	23.9	17	8 Q9T2R9	Q9T2R9 solanum tub
9	25.5	23.4	19	4 Q9UCG3	Q9UCG3 homo sapien
10	25	22.9	14	4 Q16045	Q16045 homo sapien
11	25	22.9	18	2 Q9R5F6	Q9R5F6 helicobacte
12	25	22.9	18	13 Q9PRM7	Q9PRM7 xenopus. ac
13	25	22.9	19	2 Q44850	Q44850 borrelia bu
14	25	22.9	19	4 Q9UJ18	Q9UJ18 homo sapien
15	24	22.0	12	12 Q12088	Q12088 caprine art
16	24	22.0	12	12 Q12074	Q12074 caprine art
17	24	22.0	12	12 Q12076	Q12076 caprine art
18	24	22.0	12	12 Q12078	Q12078 caprine art
19	24	22.0	12	12 Q12080	Q12080 caprine art

20	24	22.0	12	12 Q12082	Q12082 caprine art
21	24	22.0	12	12 Q12084	Q12084 caprine art
22	24	22.0	12	12 Q12086	Q12086 caprine art
23	24	22.0	12	12 Q12090	Q12090 caprine art
24	24	22.0	12	12 Q12092	Q12092 caprine art
25	24	22.0	12	12 Q12094	Q12094 caprine art
26	24	22.0	12	12 Q12106	Q12106 caprine art
27	24	22.0	12	12 Q12108	Q12108 caprine art
28	24	22.0	12	12 Q12110	Q12110 caprine art
29	24	22.0	12	12 Q12112	Q12112 caprine art
30	24	22.0	12	12 Q12114	Q12114 caprine art
31	24	22.0	12	12 Q12116	Q12116 caprine art
32	24	22.0	12	12 Q12118	Q12118 caprine art
33	24	22.0	15	2 Q46963	Q46963 escherichia
34	24	22.0	15	5 Q9TXC8	Q9TXC8 locusta mlg
35	24	22.0	16	4 Q9UCX9	Q9UCX9 homo sapien
36	24	22.0	16	4 Q9UCH1	Q9UCH1 homo sapien
37	24	22.0	19	2 Q47079	Q47079 escherichia
38	24	22.0	19	10 Q9S8W5	Q9S8W5 avena sativ
39	24	22.0	19	12 Q93210	Q93210 porcine cir
40	23	21.1	11	5 Q9V7K6	Q9V7K6 dirosophila
41	23	21.1	11	7 Q77892	Q77892 oreochromis
42	23	21.1	11	7 Q77906	Q77906 oreochromis
43	23	21.1	11	7 Q77918	Q77918 pseudotroph
44	23	21.1	13	4 Q9V674	Q9V674 homo sapien
45	23	21.1	17	6 Q9TR78	Q9TR78 didelphis m

ALIGNMENTS

RESULT 1
ID Q9PR21 PRELIMINARY; PRT; 10 AA.
AC Q9PR21;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE LYSYL-BRADYKININ-VASOACTIVE PEPTIDE KALLIDIN HOMOLOG.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proteocephalopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
RN [1]
RP SEQUENCE. 94039817.
RX MEDLINE; 94039817.
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from trout plasma.";
RL FEBS Lett. 334:75-78(1993).
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 26.6%; Score 29; DB 13; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 EREXW 13
Db 1 KRPGW 6
RESULT 2
ID Q9UC71 PRELIMINARY; PRT; 20 AA.
AC Q9UC71;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE FILAGGRIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

CC -1- FUNCTION: SHOWS HEMOLYTIC ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- TISSUE SPECIFICITY: SKIN.
 DR PIR: S09018; S09018.
 KW Amphibian skin; Amidation; Hemolysis.
 FT MOD_RES 13 13 AMIDATION.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1390 MW; C6BA768B9DFE587D CRC64;

Query Match 18.3%; Score 20; DB 1; Length 13;
 Best Local Similarity 57.1%; Pred. No. 1.9e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 GWIKOLF 18
 1 : |||
 DB 7 GILSOLF 13

Search completed: December 21, 2000, 08:32:59
 Job time: 442 sec

OS Bombyx mori (Silk moth).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Bombycoidea; Bombycidae; Bombyx.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 85083111.
 RA Rodakis G.C., Lecanidou R., Eickbush T.H.;
 RT "Diversity in a chorion multigene family created by tandem
 RL J. Mol. Evol. 20:265-273(1984).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF MANY FROM THE EGGSHELL OF THE
 CC SILK MOTH.
 CC -1- SIMILARITY: MEMBER OF THE ALPHA-BRANCH OF CHORION PROTEIN TO WHICH
 CC BELONG CLASSES A, CA AND HCA.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sdb.ch).
 CC -----
 CC EMBL: X01068; CAB57790.1; -.
 DR PIR: B23219; B23219.
 KW Eggshell; Chorion; Repeat; Multigene family; Signal.
 FT SIGNAL 1
 FT NON_TER 17
 FT SEQUENCE 17 AA; 1913 MW; 5E634508C5355C9C CRC64;
 SQ
 Query Match 19.3%; Score 21; DB 1; Length 17;
 Best Local Similarity 71.4%; Pred. No. 1.7e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LLLHLOG 7
 DB 7 LLLCVGG 13
 RESULT 13
 CRTC_SPIOI STANDARD; PRT; 20 AA.
 ID AC P30806;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE CALRETICULIN-LIKE PROTEIN (FRAGMENT).
 OS Spinacia oleracea (Spinach).
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales;
 CC Caryophyllales; Chenopodiaceae; Spinacia.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=LEAF;
 RX MEDLINE: 93176159.
 RA Menegazzi P., Guzzo F., Baldan B., Mariani P., Treves S.;
 RT "Purification of calreticulin-like protein(s) from spinach leaves";
 RL Biochem. Biophys. Res. Commun. 190:1130-1135(1993).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM.
 CC -1- PTM: GLYCOSYLATED.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 DR PIR: PC1241; PC1241.
 DR PIR: PC1240; PC1240.
 DR INTERPRO: IPR001580; -.
 DR PROSITE: PS00803; CALRETICULIN_1; PARTIAL.
 DR PROSITE: PS00804; CALRETICULIN_2; PARTIAL.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; PARTIAL.
 KW Endoplasmic reticulum; Calcium-binding; Glycoprotein.
 FT NON_TER 20
 FT SEQUENCE 20 AA; 2645 MW; 00FAB4C9DEDCB0F CRC64;
 SQ

Query Match 19.3%; Score 21; DB 1; Length 20;
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 EPWG 13
 DB 9 EDGW 12
 RESULT 14
 ID AC P80903;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 30-NOV-2000 (Rel. 35, Last sequence update)
 DE PYRUVATE SYNTHASE SUBUNIT PORD (EC 1.2.7.1) (PYRUVATE OXIDOREDUCTASE
 DE DELTA CHAIN) (PORD) (PYRUVIC-FERREDOXIN OXIDOREDUCTASE DELTA SUBUNIT)
 DE (FRAGMENT).
 GN PORD.
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
 CC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 CC Methanobacterium.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 97261844.
 RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
 RT "Structures and functions of four anaerobic 2-oxoacid oxidoreductases
 RT in Methanobacterium thermoautotrophicum";
 RL Eur. J. Biochem. 244:862-868(1997).
 CC -1- FUNCTION: THE PH OPTIMUM IS PH 10.0 AND THE OPTIMAL TEMPERATURE
 CC IS 80 DEGREES CELSIUS.
 CC -1- CATALYTIC ACTIVITY: PYRUVATE + COA + OXIDIZED FERREDOXIN =
 CC ACETYL-COA + CO(2) + REDUCED FERREDOXIN.
 CC -1- COFACTOR: BINDS TWO 4FE-4S CLUSTERS (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
 CC GAMMA CHAIN.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
 KW Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
 FT NON_TER 12
 FT SEQUENCE 12 AA; 1241 MW; 2D54065D1BD1ADD8 CRC64;
 SQ
 Query Match 18.3%; Score 20; DB 1; Length 12;
 Best Local Similarity 75.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 9 REPG 12
 DB 9 KERG 12
 RESULT 15
 ID AC P32415;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE HEMOLYTIC PROTEIN A1 (FRAGMENT).
 OS Rana esculenta (Edible frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=SKIN SECRETION;
 RX MEDLINE: 90198965.
 RA Sismaco M., de Blase D., Severini C., Alta M., Erspamer G.F.,
 RA Barra D., Bossa F.;
 RT "Purification and characterization of bioactive peptides from skin
 RT extracts of Rana esculenta";
 RL Biochim. Biophys. Acta 1033:318-323(1990).
 RL

CC -1- FUNCTION: SMOOTH MUSCLE CONTRACTION.
 KM Bradykinin; Vasodilator.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SO SEQUENCE 13 AA; 1573 MW; 2673CB3DB3ECC867 CRC64;

Query Match 20.2%; Score 22; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 9.2e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 QGERPEGM 13
 1 1 1 1 1 1
 Db 1 QZKRPEGF 8

RESULT 9
 ID NEUT_CHICK STANDARD; PRT; 13 AA.
 AC P13724;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE NEURETENSIN (NT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 88063566.
 RA Iwabuchi H., Komori S., Ohashi H., Kimura S.;
 RT "The amino acid sequence of a smooth muscle-contracting peptide from
 chicken rectum. Identity to chicken neurensin.";
 RL Jpn. J. Pharmacol. 44:445-459(1987).
 CC -1- FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE.
 KW PIR; A28505; A28505.
 DR Vasactive.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SO SEQUENCE 13 AA; 1608 MW; 4C949E71AC410DD3 CRC64;

Query Match 20.2%; Score 22; DB 1; Length 13;
 Best Local Similarity 44.4%; Pred. No. 9.2e+02;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 LHLQGERP 11
 1 1 1 1 1 1
 Db 2 LHVNKARP 10

RESULT 10
 ID Q2OG_COMTE STANDARD; PRT; 10 AA.
 AC P80466;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE QUINOLINE 2-OXIDOREDUCTASE, GAMMA CHAIN (EC 1.-.-.-) (FRAGMENT).
 OS Comamonas testosteroni (Pseudomonas testosteroni).
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-63;
 RX MEDLINE; 96035889.
 RA Schach S., Tshisuka B., Feltner S., Lingers F.;
 RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
 dioxygenase from Comamonas testosteroni 63. The first two enzymes in
 quinoline and 3-methylquinoline degradation.";
 RL Eur. J. Biochem. 232:536-544(1995).
 CC -1- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-
 1,2-DIHYDROQUINOLINE.
 CC -1- COFACTOR: FAD AND MOLYBDENUM.
 CC -1- PATHWAY: FIRST STEP IN THE DEGRADATION OF QUINOLINE AND

CC (3-METHYL)-QUINOLINE.
 CC -1- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
 CC TWO GAMMA CHAINS (PROBABLE).
 CC Oxidoreductase; Flavoprotein; FAD; Molybdenum.
 FT NON_TER 10 10
 SO SEQUENCE 10 AA; 1153 MW; C848CE64433B1DC6 CRC64;

Query Match 19.3%; Score 21; DB 1; Length 10;
 Best Local Similarity 42.9%; Pred. No. 1e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 LQGERP 11
 1 1 1 1 1 1
 Db 2 IQAEKNP 8

RESULT 11
 ID CXET_COMTE STANDARD; PRT; 13 AA.
 AC P81755;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE EPSILON-CONOTOXIN TXIX.
 OS Conus textile (Cloth-of-gold cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 RN [1]
 RP SEQUENCE, CARBOHYDRATE-LINKAGE SITE THR-10, AND STRUCTURE BY NMR.
 RC TISSUE-VENOM.
 RX MEDLINE; 99254114.
 RA Rigby A.C., Lucas-Meunier E., Kalume D.E., Czerwiec E., Hambe B.,
 RA Dahlqvist I., Fossler P., Baux G., Roepstorff P., Baleja J.D.,
 RA Furler B.C., Furler B., Stenflo J.P.;
 RT "A conotoxin from Conus textile with unusual posttranslational
 modifications reduces presynaptic Ca2+ influx.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:5758-5763(1999).
 CC -1- FUNCTION: CONOTOXIN WHICH ACTS AT PRESYNAPTIC MEMBRANES, BLOCKING
 THE CALCIUM CHANNELS.
 CC -1- PTM: O-GLYCAN CONSISTS OF THE DISACCHARIDE GAL-GALNAC.
 CC PDB; 1WCF; 08-JUN-99.
 DR Presynaptic neurotoxin; Calcium channel inhibitor; Venom; Vitamin K;
 KW Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Bromination;
 KW 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 9
 FT MOD_RES 1 1 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 4 4 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD_RES 7 7 BROMINATION.
 FT MOD_RES 13 13 HYDROXYLATION.
 FT CARBOHYD 10 10 O-LINKED (GALNAC...)
 SO SEQUENCE 13 AA; 1388 MW; 386C9E1C74AFA378 CRC64;

Query Match 19.3%; Score 21; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 EPGW 13
 1 1 1 1 1 1
 Db 4 EDGW 7

RESULT 12
 ID CHH3_BOMMO STANDARD; PRT; 17 AA.
 AC P20729;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE CHORION CLASS HIGH-CYSTEINE HCA PROTEIN 13 PRECURSOR (HC-A.13)
 (FRAGMENT).

DE (DCC II).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
OC Tabanidae; Tabanus.
RN [1]
RP SEQUENCE.
RC TISSUE-CORPORA CARDIACA;
RX MEDLINE; 90046758.
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -1- ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR; B33995; B33995.
DR INTERPRO; IPR002047; -.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;

Query Match 22.0%; Score 24; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 34e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FGM 13
Db 6 FGM 8

RESULT 6
AROO_AMYME STANDARD; PRT; 20 AA.
ID AROO_AMYME
AC P46380;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10) (3-DEHYDROQUINASE)
DE (TYPE II DHOASE) (FRAGMENT).
GN AROO.
OS Amycolatopsis methanolica.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Pseudonocardiales; Pseudonocardiaceae;
OC Amycolatopsis.
RN [1]
RP SEQUENCE.
RC STRAIN=NCIB 11946;
RX MEDLINE; 93123995.
RA Everink G.J.W., Hessels G.I., Vrijbloed J.W., Coggins J.R.,
RA Dijkhuizen L.;
RT "Purification and characterization of a dual function
RT 3-dehydroquinate dehydratase from Amycolatopsis methanolica";
RL J. Gen. Microbiol. 138:2449-2457(1992).
CC -1- FUNCTION: CATALYZE A TRANS-DEHYDRATION VIA AN ENOLATE
CC INTERMEDIATE. IS INVOLVED IN BOTH THE CATABOLISM OF QUINATE AND
CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS. HAS A TEMPERATURE
CC OPTIMAL OF 76 DEGREES CELSIUS AND PH OPTIMAL OF 9.0. TYPE II
CC ENZYMES ARE THERMOSTABLE.
CC -1- CATALYTIC ACTIVITY: 3-DEHYDROQUINATE = 3-DEHYDROSHIMIMATE + H(2)O.
CC -1- PATHWAY: THIRD STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
CC -1- SUBUNIT: HOMODODECAMER.
CC -1- SIMILARITY: BELONGS TO THE TYPE-II 3-DEHYDROQUINASE FAMILY.
DR INTERPRO; IPR001874; -.
DR PROSITE; PS01029; DEHYDROQUINASE-II; PARTIAL.
KW Quinate metabolism; Aromatic amino acid biosynthesis; lyase.

FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2197 MW; C24AA183E5CFDFA CRC64;

Query Match 22.0%; Score 24; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GEREP 11
Db 15 GKREP 19

RESULT 7
LPK1_LOCM1 STANDARD; PRT; 16 AA.
ID LPK1_LOCM1
AC P20404;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE LOCUSTAPYROKININ 1 (LOW-PK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
RN [1]
RP SEQUENCE.
RC TISSUE-CORPORA CARDIACA;
RX MEDLINE; 91224474.
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, primary structure, and synthesis of locustapyrokinin: a
RT myotonic peptide of Locusta migratoria";
RL Gen. Comp. Endocrinol. 81:97-104(1991).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A49761; A49761.
DR INTERPRO; IPR001484; -.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1827 MW; A7178BBDCA0AFDD6 CRC64;

Query Match 21.1%; Score 23; DB 1; Length 16;
Best Local Similarity 57.1%; Pred. No. 8e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 GWIKOLF 18
Db 6 GWPQOPF 12

RESULT 8
BRK_PARID STANDARD; PRT; 13 AA.
ID BRK_PARID
AC P42717;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE WASPKININ.
OS Parapolybia indica.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vespoidae; Vespidae; Polistinae; Parapolybia.
RN [1]
RP SEQUENCE.
RC TISSUE=VENOM.
RA Toki T., Yasuhara T., Nakajima T.;
RT "Isolation and sequential analysis of peptides on the venom sac of
RT Parapolybia indica";
RL Elisel Dobutsu 39:105-111(1988).

RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hyperthalamosemic activity isolated from the corpora cardiaca of horse
 RT files (Diptera)." ;
 RT Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DILYGERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE DILYGERIDES AS AN ENERGY SOURCE.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: A33995; A33995.
 DR INTERPRO: IPR002047; -.
 DR PROSITE: PS00256; AKH; 1.
 KM Neuropeptide; Amidation; flight.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 22.0%; Score 24; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PCW 13
 DB 6 PCW 8

RESULT 3
 ID RPCH_PANBO STANDARD; PRT; 8 AA.
 AC P08939;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE RED PIGMENT CONCENTRATING HORMONE (RPCH).
 OS Pandanus borealis (Northern red shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidae;
 OC Pandalidae; Pandanus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 75054965.
 RA Ferlund P.;
 RT "Structure of the red-pigment-concentrating hormone of the shrimp,
 RT Pandanus borealis." ;
 RT Biochim. Biophys. Acta 371:304-311(1974).
 CC -1- FUNCTION: THIS HORMONE ADAPTS THE ANIMAL TO LIGHT BACKGROUNDS BY
 CC STIMULATING CONCENTRATION OF THE PIGMENT OF ITS RED BODY-
 CC CHROMATOPHORES.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: S07139; S07139.
 DR INTERPRO: IPR002047; -.
 DR PROSITE: PS00256; AKH; 1.
 KM Pigment; Hormone; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 948 MW; 86786775B9C44736 CRC64;

Query Match 22.0%; Score 24; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PCW 13
 DB 6 PCW 8

RESULT 4
 ID HTF_NAUCI STANDARD; PRT; 10 AA.

5

AC P10939;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPERTREHALOSAEMIC HORMONE (HTH) (HYPERTREHALOSAEMIC NEUROPEPTIDE).
 OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
 OS Leucophaea maderae (Madeira cockroach),
 OS Blattella germanica (German cockroach), and
 OS Gromphadorina portenlosa (Cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberoidea; Blaberidae; Nauphoeta.
 RN [1]
 RP SEQUENCE.
 RC SPECIES=N.CINEREA; TISSUE=CORPORA CARDIACA;
 RX MEDLINE; 87100208.
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Amino acid sequence of a hypertrehalosaemic neuropeptide from the
 RT corpus cardiaca of the cockroach, Nauphoeta cinerea." ;
 RT Biochem. Biophys. Res. Commun. 141:774-781(1986).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=L.MADERAE; G.PORTENTOSA, AND B.GERMANICA;
 RX MEDLINE; 90253659.
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gromphadorina portenlosa, Blattella germanica and Blattella orientalis
 RT and of the stick insect Ectophasma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry." ;
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=B.GERMANICA;
 RX MEDLINE; 91179584.
 RA Veenstra J.A., Camps F.;
 RT "Structure of the hypertrehalosaemic neuropeptide of the German
 RT cockroach, Blattella germanica." ;
 RL Neuropeptides 15:107-109(1990).
 CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: A26381; A26381.
 DR PIR: S08997; S08997.
 DR PIR: S08998; S08998.
 DR PIR: S09137; S09137.
 DR PIR: A60421; A60421.
 DR INTERPRO: IPR002047; -.
 DR PROSITE: PS00256; AKH; 1.
 KM Neuropeptide; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1092 MW; 05623678675B9C4 CRC64;

Query Match 22.0%; Score 24; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PCW 13
 DB 6 PCW 8

RESULT 5
 ID HTF_TABAT STANDARD; PRT; 10 AA.
 AC P14596;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE HYPERTREHALOSAEMIC FACTOR (HTHF) (DIPTERAN CORPORA CARDIACA FACTOR II)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:32:59 ; Search time 62.7 Seconds
(without alignments)
10.191 Million cell updates/sec

Title: US-08-934-367-12

Perfect score: 109
Sequence: 1 LLLHLQGEREPQWIKQLFTN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 segs, 31947931 residues

Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	25.7	19	1 TRP3_LEUMA	P81735 leucophaea
2	24	22.0	8	1 AKH_TABAT	P14585 tabanus atr
3	24	22.0	8	1 RICH_PANBO	P08939 pandanus bo
4	24	22.0	10	1 HTF_NAUCI	P10939 nauphoeta c
5	24	22.0	10	1 HTF_TABAT	P14596 tabanus atr
6	24	22.0	20	1 AROC_AMYME	P46380 amycolators
7	23	21.1	16	1 LPK1_LOCM1	P20404 locusta mig
8	22	20.2	13	1 BRK_PARID	P42717 parapolybia
9	22	20.2	13	1 NEUT_CHICK	P13724 gallus gall
10	21	19.3	10	1 Q2OG_COMTE	P80466 comanonas t
11	21	19.3	13	1 CXET_COMTE	P81755 conus texti
12	21	19.3	17	1 CHH3_BOOMO	P20729 bombyx mori
13	21	19.3	20	1 CRIC_SPIOL	P30806 spinacia ol
14	20	18.3	12	1 FORD_MERTM	P80903 methanodact
15	20	18.3	13	1 HPAL_RANES	P32415 rana escule
16	20	18.3	14	1 CAT2_FASHE	P80342 fasciola he
17	20	18.3	15	1 TAL_TREBR	P4070 tremella br
18	20	18.3	19	1 CAT3_FASHE	P80532 fasciola he
19	20	18.3	19	1 LANA_ACTIG	P56650 actinoplane
20	20	18.3	20	1 CAT1_FASHE	P09093 fasciola he
21	19.5	17.9	20	1 COG1_PANCM	P20731 paralithode
22	19	17.4	7	1 UH11_RAT	P56576 ratus norv
23	19	17.4	10	1 GON1_PETMA	P44378 petromyzon
24	19	17.4	10	1 GON3_ONCKE	P20367 oncothynchu
25	19	17.4	10	1 GONL_SOUAC	P27429 squalus aca
26	19	17.4	12	1 RS19_ELIEP	P47881 elm yellow
27	19	17.4	13	1 FARB_ASCSU	P43173 ascaris suu
28	19	17.4	13	1 NEUT_RANVE	P15156 rana tempor
29	19	17.4	14	1 RS19_CLOPP	P46228 clover prol
30	19	17.4	14	1 RS19_LOMBP	P468878 loofah wilt
31	19	17.4	15	1 VORA_MERTM	P80907 methanodact
32	19	17.4	18	1 NPA_BOVIN	P15506 bos taurus
33	19	17.4	19	1 FIBB_HORSE	P14471 equus caball

34	19	17.4	19	1 PYRB_PSEFL	P56585 pseudomonas
35	19	17.4	20	1 COG1_CHIOP	P24153 chionoecete
36	18	16.5	8	1 AKH_LIBAU	P25418 libellula a
37	18	16.5	8	1 CCKN_MACEU	P30369 macropus eu
38	18	16.5	8	1 HTFL_PERAM	P04548 periplaneta
39	18	16.5	8	1 HTF2_PERAM	P04549 periplaneta
40	18	16.5	8	1 HTF_TENMO	P25419 tenebrio mo
41	18	16.5	8	1 UF06_MOUSE	P38644 mus musculu
42	18	16.5	10	1 CAER_LITXA	P56264 litorea xan
43	18	16.5	10	1 HTFL_ROMMI	P18110 romalea mic
44	18	16.5	10	1 HTF2_CARMO	P1385 carausius m
45	18	16.5	11	1 BRK_MEGFL	P12797 megascolla

ALIGNMENTS

RESULT 1	TRP3_LEUMA	STANDARD;	PRT;	19 AA.
AC	P81735;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	TACHYKININ-RELATED PEPTIDE 3 (LEWTRP 3).			
OS	Leucophaea maderae (Madeira cockroach).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;			
OC	Blattelloidea; Blattellidae; Leucophaea.			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=MIDGUT;			
RX	MEDLINE: 97053012.			
RA	Muren J.E., Naessel D.R.;			
RT	"Isolation of five tachykinin-related peptides from the midgut of			
RT	the cockroach Leucophaea maderae: existence of N-terminally extended			
RT	isoforms.";			
RL	Regul. Pept. 65:185-196(1996).			
CC	-1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY			
CC	OF SPONTANEOUS CONTRACTIONS AND TONS OF HINDGUT MUSCLE.			
CC	-1- TISSUE SPECIFICITY: MIDGUT.			
CC	-1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.			
CC	Tachykinin; Neuropeptide; Amidation.			
FT	MOD_RES 19			
SO	SEQUENCE 19 AA; 1930 MW; 99B5471A011625E5 CRC64;			
Query Match 25.7%; Score 28; DB 1; Length 19;				
Best Local Similarity 83.3%; Pred. No. 1.5e+02;				
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	7 GEREFG 12			
Db	2 GERAG 7			
RESULT 2				
ID	AKH_TABAT	STANDARD;	PRT;	8 AA.
AC	P14595;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	01-FEB-1994 (Rel. 28, Last annotation update)			
DE	ADIPONICTIC HORMONE (AKH) (DIPTERAN CORPORA CARDIACA FACTOR 1)			
DE	(DCC 1).			
OS	Tabanus atratus (Horse fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;			
OC	Tabanidae; Tabanus.			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=CORPORA CARDIACA;			
RX	MEDLINE: 90046758.			

A:Reference number: A43405; MWID:92388154
A:Accession: A43405
A:Molecule type: protein
A:Residues: 1-10 <VE>
C:Superfamily: 6-phosphofructo-2-kinase / fructose-2,6-bisphosphate/2-phosphatase; phosph
C:Keywords: phosphoric monoester hydrolase; phosphotransferase

Query Match 22.0%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 HLOGE 8
||:||
Db 5 HIKGE 9

RESULT 14

A60421
hypertrehalosemic hormone - German cockroach
N:Alternate names: Bld-HrTH
C:Species: Blattea germanica (German cockroach)
C>Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 31-Oct-1997
C:Accession: A60421; S09137
R:Veenstra, J.A.; Camps, F.
Neuropeptides 15, 107-109, 1990
A>Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, Blatte
A:Reference number: A60421; MWID:91179584
A:Accession: A60421
A:Molecule type: protein
A:Residues: 1-10 <VE>
R:Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A>Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpor
entails and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A:Reference number: S08995; MWID:90233659
A:Accession: S09137
A:Molecule type: protein
A:Residues: 1-10 <GAE>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 22.0%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGW 13
|||
Db 6 PGW 8

RESULT 15

S08997
hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)
C:Species: Gromphadorina portentosa
C>Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 24-Oct-1997
C:Accession: S08997
R:Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A>Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpor
entails and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A:Reference number: S08995; MWID:90233659
A:Accession: S08997
A:Molecule type: protein
A:Residues: 1-10 <GAE>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 22.0%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGW 13
|||
Db 6 PGW 8

Search completed: December 21, 2000, 08:30:07
Job time: 271 sec

A:Residues: 1-4 <KUR>
C:Keywords: neuropeptide

Query Match 22.0%; Score 24; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGM 13
|||
DB 2 PGM 4

RESULT 9
A61348
red pigment-concentrating hormone - northern shrimp
N:Alternate names: blanching hormone
C:Species: Pandalus borealis (northern shrimp)
C:Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C:Accession: A61348; S07139
R:Jenssen, P.; Josefsson, L.
Science 177, 173-175, 1972
A:Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A:Reference number: A61348; MUID:72226738
A:Accession: A61348
A:Molecule type: protein
A:Residues: 1-8 <FER1>
R:Fernlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A:Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus borealis.
A:Reference number: S07139; MUID:75054965
A:Accession: S07139
A:Molecule type: protein
A:Residues: 7'E', 2-8 <FER2>
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have used pigment-containing cells.
C:Superfamily: adipokinetin hormone
C:Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 22.0%; Score 24; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGM 13
|||
DB 6 PGM 8

RESULT 10
A33995
adipokinetin hormone - black horse fly
C:Species: Tabanus atratus (black horse fly)
C:Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997
C:Accession: A33995
R:Jaffee, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A:Title: Primary structure of two neuropeptide hormones with adipokinetin and hypotrehalose
A:Reference number: A33995; MUID:90046758
A:Accession: A33995
A:Molecule type: protein
A:Residues: 1-8 <JAF>
C:Superfamily: adipokinetin hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 22.0%; Score 24; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGM 13
|||
DB 6 PGM 8

RESULT 11
S55310
adipokinetin hormone - damselfly (Pseudagrion inconspicuum)
N:Alternate names: Psi-AKH
C:Species: Pseudagrion inconspicuum
C:Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
C:Accession: S55310
R:Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A:Title: A novel adipokinetin octapeptide found in the damselflies Pseudagrion inconspicuum
A:Reference number: S55310; MUID:94379987
A:Accession: S55310
A:Molecule type: protein
A:Residues: 1-8 <JAN>
C:Superfamily: adipokinetin hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 22.0%; Score 24; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGM 13
|||
DB 6 PGM 8

RESULT 12
A58620
adipokinetin hormone - damselfly (Ischnura senegalensis)
C:Species: Ischnura senegalensis
C:Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
C:Accession: A58620
R:Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A:Title: A novel adipokinetin octapeptide found in the damselflies Pseudagrion inconspicuum
A:Reference number: S55310; MUID:94379987
A:Accession: A58620
A:Molecule type: protein
A:Residues: 1-8 <JAN>
C:Superfamily: adipokinetin hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 22.0%; Score 24; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGM 13
|||
DB 6 PGM 8

RESULT 13
A43405
6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2,6-bisphosphate 2-phosphatase (EC 3.1.3.11)
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Mar-2000
C:Accession: A43405
R:Ventura, F.; Rosa, J.L.; Ambrosio, S.; Pilakis, S.J.; Bartons, R.
J. Biol. Chem. 267, 17939-17943, 1992
A:Title: Bovine brain 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase. Evidence

RESULT 3
S39030
lysyl-bradykinin - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 19-Apr-1996
C:Accession: S39030
R:Conlon, J.M.; Olson, K.R.
FEBS Lett. 334, 75-78, 1993
A:Title: Purification of a vasoactive peptide related to lysyl-bradykinin from trout pia
A:Reference number: S39030; MUID:94039817
A:Accession: S39030
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <CON>

Query Match 26.6%; Score 29; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 EREPGW 13
: | | |
Db 1 KRPPGW 6

RESULT 4
PH1788
T cell receptor alpha chain V region (clone 2PBL V alpha 24-4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1788
R:Porcell, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585
A:Accession: PH1788
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <FOR>

Query Match 24.8%; Score 27; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 HLOGER 10
: | | |
Db 1 HLCGER 7

RESULT 5
PH1802
T cell receptor alpha chain V region (clone 3PBL V alpha 24-8) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1802
R:Porcell, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585
A:Accession: PH1802
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-17 <FOR>

Query Match 22.9%; Score 25; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 HLOGER 9
: | | |
Db 1 HLCGER 6

RESULT 6
PH1822
T cell receptor alpha chain V region (clone 5PBL V alpha 24-5) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1822
R:Porcell, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blo
A:Reference number: PH1754; MUID:93301585
A:Accession: PH1822
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-17 <FOR>

Query Match 22.9%; Score 25; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 HLOGER 9
: | | |
Db 1 HLCGER 6

RESULT 7
F49215
urease (EC 3.5.1.5) small chain urea - Helicobacter mustelae (ATCC 43772) (fragment)
C:Species: Helicobacter mustelae
C:Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 30-May-1997
C:Accession: F49215
R:Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.
Infect. Immun. 60, 5259-5266, 1992
A:Title: Purification and characterization of the urease enzymes of Helicobacter spec
A:Reference number: A49215; MUID:93084378
A:Accession: F49215
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <TUR>
A:Note: Sequence extracted from NCBI backbone (NCBI:119487)
C:Superfamily: urease 26k chain; urease 11k chain homology; urease 12k chain homology
C:Keywords: hydrolase

Query Match 22.9%; Score 25; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LLLHLOGE 8
: | | |
Db 9 MMLHYAGE 16

RESULT 8
A34626
RPGH-related neuropeptide - ferruginous spindie
C:Species: Fuscus ferrugineus (ferruginous spindie)
C:Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C:Accession: A34626
R:Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake,
Biochem. Biophys. Res. Commun. 167, 273-279, 1990
A:Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A:Reference number: A34626; MUID:90179762
A:Accession: A34626
A:Status: preliminary
A:Molecule type: protein

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:30:07 ; Search time 112.59 seconds

(without alignments)
11.273 Million cell updates/sec

Title: US-08-934-367-12

Sequence: 1 LLLHIGGERPGWIKQLFTN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0
Maximum DB seq length: 20Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-65:*

1: pir1:*\n2: pir2:*\n3: pir3:*\n4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	31	28.4	18	2	G02018	proteasome chain L
2	30	27.5	16	2	PH1790	T cell receptor al
3	29	26.6	10	2	S39030	lysl-bradykinin -
4	27	24.8	15	2	PH1788	T cell receptor al
5	25	22.9	17	2	PH1802	T cell receptor al
6	25	22.9	17	2	PH1822	T cell receptor al
7	25	22.9	18	2	F49215	urease (EC 3.5.1.5
8	24	22.0	4	2	A34626	RCR-related neuro
9	24	22.0	8	2	A61348	red pigment-concen
10	24	22.0	8	2	A33995	adipokineic hormo
11	24	22.0	8	2	S55310	adipokineic hormo
12	24	22.0	8	2	A58620	adipokineic hormo
13	24	22.0	10	2	A43405	6-phosphofructo-2-
14	24	22.0	10	2	A60421	hypertrehalosemic
15	24	22.0	10	2	S08997	hypertrehalosemic
16	24	22.0	10	2	S08998	hypertrehalosemic
17	24	22.0	10	2	A26381	hypertrehalosemic
18	24	22.0	10	2	B33995	hypertrehalosemic
19	24	22.0	15	2	A26228	spot 42 protein -
20	24	22.0	15	2	PH1329	Ig heavy chain DJ
21	24	22.0	15	2	S38976	chromogranin A - b
22	24	22.0	16	2	PT0282	Ig heavy chain CDR
23	24	22.0	19	2	S29212	protein C - oat (f
24	24	22.0	20	2	A47687	3-dehydroquinatide
25	23	21.1	7	2	A61081	tyrosophyllin, basi
26	23	21.1	11	2	S68649	spermatheisin AON-3
27	23	21.1	15	2	S67975	apolipoprotein Cb2
28	23	21.1	16	1	A49761	locustapryokinin -
29	23	21.1	17	2	PH0778	T-cell receptor al

30	23	21.1	18	2	S71592	serine proteinase
31	23	21.1	19	2	PH1339	Ig heavy chain DJ
32	22	20.2	9	2	S78426	52.5k protein - sp
33	22	20.2	9	2	G56978	collagen alpha 1(I
34	22	20.2	11	2	D56979	collagen alpha 1(I
35	22	20.2	11	2	PD0442	NTPSNAP2 protein -
36	22	20.2	12	2	PQ0776	NADH dehydrogenase
37	22	20.2	13	2	A28505	neurotensin-like P
38	22	20.2	14	2	PH1347	Ig heavy chain DJ
39	22	20.2	14	2	PH1311	Ig heavy chain DJ
40	22	20.2	14	2	PH1321	Ig heavy chain DJ
41	22	20.2	14	2	PH1305	Ig heavy chain DJ
42	22	20.2	14	2	PH1306	Ig heavy chain DJ
43	22	20.2	15	2	PT0222	Ig heavy chain CDR
44	22	20.2	15	2	PH1314	Ig heavy chain DJ
45	22	20.2	15	2	PH1310	Ig heavy chain DJ

ALIGNMENTS

RESULT 1
G02018
proteasome chain IMP7 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 22-Jun-1999
C:Accession: G02018
R:Kim, T.
submitted to the EMBL Data Library, July 1995
A:Reference number: G09054
A:Accession: G02018
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18 <KIM>
A:Cross-references: EMBL:U32862; NID:q1045468; PIDN:AAA80234.1; PID:q1045469
C:Genetics:
A:Gene: IMP7
C:Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 28.4%; Score 31; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 1; Indels 0;
OY 9 REPGWIK 15
DB 4 KEDGWVK 10
RESULT 2
PH1790
T cell receptor alpha chain V region (clone 2PBL V alpha 24-6) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1790
R:Forcellini, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blo
A:Reference number: PH1754; MUID:93301585
A:Accession: PH1790
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <POR>

Query Match 27.5%; Score 30; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 HLOGEREP 11
DB 1 HLOGERGP 8

Thu Dec 21 08:51:15 2000

us-08-934-367-12.ra1

OY 12 GWIKOLF 18
11: 111
Db 5 GWLAOLF 11

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RESULT 14
PCT-US95-09262-13
; Sequence 13, Application PC/TUS9509262
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; City: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09262
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/10040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.38"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-13
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Query Match 30.3%; Score 33; DB 4; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWIKOLF 18
11: 111
Db 5 GWLAOLF 11

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RESULT 15
US-08-621-803-227
; Sequence 227, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; City: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 227:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.388"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-227
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Query Match 28.4%; Score 31; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWIKOLF 18
11: 111
Db 1 GWLIOLF 7

Search completed: December 21, 2000, 08:31:49
Job time: 372 sec

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02465
FILING DATE: 11-JAN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Noonan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,1133
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "BPI.38"
PCT-US94-02465-40

Query Match 30.3%; Score 33; DB 4; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 GWIKOLF 18
11:111
Db 5 GWIAOLF 11

RESULT 12
PCT-US95-00498-40
Sequence 40, Application PC/TUS9500498
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
TITLE OF INVENTION: Materials
NUMBER OF SEQUENCES: 237
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00498
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27129/32415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.38"
PCT-US95-00498-40

Query Match 30.3%; Score 33; DB 4; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 GWIKOLF 18
11:111
Db 5 GWIAOLF 11

RESULT 13
PCT-US95-00656-40
Sequence 40, Application PC/TUS9500656
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Anti-Fungal Materials and Methods
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00656
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27129/32415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.38"
PCT-US95-00656-40

Query Match 30.3%; Score 33; DB 4; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

APPLICANT: Little II, Roger G
APPLICANT: Lim, Edward
APPLICANT: Fadem, Mitchell B.
TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES: 252
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,259A
FILING DATE: 21-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/504,841
FILING DATE: 20-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11021US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 312/707-9155
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.38"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-13
Query Match 30.3%; Score 33; DB 2; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 12 GWIKOLF 18
DB 5 GWLAOLF 11
RESULT 10
US-09-119-263-40
; Sequence 40, Application US/09119263
; Patent No. 6054431
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; APPLICANT: Lambert, Lewis H.
; APPLICANT: Little, Roger G.
; TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
; TITLE OF INVENTION: Materials
; NUMBER OF SEQUENCES: 237
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois

COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,263
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/758,116
FILING DATE:
APPLICATION NUMBER: 08/372,783
FILING DATE:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27129/32415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.38"
US-09-119-263-40
Query Match 30.3%; Score 33; DB 3; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 12 GWIKOLF 18
DB 5 GWLAOLF 11
RESULT 11
PCT-US94-02465-40
; Sequence 40, Application PC/TUS9402465
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Biologically Active Peptides from
; TITLE OF INVENTION: Functional Domains of Bactericidal/Permeability-Increasing
; TITLE OF INVENTION: Protein and Uses Thereof
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "BPI.38"
US-08-473-344-40

Query Match 30.3%; Score 33; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWIKOLF 18
11: 111
DB 5 GWLAOLF 11

RESULT 7
US-08-621-803-39
; Sequence 39, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; NUMBER OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.38"
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note="The C-Terminus is Amidated."
US-08-621-803-39

Query Match 30.3%; Score 33; DB 2; Length 14;

Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 12 GWIKOLF 18
11: 111
DB 5 GWLAOLF 11

RESULT 8
US-08-485-445A-40
; Sequence 40, Application US/08485445A
; Patent No. 5856438
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.
; TITLE OF INVENTION: Biologically Active Peptides from
; TITLE OF INVENTION: Functional Domains of Bactericidal/
; TITLE OF INVENTION: Permeability-Increasing Protein and
; NUMBER OF SEQUENCES: 226
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: Suite 3400, 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,445A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11018US08/100-224.P4.C1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-707-8889
; TELEFAX: 312-707-9155
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "BPI.38"
US-08-485-445A-40

Query Match 30.3%; Score 33; DB 2; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWIKOLF 18
11: 111
DB 5 GWLAOLF 11

RESULT 9
US-08-621-259A-13
; Sequence 13, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:

;; TITLE OF INVENTION: Biologically Active Peptides from
;; TITLE OF INVENTION: Functional Domains of Bactericidal/
;; TITLE OF INVENTION: Permeability-Increasing Protein and
;; TITLE OF INVENTION: Uses Thereof
;; NUMBER OF SEQUENCES: 226
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Allegretti & Witcoff, Ltd.
;; STREET: Suite 3000, 10 S. Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
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;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 08/209,762
;; FILING DATE: 11-MAR-1994
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 08/183,222
;; FILING DATE: 14-JAN-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McDonnell, John J.
;; REGISTRATION NUMBER: 26,949
;; REFERENCE/DOCKET NUMBER: 93,1133-
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000
;; TELEFAX: 312-715-1234
;; INFORMATION FOR SEQ ID NO: 40:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: misc.feature
;; OTHER INFORMATION: "BPI.38"
;; US-08-306-473A-40
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Query Match 30.3%; Score 33; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 12 GWIKOLF 18
11:111
DB 5 GWLAOLF 11
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RESULT 5
US-08-209-762-40
;; Sequence 40, Application US/08209762
;; Patent No. 5733872
;; GENERAL INFORMATION:
;; APPLICANT: Little, Roger G.
;; TITLE OF INVENTION: Biologically Active Peptides from
;; TITLE OF INVENTION: Functional Domains of Bactericidal/Permeability-Increasing
;; TITLE OF INVENTION: Protein and Uses Thereof
;; NUMBER OF SEQUENCES: 98
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Allegretti & Witcoff, Ltd.
;; STREET: 10 South Wacker Drive, Suite 3000
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/209,762
;; FILING DATE: 11-JAN-1994
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5733872nan, Kevin E
;; REGISTRATION NUMBER: 35,303
;; REFERENCE/DOCKET NUMBER: 93,1133
;; TELECOMMUNICATION INFORMATION:
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;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: misc.feature
;; OTHER INFORMATION: "BPI.38"
;; US-08-209-762-40
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Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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DB 5 GWLAOLF 11
;
RESULT 6
US-08-473-344-40
;; Sequence 40, Application US/08473344
;; Patent No. 5763567
;; GENERAL INFORMATION:
;; APPLICANT: Little, Roger G.
;; TITLE OF INVENTION: Biologically Active Peptides from
;; TITLE OF INVENTION: Functional Domains of Bactericidal/Permeability-Increasing
;; TITLE OF INVENTION: Protein and Uses Thereof
;; NUMBER OF SEQUENCES: 98
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Banner & Allegretti, Ltd.
;; STREET: 10 South Wacker Drive, Suite 3000
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/473,344
;; FILING DATE: 7-JUN-1995
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/306,473
;; FILING DATE: 15-SEP-1995
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/209,762
;; FILING DATE: 11-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McDonnell, John J.
;; REGISTRATION NUMBER: 26,949
;; REFERENCE/DOCKET NUMBER: 93,1133-J
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000

US-08-311-611A-40

Query Match 30.3%; Score 33; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 GWIKOLF 18
DB 5 GWIKOLF 11

RESULT 2
US-08-372-783-40
; Sequence 40, Application US/08372783
; Patent No. 5578572
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; APPLICANT: Lambert, Lewis H.
; APPLICANT: Little, Roger G.
; TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
; NUMBER OF SEQUENCES: 237
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,783
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
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; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.38"
US-08-372-783-40

Query Match 30.3%; Score 33; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 12 GWIKOLF 18
DB 5 GWIKOLF 11

DB 5 GWIKOLF 11

RESULT 3
US-08-372-105-40
; Sequence 40, Application US/08372105
; Patent No. 5627153
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.
; APPLICANT: Lim, Edward
; APPLICANT: Lambert, Lewis H.
; APPLICANT: Scannon, Patrick J.
; TITLE OF INVENTION: Anti-Fungal Materials and Methods
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,105
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.38"
US-08-372-105-40

Query Match 30.3%; Score 33; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 12 GWIKOLF 18
DB 5 GWIKOLF 11

RESULT 4
US-08-306-473A-40
; Sequence 40, Application US/08306473A
; Patent No. 5652332
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:31:49 ; Search time 99.91 seconds
(without alignments)
3.355 Million cell updates/sec

Title: US-08-934-367-12
Perfect score: 109
Sequence: 1 LLLHLOGEREPGKINQLFTN 20

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Searched: 164575 seqs, 16761186 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	33	30.3	14	US-08-372-783-40	Sequence 40, Appl
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4	33	30.3	14	US-08-306-473A-40	Sequence 40, Appl
5	33	30.3	14	US-08-209-762-40	Sequence 40, Appl
6	33	30.3	14	US-08-473-344-40	Sequence 39, Appl
7	33	30.3	14	US-08-621-803-39	Sequence 40, Appl
8	33	30.3	14	US-08-485-445A-40	Sequence 13, Appl
9	33	30.3	14	US-08-621-259A-13	Sequence 40, Appl
10	33	30.3	14	US-09-119-263-40	Sequence 40, Appl
11	33	30.3	14	PCT-US94-02465-40	Sequence 40, Appl
12	33	30.3	14	PCT-US95-00656-40	Sequence 13, Appl
13	33	30.3	14	PCT-US95-09262-13	Sequence 227, App
14	33	30.3	14	US-08-621-803-227	Sequence 219, App
15	33	28.4	10	US-08-621-259A-219	Sequence 228, App
16	33	28.4	10	US-08-621-803-228	Sequence 220, App
17	33	28.4	11	US-08-621-259A-220	Sequence 230, App
18	33	28.4	11	US-08-621-803-230	Sequence 222, App
19	33	28.4	12	US-08-621-259A-222	Sequence 33, Appl
20	33	28.4	13	US-08-261-660A-33	Sequence 42, Appl
21	33	28.4	13	US-08-261-660A-42	Sequence 33, Appl
22	33	28.4	13	PCT-US94-06931-42	Sequence 42, Appl
23	33	28.4	13	PCT-US94-06931-33	Sequence 33, Appl
24	33	28.4	14	US-08-311-611A-15	Sequence 15, Appl
25	33	28.4	14	US-08-311-611A-33	Sequence 33, Appl
26	33	28.4	14	US-08-311-611A-34	Sequence 34, Appl
27	33	28.4	14	US-08-311-611A-35	Sequence 35, Appl
28	33	28.4	14	US-08-311-611A-35	Sequence 35, Appl

29	31	28.4	14	US-08-311-611A-36	Sequence 36, Appl
30	31	28.4	14	US-08-311-611A-44	Sequence 44, Appl
31	31	28.4	14	US-08-311-611A-45	Sequence 45, Appl
32	31	28.4	14	US-08-311-611A-46	Sequence 46, Appl
33	31	28.4	14	US-08-311-611A-81	Sequence 81, Appl
34	31	28.4	14	US-08-311-611A-89	Sequence 89, Appl
35	31	28.4	14	US-08-311-611A-91	Sequence 91, Appl
36	31	28.4	14	US-08-311-611A-106	Sequence 106, App
37	31	28.4	14	US-08-311-611A-107	Sequence 107, App
38	31	28.4	14	US-08-311-611A-109	Sequence 110, App
39	31	28.4	14	US-08-311-611A-110	Sequence 112, App
40	31	28.4	14	US-08-311-611A-122	Sequence 142, App
41	31	28.4	14	US-08-311-611A-142	Sequence 15, Appl
42	31	28.4	14	US-08-372-783-15	Sequence 33, Appl
43	31	28.4	14	US-08-372-783-93	Sequence 34, Appl
44	31	28.4	14	US-08-372-783-94	Sequence 62, Appl
45	31	28.4	14	PCT-US95-09262-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-08-311-611A-40
; Sequence 40, Application US/08311611A
; Patent No. 5523288
; GENERAL INFORMATION:
; APPLICANT: Cohen, Jonathan
; APPLICANT: Kung, Ada H.C.
; APPLICANT: Lambert, Jr., Lewis H.
; TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial
; TITLE OF INVENTION: Infection by Administration of
; TITLE OF INVENTION: Bactericidal/Permeability-Increasing
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borum
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/311,611A
; APPLICATION NUMBER: US/08/311,611A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,401
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/125,651
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 32251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "BPI.38"

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95105146.
RA Flynn T.R., Hollenberg A.N., Cohen O., Menke J.B., Usala S.J.,
RA Tollin S., Hegarty M.K., Wondisford F.E.;
RT "A novel C-terminal domain in the thyroid hormone receptor selectively
mediates thyroid hormone inhibition.";
RL J. Biol. Chem. 269:32713-32716(1994).
SQ SEQUENCE 16 AA; 1920 MW; 79A831A4F3C8E22F CRC64;

Query Match 22.9%; Score 22; DB 4; Length 16;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 11 KLFSLDPQ 20
II : : I I
DB 4 KILMKVTDLQ 13

Search completed: December 21, 2000, 08:35:39
Job time: 602 sec

09TS18
ID 09TS18 PRELIMINARY: PRT: 20 AA.
AC 09TS18:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CYTOTOXIN-BINDING PROTEIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94039134.
RA Lutz F., Mohr M., Grimmig M., Leidolf R., Linder D.:
RT *Pseudomonas aeruginosa cytotoxin-binding protein in rabbit
erythrocyte membranes. An oligomer of 28 kDa with similarity to
transmembrane channel proteins. J.
RL Eur. J. Biochem. 217:1123-1128(1993).
SO SEQUENCE 20 AA; 2414 MW; 40B82D7DB5283D2D CRC64;

Query Match 24.0%; Score 23; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 9 KKKLF 13
DB 5 KKKLF 9

RESULT 12
ID P82138 PRELIMINARY: PRT: 20 AA.
AC P82138:
DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S15 (FRAGMENT).
OS Spirochaetaceae (Spirochaeta).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Caryophyllidae; Caryophyllales;
OC Chenopodiaceae; Spinacia.
RN [1]
RP SEQUENCE.
RC STRAIN-CV. ALVARO; TISSUE-LEAF;
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.:
RT Identification of all the proteins in the small subunit of an
organella (chloroplast) ribosome. J.
RL J. Biol. Chem. 0:0-0(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND OTHER PLASTIDS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- SIMILARITY: BELONGS TO THE S15P FAMILY OF RIBOSOMAL PROTEINS.
DR INTERPRO: IPR000589; -
DR PROSITE: PS00362; RIBOSOMAL_S15; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 20
SO SEQUENCE 20 AA; 2294 MW; B613012072A648A3 CRC64;

Query Match 24.0%; Score 23; DB 8; Length 20;
Best Local Similarity 44.4%; Pred. No. 2.9e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 9 KKKLFSL 17
DB 2 KKNSEISVI 10

RESULT 13
ID 008806 PRELIMINARY: PRT: 20 AA.

AC 008806:
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE SERINE PROTEINASE INHIBITOR 14 (SERINE PROTEINASE INHIBITOR MNS26)
DE (FRAGMENT).
GN Sp14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA Sun J., Ooms L., Bird C.H., Sutton V.R., Trapani J.A., Bird P.I.:
RL J. Biol. Chem. 0:0-0(0).
DR EMBL: U96709; AAB57821.1; -
DR MGD: MGI:894672; Sp14.
FT NON_TER 1
FT NON_TER 20
SO SEQUENCE 20 AA; 2039 MW; 38571040F8263692 CRC64;

Query Match 24.0%; Score 23; DB 11; Length 20;
Best Local Similarity 46.7%; Pred. No. 2.9e+03;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 3 VQASYSKKKFLSL 17
DB 4 VAASAGKILFSSMV 18

RESULT 14
ID P78533 PRELIMINARY: PRT: 15 AA.
AC P78533:
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE DEOXYGUANOSINE KINASE (EC 2.7.1.113) (FRAGMENT).
GN DCK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Johansson M., Karlsson A.:
RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + DEOXYGUANOSINE - ADP + dGMP.
DR EMBL: U62042; AAB48932.1; -
KW transferase.
FT NON_TER 15
FT NON_TER 15
SO SEQUENCE 15 AA; 1706 MW; 53575609CC614F8E CRC64;

Query Match 22.9%; Score 22; DB 4; Length 15;
Best Local Similarity 71.4%; Pred. No. 3.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 11 KFLSL 17
DB 5 RLFLSL 11

RESULT 15
ID 09UD41 PRELIMINARY: PRT: 16 AA.
AC 09UD41:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE BETA-ISOFORM THYROID HORMONE RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

Query Match 25.0%; Score 24; DB 2; Length 18;
 Best Local Similarity 71.4%; Pred. No. 1.8e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 10 KKLFLSL 16
 1111 :1
 DB 2 KKLFLAL 8

RESULT 7
 ID O9RAE9 PRELIMINARY; PRT; 20 AA.
 AC O9RAE9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE COA THIOESTERASE (FRAGMENT).
 OS Rhodopseudomonas palustris.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Bradyrhizobium group; Rhodopseudomonas.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 96171228.
 RA Kiver J., Xu Y., Gibson J.;
 RT Metabolism of cyclohexane carboxylic acid by the photosynthetic
 bacterium Rhodopseudomonas palustris.";
 RT Arch. Microbiol. 164:337-345(1995).
 RL Arch. Microbiol. 164:337-345(1995).
 SQ SEQUENCE 20 AA; 2259 MW; 870D483384D4315 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 20;
 Best Local Similarity 46.2%; Pred. No. 2e+03;
 Matches 6; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

OY 10 KKLFLSL 20
 1111 :1
 DB 2 KKLFLSL 14

RESULT 8
 ID P78199 PRELIMINARY; PRT; 17 AA.
 AC P78199;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE PROBABLE N-ACTEYLTRANSFERASE (PC 3.5.1.28) (FRAGMENT).
 GN AMT.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-K12;
 RX MEDLINE: 97349980.
 RA Yamamoto Y., Abba H., Baba T., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
 RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
 RA Oshima T., Oyama S., Saito N., Sempel G., Satoh Y., Sivasundaram S.,
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
 RA Yamagata S., Horiuchi T.;
 RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
 -K12 genome corresponding to 50,0-68.8 min on the linkage map and
 RT analysis of its sequence features.";
 RL DNA Res. 4:91-113(1997).
 DR EMBL: D90874; BAA16324.1; -.
 FT NON_TER 1
 SQ SEQUENCE 17 AA; 2192 MW; 02EDC1B821D3431D CRC64;

Query Match 24.0%; Score 23; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 2.5e+03;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 OY 4 QASYSKR 11
 1111 :1
 DB 10 QAKSKKR 17

RESULT 9
 ID Q56610 PRELIMINARY; PRT; 18 AA.
 AC Q56610;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE ACCA (FRAGMENT).
 GN ACCA.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-C6706;
 RX MEDLINE: 97074686.
 RA Franco A., Peir-Eu Y., Johnson J., Barry E.M., Guerra H., Maurer R.,
 RA Morris J.G.;
 RT "Cloning and characterization of dnaE, encoding the catalytic subunit
 of replicative DNA polymerase III, from Vibrio cholerae strain
 RT C6706.";
 RL Gene 175:281-283(1996).
 DR EMBL: U30472; AAC44579.1; -.
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 2153 MW; 18BCDAD212842EF CRC64;

Query Match 24.0%; Score 23; DB 2; Length 18;
 Best Local Similarity 57.1%; Pred. No. 2.6e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 14 LSLDFQ 20
 1111 :1
 DB 3 LNFLDFE 9

RESULT 10
 ID Q9QVB0 PRELIMINARY; PRT; 18 AA.
 AC Q9QVB0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE (Ca2+-Mg2+)-ATPASE (FRAGMENT).
 GN Rattus sp.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 93054417.
 RA Ezaki J., Himeno M., Kato K.;
 RT "Purification and characterization of (Ca2+-Mg2+)-ATPase in rat liver
 RT lysosomal membranes.";
 RL J. Biochem. 112:33-39(1992).
 SQ SEQUENCE 18 AA; 2008 MW; 8314BA373ED6AA47 CRC64;

Query Match 24.0%; Score 23; DB 11; Length 18;
 Best Local Similarity 44.4%; Pred. No. 2.6e+03;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 9 KKLFLSL 17
 1111 :1
 DB 6 KERFVFL 14

RESULT 11

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GN NISG.
OS Lactococcus lactis.
OC Plasmid pLEB513.
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-N8; TRANSPOSON-TN5481;
RA Immonen T., Wahlstrom G., Takala T., Saris P.E.J.;
RT *Evidence for a mosaic structure of the Tn5481 in Lactococcus lactis
RT N8.*;
RL DNA Seq. 9:245-261(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-N8; TRANSPOSON-TN5481;
RA Immonen T., Saris P.E.J.;
RT *Characterization of the nisFEG operon of the nisin Z producing
RT Lactococcus lactis subsp. lactis N8 strain.*;
RL DNA Seq. 9:263-274(1998).
DR EMBL: AJ000993; CAA04441.1; -.
KW plasmid.
FT NON_TER.
SQ SEQUENCE 19 AA; 2139 MW; 6A429DC80E673613 CRC64;

Query Match
Best Local Similarity 27.1%; Score 26; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 TVQASYSKKKL 12
Db 7 TILVALSKKKI 18

RESULT 3
P97522 PRELIMINARY; PRT; 18 AA.
AC P97522;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE CFTR GENE.
GN CFTR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RA Vulliamier S., Denamur E.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: X95927; CAA65168.1; -.
SQ SEQUENCE 18 AA; 2158 MW; 5C5855056C1CE6DE CRC64;

Query Match
Best Local Similarity 26.0%; Score 25; DB 11; Length 18;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 3 VOASYSKKKLFLSLDFO 20
Db 1 WQSPLEKASFYSKLFPR 18

RESULT 4
O9URE0 PRELIMINARY; PRT; 15 AA.
AC O9URE0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE TYPE II TOPOISOMERASE, TOPOISOMERASE II.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;

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OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RA Elisea S.H., Hsiung Y., Ntliis J.L., Osheroff N.;
RL J. Biol. Chem. 270:1913-1920(1995).
SQ SEQUENCE 15 AA; 2094 MW; 0A6A37F6E81E85F6 CRC64;

Query Match
Best Local Similarity 25.0%; Score 24; DB 3; Length 15;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 7 YSKKKFLS 15
Db 2 YOKRKDYMS 10

RESULT 5
O9UCH4 PRELIMINARY; PRT; 15 AA.
AC O9UCH4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE NATURAL KILLER ENHANCING FACTOR, NKEF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE: 93215001.
RA Shau H., Gupta R.K., Golub S.H.;
RT *Identification of a natural killer enhancing factor (NKEF) from human
RT erythroid cells.*;
RL Cell. Immunol. 147:1-11(1993).
SQ SEQUENCE 15 AA; 1738 MW; 4909DA4793D382BF CRC64;

Query Match
Best Local Similarity 25.0%; Score 24; DB 4; Length 15;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 3 VOASYSKKKLFL 14
Db 2 VOAFQCKVNVFL 13

RESULT 6
O06514 PRELIMINARY; PRT; 18 AA.
AC O06514;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-JUL-1997 (TREMBlrel. 04, Last annotation update)
DE DNA, MOSAIC MERCURY RESISTANCE TRANSPOSABLE ELEMENT
DE (MER-OPERON)1040 BP (FRAGMENT).
GN MERP.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CH210; TRANSPOSON-TN5059;
RX MEDLINE: 97303088.
RA Nikiforov V., Kholodil G., Minakhin L., Gorlenko Z., Kalyeva E.,
RA Mindlin S., Nikiforov V.;
RT *Intercontinental spread of promiscuous mercury-resistance transposons
RT in environmental bacteria.*;
RL Mol. Microbiol. 24:321-329(1997).
DR EMBL: Y09026; CAA70241.1; -.
FT NON_TER.
SQ SEQUENCE 18 AA; 1899 MW; 484A2D7197814DF9 CRC64;

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:35:39 ; Search time 157.2 Seconds
(without alignments)
11.880 Million cell updates/sec

Title: US-08-934-367-11
Perfect score: 96
Sequence: 1 TTVOASYSKKKFLSLDLPQ 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mbc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	27.1	18	3 Q02414	Q02414 aspergillus
2	26	27.1	19	2 Q9RL04	Q9RL04 lactococcus
3	25	26.0	18	11 P97522	P97522 ratius norv
4	24	26.0	15	3 Q9URE0	Q9URE0 saccharomyc
5	24	25.0	15	4 Q9UCH4	Q9UCH4 homo sapien
6	24	25.0	18	2 Q06514	Q06514 escherichia
7	24	25.0	20	2 Q9R4E9	Q9R4E9 rhodospseudo
8	23	24.0	17	2 P78199	P78199 escherichia
9	23	24.0	18	2 Q56610	Q56610 vibrio chol
10	23	24.0	18	11 Q9QVB0	Q9QVB0 rattus sp.
11	23	24.0	20	6 Q9RS18	Q9RS18 oryctolagus
12	23	24.0	20	8 P82138	P82138 spinacia ol
13	23	24.0	20	11 Q08806	Q08806 mus musculu
14	22	22.9	15	4 P78533	P78533 homo sapien
15	22	22.9	16	4 Q9UD41	Q9UD41 homo sapien
16	22	22.9	16	6 Q9TRA2	Q9TRA2 sus scrofa
17	22	22.9	17	11 Q92170	Q92170 mus musculu
18	22	22.9	19	4 Q9UMM9	Q9UMM9 homo sapien
19	22	22.9	19	6 Q9TRF3	Q9TRF3 macropus gl

20	21	21.9	9	2 Q45852	Q45852 clostridium
21	21	21.9	12	11 Q54970	Q54970 mus musculu
22	21	21.9	14	2 Q9R506	Q9R506 burkholderi
23	21	21.9	18	11 Q9QUZ8	Q9QUZ8 rattus sp.
24	21	21.9	19	3 Q92321	Q92321 saccharomyc
25	21	21.9	20	2 Q49448	Q49448 mycoplasma
26	21	21.9	20	9 Q37868	Q37868 bacterioph
27	21	21.9	20	12 Q86935	Q86935 human herpe
28	21	21.9	20	12 Q86936	Q86936 human herpe
29	21	21.9	20	12 Q86937	Q86937 human herpe
30	21	21.9	20	12 Q86938	Q86938 human herpe
31	21	21.9	20	12 Q86939	Q86939 human herpe
32	21	21.9	20	12 Q86940	Q86940 human herpe
33	21	21.9	20	12 Q86941	Q86941 human herpe
34	21	21.9	20	12 Q86942	Q86942 human herpe
35	20.5	21.4	19	13 Q9PRP1	Q9PRP1 gallus gall
36	20	20.8	13	11 Q62354	Q62354 mus musculu
37	20	20.8	13	11 Q62355	Q62355 mus musculu
38	20	20.8	15	2 Q68425	Q68425 buchnera ap
39	20	20.8	15	2 Q9R4Y0	Q9R4Y0 pseudomonas
40	20	20.8	16	2 Q47605	Q47605 escherichia
41	20	20.8	16	2 Q9R4L0	Q9R4L0 spiroplasma
42	20	20.8	16	10 Q9S8A4	Q9S8A4 secale cere
43	20	20.8	16	12 Q79458	Q79458 human immun
44	20	20.8	17	8 Q9ZY77	Q9ZY77 trissolcus
45	20	20.8	18	2 Q46390	Q46390 clostridium

ALIGNMENTS

RESULT 1	Q02414	PRELIMINARY;	PRT;	18 AA.
ID	Q02414;			
AC	Q02414;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)			
DE	OROTIDINE-5'-MONOPHOSPHATE DECARBOXYLASE (FRAGMENT).			
GN	PYRG.			
OS	Aspergillus awamori.			
OC	Eukaryota; Fungi; Ascomycota; Eurotiiales; Trichocomaceae;			
NC	anamorphic Trichocomaceae; Aspergillus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 96031709.			
RA	Gouka R.J., Hessing J.G., Stam H., Musters W., Hondel C.A.;			
RT	"A novel strategy for the isolation of defined pyrg mutants and the development of a site-specific integration system for Aspergillus awamori."			
RL	Curr. Genet. 27:536-540(1995).			
DR	EMBL; S79674; AAB35350.1; -.			
FT	NON_TER	1	1	
SO	SEQUENCE	18 AA;	1891 MW;	E1A0E34C7D23688E CRC64;
QY	2 TVQASYSKKKFLSLD 18			
DB	2 TVQASYSKKKFLSLD 18			
RESULT 2	Q9RL04	PRELIMINARY;	PRT;	19 AA.
ID	Q9RL04;			
AC	Q9RL04;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)			
DE	NISG PROTEIN (FRAGMENT).			

Query Match 27.1%; Score 26; DB 3; Length 18;
Best Local Similarity 41.2%; Pred. No. 8.1e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

RL Arch. Insect Biochem. Physiol. 39:1-8(1998).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
CC AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
CC BIOSYNTHESIS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-TU/EF-1A SUBFAMILY.
DR INTERPRO: IPR000795; -
DR PROSITE: PS00301; EFACOR_GTP: PARTIAL.
DR Elongation factor: Protein biosynthesis; GTP-binding.
FW NON_TER 15 15
SQ SEQUENCE 15 AA: 1670 MW: 1EB7DA05B09B3751 CRC64;

QY Query Match 19.8%; Score 19; DB 1; Length 15;
Best Local Similarity 20.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 8 SKKRLFLSL 17
1 AKKIHINIV 10

RESULT 14
RL6_VIBPR STANDARD: PRT: 16 AA.
AC Q56715;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 50S RIBOSOMAL PROTEIN L6 (FRAGMENT).
GN RPLF.
OS Vibrio proteolyticus (Aeromonas proteolytica).
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15338;
RX MEDLINE: 97149305.
RA Selterquist R.A., Smith G.K., Oakley T.H., Lee Y.H., Fox G.E.;
RT "Sequence, overproduction and purification of Vibrio proteolyticus
RT ribosomal protein L18 for in vitro and in vivo studies."
RL Gene 183:237-242(1996).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
CC LOCATED AT THE AMINOACYL-TRNA BINDING SITE OF THE
CC PEPTIDYLTRANSFERASE CENTER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L6P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL: U38943; AAB41328.1; -
DR INTERPRO: IPR002358; -
DR PROSITE: PS00525; RIBOSOMAL_L6_1; PARTIAL.
KW Ribosomal protein; tRNA-binding.
FT NON_TER 1 1
SQ SEQUENCE 16 AA: 1935 MW: A8C19078DF581B6C CRC64;

Query Match 19.8%; Score 19; DB 1; Length 16;
Best Local Similarity 44.4%; Pred. No. 2.5e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 VOASYSKKK 11
1: :|||
Db 8 VRTKRAKK 16

RESULT 15

PHSL_DESBN
ID PHSL_DESBN STANDARD: PRT: 19 AA.
AC P13066;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PERIPLASMIC [NIFESE] HYDROGENASE LARGE SUBUNIT (EC 1.18.99.1) (NIFESE
DE HYDROGENIVASE LARGE CHAIN) (FRAGMENT).
OS Desulfotribrio baculatus (strain Norway 4).
OC Bacteria; Proteobacteria; delta subdivision; Desulfotribriobium.
RN [1]
RP SEQUENCE.
RX MEDLINE: 88106446.
RA Prickril B.C., He S.H., Li C., Menon N., Choi E.S., Przybyla A.E.,
RA Derrattarian D.V., Peck H.D. Jr., Faugue G., le Gall J., Teixeira M.,
RA Moura I., Moura J.J.G., Patil D., Huynh B.H.;
RT "Identification of three classes of hydrogenase in the genus,
RT Desulfotribrio."
RL Biochem. Biophys. Res. Commun. 149:369-377(1987).
CC -1- CATALYTIC ACTIVITY: 2 REDUCED FERREDOXIN + 2 H(+) = 2 OXIDIZED
CC FERREDOXIN + H(2).
CC -1- COFACTOR: ONE NICKEL ION, TWO 4FE-4S CLUSTERS AND ONE
CC SELENOCYSTEINE.
CC -1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL SUBUNIT.
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE [NIFESE]/[NIFESE] HYDROGENASE LARGE
CC SUBUNIT FAMILY.
DR PIR: H27480; H27480.
DR INTERPRO: IPR001501; -
DR PROSITE: PS00507; NI_HGENASE_L_1; PARTIAL.
DR PROSITE: PS00508; NI_HGENASE_L_2; PARTIAL.
KW Oxidoreductase; Periplasmic; Nickel; Selenium; Selenocysteine.
FT NON_TER 19 19
SQ SEQUENCE 19 AA: 1942 MW: 2BFCD2D360F00367 CRC64;

Query Match 19.8%; Score 19; DB 1; Length 19;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 ASYSKKKL 12
1: :|||
Db 7 AADGKKKI 14

Search completed: December 21, 2000, 08:32:59
Job time: 442 sec

FT NON_TER 15 15
SQ SEQUENCE 15 AA: 1732 MW: 5309A3CADDADA1 CRC64:

Query Match
Best Local Similarity 20.8%; Score 20; DB 1; Length 15;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 SYSKKRL 12
DB 1 NYMKPL 7

RESULT 10
RIPK_TRIKI STANDARD; PRT: 16 AA.

AC P16093;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE RIBOSOME-INACTIVATING PROTEIN TRICHOKIRIN (RNA N-GLYCOSIDASE)
DE (EC 3.2.2.22) (FRAGMENT)
OS Trichosanthes kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Cucurbitales; Cucurbitaceae; Trichosanthes.
RN [1]
RP SEQUENCE:
RC TISSUE=SEED;
RX MEDLINE: 89005108.

RA Casellas P., Dussosoy D., Falasca A.I., Barbieri L.,
RA Guilleminot J.C., Ferrara P., Bolognesi A., Centini P., Stirpe F.;
RT "Trichokirin, a ribosome-inactivating protein from the seeds of
RT Trichosanthes kirilowii Maximowicz. Purification, partial
RT characterization and use for preparation of immunotoxins.";
RT Eur. J. Biochem. 176:581-588(1988).

CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.

CC -1- PTM: GLYCOSYLATED.

CC -1- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
CC PROTEINS. BELONGS TO TYPE 1 RIP.

DR PIR: S01669; S01669.

DR INTERPRO: IP001574; -;
DR PROSITE: PS00275; SHIGA_RICIN; PARTIAL.

KW Protein synthesis inhibitor; Hydrolase; Toxin; Glycoprotein.

FT NON_TER

SQ SEQUENCE 16 AA: 1605 MW: 5E268A7F345935A2 CRC64:

Query Match
Best Local Similarity 20.8%; Score 20; DB 1; Length 16;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 ASYSK 9
DB 12 ASTEK 16

RESULT 11
B44K_PORGI

ID B44K_PORGI STANDARD; PRT: 8 AA.

AC P8186;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE 44 KDA IMMUNOGENIC PROTEIN (FRAGMENT).

OS Porphyromonas gingivalis (Bacteroides gingivalis).

OC Bacteria; CFB group; Bacteroidaceae; Porphyromonas.

RN [1]

RP SEQUENCE.

RX STRAIN=VPB 3492;

RA MEDLINE: 20198497.

RA Norris J.M., Love D.N.;

RT "Serum antibody responses of cats to soluble whole cell antigens of
RT feline porphyromonas gingivalis.";
RT Vet. Microbiol. 73:37-49(2000).
CC -1- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
KW Antigen.
FT NON_TER

Query Match
Best Local Similarity 19.8%; Score 19; DB 1; Length 8;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 ASYSKKRL 12
DB 1 APYOKRNI 8

RESULT 12
MAST_VESBA

ID MAST_VESBA STANDARD; PRT: 14 AA.

AC P21654;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 01-AUG-1992 (Rel. 23, Last annotation update)

DE MASTOPARAN B.

OS Vespa basalis (Hornet).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Vespidae; Vespinae; Vespinae; Vespa.

RN [1]

RP SEQUENCE.

RC TISSUE=VENOM;

RX MEDLINE: 91174755.

RA Lo C.-L., Hwang L.-L.;

RT "Structure and biological activities of a new mastoparan isolated
RT from the venom of the hornet Vespa basalis.";

RT Biochem. J. 274:453-456(1991).

CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
CC THAT COUPLE TO PHOSPHOLIPASE C.

DR PIR: S14336; S14336.

KW Mast cell degranulation; Venom; Amidation.

FT MOD_RES 14 AMIDATION.

SQ SEQUENCE 14 AA: 1613 MW: D35944CA193A19A2 CRC64:

Query Match
Best Local Similarity 19.8%; Score 19; DB 1; Length 14;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 SYSKKRL 12
DB 8 SMKKVL 14

RESULT 13
EF1A_MICCR

ID EF1A_MICCR STANDARD; PRT: 15 AA.

AC P8126;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (FRAGMENT).

OS Microplitis croceipes.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;

OC Ichneumonidae; Braconidae; Microgasterinae; Microplitis.

RN [1]

RP SEQUENCE.

RX MEDLINE: 99033459.

RA Stuart M.K.;

RT "An antibody diagnostic for hymenopteran parasitism is specific for a
RT homologue of elongation factor-1 alpha.";

RESULT 6
M17_BOVIN STANDARD; PRT; 20 AA.
ID M17_BOVIN
AC P35451;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 17 KDA MILK GLYCOPROTEIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RC TISSUE=MILK;
RX MEDLINE: 93308294.
RA Soerensen E.S., Petersen T.E.:
RT "Purification and characterization of three proteins isolated from
the protease pepone fraction of bovine milk.";
RL J. Dairy Res. 60:189-197(1993).
CC -1- PTM: N-GLYCOSYLATED.
CC -1- SIMILARITY: TO CAMEL WHEY PROTEIN.
KW Glycoprotein; Milk.
FT NON_TER 1 20
SQ SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;

Query Match 21.9%; Score 21; DB 1; Length 20;
Best Local Similarity 35.3%; Pred. No. 1.4e+03;
Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 TTVOASYSKKKLFSL 17
Db 1 SSXQPSQNPKLPLSL 17

RESULT 7
TL18_SPIOI STANDARD; PRT; 20 AA.
ID TL18_SPIOI
AC P82536;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE THYLAKOID LUMENAL 18 KDA PROTEIN (P18) (FRAGMENT).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
OC Caryophyllales; Chenopodiaceae; Spinacia.
RN [1]
RP SEQUENCE.
RA Kieselbach T., Bystedt M., Schroeder W.P.:
RT Submitted (May-2000) to the SWISS-PROT data bank.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2192 MW; 752C21963F49FA64 CRC64;

Query Match 21.9%; Score 21; DB 1; Length 20;
Best Local Similarity 30.8%; Pred. No. 1.4e+03;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 TTVOASYSKKKLF 13
Db 5 TPLQSKVTNKVVF 17

RESULT 8
PA2B_VIPBO STANDARD; PRT; 12 AA.
ID PA2B_VIPBO
AC P31859;
DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PHOSPHOLIPASE A2, BASIC (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE
DE 2-ACYLHYDROLASE) (FRAGMENT).
OS Vipera berus orientalis (Viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
RN [1]
RP SEQUENCE.
RC TISSUE=VENOM;
RX MEDLINE: 74128698.
RA Delori P.J.:
RT "Purification and physicochemical, chemical and biological properties
of a toxic A2 phospholipase isolated from the venom of viperidae
snakes: Vipera berus.";
RL Biochimie 55:1031-1045(1973).
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-
PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
DR INTERPRO: IPR001211; -.
DR PROSITE: PS00118; PA2_HIS; PARTIAL.
DR PROSITE: PS00119; PA2_ASP; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Venom.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1412 MW; D054351A89969879 CRC64;

Query Match 20.8%; Score 20; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 SLDF 19
Db 1 SLDF 5

RESULT 9
FGFL_CANFA STANDARD; PRT; 15 AA.
ID FGFL_CANFA
AC P18651;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HEPARIN-BINDING GROWTH FACTOR 1 (HBGF-1) (ACIDIC FIBROBLAST GROWTH
DE FACTOR) (AFGF) (ALPHA-ENDOTHELIAL CELL GROWTH FACTOR) (FRAGMENT).
GN FGFL OR FGF-1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE.
RX MEDLINE: 89231704.
RA Quinkler W., Maasberg M., Bernotat-Danielowski S., Luethe N.,
RA Sharma H.S., Schaper W.:
RT "Isolation of heparin-binding growth factors from bovine, porcine and
canine hearts.";
RL Eur. J. Biochem. 181:67-73(1989).
CC -1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN
VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
CONCENTRATION OF THESE 2 GROWTH FACTORS.
CC -1- SUBUNIT: MONOMER.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN, ALTHOUGH LESS STRONGLY
THAN DOES BFGF.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
DR PIR: S03955; S03955.
DR HSSP: P05230; 2AXM.
DR INTERPRO: IPR002209; -.
DR PROSITE: PS00247; HBGF_FGF; PARTIAL.
KW Growth factor; Mitogen; Vascularization; Heparin-binding.

RX MEDLINE: 79255521.
 RA Possani L.D., Alagon A.C., Fletcher P.L. Jr., Varela M.J., Julia J.Z.,
 RT "Purification and characterization of a phospholipase A2 from the
 RT venom of the coral snake, Micrurus fulvius microgaleus (Brown and
 RT Smith).";
 RL Biochem. J. 179:603-606(1979).
 CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
 CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
 CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-
 CC PHOSPHOCHOLINE + A FATTY ACID ANION.
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
 DR INTERPRO: IPR001211; -
 DR PROSITE: PS00118; PA2_HIS: PARTIAL.
 DR PROSITE: PS00119; PA2_ASP: PARTIAL.
 KM Hydrolase; Lipid degradation; Calcium; Venom.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA: 1398 MW: CC21992A89F0339 CRC64;

Query Match 24.0%; Score 23; DB 1; Length 12;
 Best Local Similarity 66.7%; Pred. No. 3.6e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 15 SLDDFQ 20
 111:11
 DB 1 SLBFFK 6

RESULT 3
 CPBX_CAVPO STANDARD; PRT: 20 AA.
 ID CPBX_CAVPO
 AC P34033;
 DT 01-FEB-1994 (Rel. 28; Created)
 DT 01-FEB-1994 (Rel. 28; Last sequence update)
 DT 30-MAY-2000 (Rel. 39; Last annotation update)
 DE CYTOCHROME P45011B (EC 1.14.14.1) (FRAGMENT).
 OS Cavia Porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Mammalia; Rodentia; Hystriocognathi; Cavidae; Cavia.
 RN [1]
 RP SEQUENCE. AND CHARACTERIZATION.
 RC STRAIN-HARTLEY; TISSUE-LIVER;
 RX MEDLINE: 91054472.
 RA Natimatsu S., Akutsu Y., Matsunaga T., Watanabe K., Yamamoto I.,
 RA Yoshimura H.;
 RT "Purification of a cytochrome P450 isozyme belonging to a subfamily
 RT of P450 11B from liver microsomes of guinea pigs.";
 RL Biochem. Biophys. Res. Commun. 172:607-613(1990).
 CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
 CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
 CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. THIS ISOZYME IS ACTIVE
 CC UPON P-NITROANISOLE, ANILINE, D-BENZPHEMININE, DELTA(9)-
 CC TETRAHYDROCANNABINOL (THC) AND STRYCHNINE.
 CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
 CC OXIDIZED FLAVOPROTEIN + H(2)O.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR PIR: A36154; A36154.
 DR INTERPRO: IPR001128; -
 DR PROSITE: PS00086; CYTOCHROME_P450: PARTIAL.
 KM Oxidoreductase; Monooxygenase; Electron Transport; Membrane; Heme;
 KM Microsome; Endoplasmic reticulum.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA: 2259 MW: 78DC81280C970A55 CRC64;

Query Match 24.0%; Score 23; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 12 LFLSL 17
 111:11
 DB 7 LFLALL 12

RESULT 4
 VR90_BORPE STANDARD; PRT: 20 AA.
 ID VR90_BORPE
 AC P81549;
 DT 15-JUL-1999 (Rel. 38; Created)
 DT 15-JUL-1999 (Rel. 38; Last sequence update)
 DT 15-JUL-1999 (Rel. 38; Last annotation update)
 DE VIRULENCE-ASSOCIATED OUTER MEMBRANE PROTEIN VIR90 (FRAGMENT).
 GN VIR90.
 OS Bordetella pertussis.
 OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 OC Bordetella.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-TOHAMA I;
 RX MEDLINE: 99179239.
 RA Passerini de Rossi B.N., Friedman L.E., Gonzalez Flecha F.L.,
 RA Castello P.R., Franco M.A., Rossi J.P.F.C.;
 RT "Identification of Bordetella pertussis virulence-associated outer
 RT membrane proteins.";
 RL FEMS Microbiol. Lett. 172:9-13(1999).
 KM Outer membrane; Virulence.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA: 2116 MW: D24E1DC6A65206C CRC64;

Query Match 22.9%; Score 22; DB 1; Length 20;
 Best Local Similarity 57.1%; Pred. No. 9.4e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 TVQASY 8
 11:11
 DB 11 TVGEYS 17

RESULT 5
 XYNB_DICB4 STANDARD; PRT: 10 AA.
 ID XYNB_DICB4
 AC P80717;
 DT 01-NOV-1997 (Rel. 35; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 01-NOV-1997 (Rel. 35; Last annotation update)
 DE ENDO-1,4-BEPA-XYLANASE B (EC 3.2.1.8) (XYLANASE B)
 OS Dictyoglomus sp. (Strain B4b).
 OC Bacteria; Dictyoglomus group; Dictyoglomus.
 RN [1]
 RP SEQUENCE.
 RC Adamson A.K., Jacobsen S., Ahling B.K.;
 RL Submitted (OCT-1996) to the SWISS-PROT data bank.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL
 CC HYDROLASES).
 DR INTERPRO: IPR001000; -
 DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10: PARTIAL.
 KM Xylan degradation; Hydrolase; Glycosidase.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA: 1144 MW: 4554322AA72041A3 CRC64;

Query Match 21.9%; Score 21; DB 1; Length 10;
 Best Local Similarity 55.6%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 10 KKLFLSLD 18
 11:11
 DB 2 KKLTLDLKD 10

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:32:59 ; Search time 62.7 Seconds
(without alignments)
10.191 Million cell updates/sec

Title: US-08-934-367-11

Perfect score: 96

Sequence: 1 TTVOQASYSKKKLFLSLDFQ 20

ALIGNMENTS

34	17	17.7	18	1	RL23_HALCU	P05975 halobacteri
35	17	17.7	20	1	CATA_ACIRA	P81422 actinobact
36	17	17.7	20	1	RIPX_CUCPE	P80750 cucurbita p
37	16	16.7	8	1	AKH_MEML	P25423 melonlontha
38	16	16.7	8	1	COXG_RAT	P80430 rattus norv
39	16	16.7	8	1	CPD1_ENTFA	P13269 enterococu
40	16	16.7	10	1	COXM_RAT	P80431 rattus norv
41	16	16.7	10	1	PNEU_RAT	P21996 rattus norv
42	16	16.7	11	1	CS15_BACSU	P81095 bacillus su
43	16	16.7	11	1	UXB2_YEAST	P09013 saccharomyc
44	16	16.7	14	1	MAST_VESSE	P01514 vesputia lew
45	16	16.7	14	1	RS19_PPWPB	Q52093 pigeon pea

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	25.0	18	UC21_MAIZE	P80627 zea mays (m
2	24.0	12	PA21_MICFM	P25072 micriturus fu
3	24.0	20	CPBX_CAVPO	P34033 cavia porce
4	22.9	20	VR90_BORPE	P81549 bordetella
5	21.9	10	XVNB_DICB4	P0717 dictyoglomu
6	21.9	20	MI17_BOVIN	P35451 bos taurus
7	21.9	12	TL18_SPTOL	P2536 spinnacia ol
8	20.8	12	PA2B_VITBO	P1859 vipera beru
9	20.8	15	FGF1_CANFA	P18651 canis famli
10	20.8	16	R1PK_TRIKI	P16093 trichosanthe
11	19.8	8	B44K_PORGI	P1886 porphyromon
12	19.8	14	MAST_VESBA	P21654 vespa basal
13	19.8	15	ELIA_MICCR	P81266 micropplitis
14	19.8	16	RL6_VITBR	Q56715 vibrrio prot
15	19.8	19	PHSL_DESBN	P13066 desulfoviblr
16	19.8	20	STVA_STYCL	P1469 styela clav
17	18.8	9	ULAE_HUMAN	P31931 homo sapien
18	18.8	13	UVRD_SALTY	Q05311 salmonella
19	18.8	13	YPE2_LACTC	P41147 lactococcus
20	18.8	16	ARCD_PSEPU	P81147 pseudomonas
21	18.8	17	ATP1_PAVLU	P28529 pavlova lut
22	18.8	19	UP24_UPEIN	P82030 uperoletia i
23	18.8	20	AMP_FUSNU	P11207 fusobacteri
24	18.8	20	CRP_MUSCA	P19094 mustelus ca
25	17.7	8	CCKN_MACEU	P30369 macrodus eu
26	17.7	11	TKN_ELEMO	P01293 eleodon mos
27	17.7	12	NO40_SORBN	P45960 glycine max
28	17.7	14	MAST_VESBA	P01515 vespa xanth
29	17.7	14	MAST_VESXA	P06640 zea mays (m
30	17.7	14	UC34_MAIZE	P19628 protoperlus
31	17.7	15	CBPB_PROAT	P10521 megadombus
32	17.7	17	BO11_MESPE	Q52838 thizobium i
33	17.7	18	NODD_RHTLO	

RESULT 1
UC21_MAIZE STANDARD; PRT; 18 AA.
AC P80627:

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLOGED COLEOPTILE (SPOT 443)

DE (FRAGMENT).

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

RN [1]

RP SEQUENCE.

RA Tissue=COLEOPTILE;

RA Toulzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,

RA Pernollet J.-C., Zivy M., de Vienne D.,

RT "The maize 2D-dimensional gel protein database: towards an integrated

RT genome analysis program.";

RL Theor. Appl. Genet. 93:997-1005(1996).

CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 5.9, ITS MW IS: 26.5 KDA.

CC -I- SIMILARITY: TO L-ASCORATE PEROXIDASES.

DR HSSP; P48534; IAPX.

DR MAIZE-2DPAGE; P80627; COLEOPTILE.

DR MAIZEEDB; 123953; -.

FT NON_TER 1 1

FT NON_TER 18 18

SQ SEQUENCE 18 AA; 1938 MW; F32F6FEF038BABA8A CRC64;

Query Match 25.0%; Score 24; DB 1; Length 18;
Best local similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVQASYS 8

Db 6 TVSAEYS 12

RESULT 2

PA21_MICFM STANDARD; PRT; 12 AA.

AC P25072;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE PHOSPHOLIPASE A2 ISOZYME 1 (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE

DE 2-ACYLHYDROLASE) (FRAGMENT).

OS Micriturus fulvius microgabineus (Mexican coral snake);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;

RN [1]

RP SEQUENCE.

RC TISSUE=VENOM;

A:Title: Purification of the sequence-specific transcription factor CTCBF, involved in
 A:Reference number: S54272; MUID:95188883
 A:Accession: S54272
 A:Status: Preliminary
 A:Molecule type: protein
 A:Residues: 1-18 <GEN>

Query Match 22.9%; Score 22; DB 2; Length 18;
 Best Local Similarity 33.3%; Pred. No. 2.6e+03;
 Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TTVOASYSKKL 12
 : | : | : : |
 Db 6 STCKVEYSEEL 17

RESULT 14
 G22565
 R-phycoerythrin gamma-B chain - red alga (Gastroclonium coulteri) (fragment)
 C:Species: Gastroclonium coulteri
 C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
 C:Accession: G22565
 R:Klotz, A.V.; Glazer, A.N.
 J. Biol. Chem. 260, 4856-4863, 1985
 A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
 A:Reference number: A22565; MUID:85182601
 A:Accession: G22565
 A:Molecule type: protein
 A:Residues: 1-13 <KLO>

Query Match 21.9%; Score 21; DB 2; Length 13;
 Best Local Similarity 44.4%; Pred. No. 2.8e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TTVOASYSK 9
 | | : : |
 Db 5 TVQQAFAEK 13

RESULT 15
 S29209
 avenin alpha-2 - oat (fragment)
 N:Alternate names: CIP-3; coeliac immunoreactive protein 3
 C:Species: Avena sativa (oat)
 C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
 C:Accession: S29209
 R:Rochelet, A.; Collila, F.; Ortiz, M.L.; Mendez, E.
 FEBS Lett. 310, 37-40, 1992
 A:Title: Identification of the three major coeliac immunoreactive proteins and one alpha
 A:Reference number: S29207; MUID:92405739
 A:Accession: S29209
 A:Molecule type: protein
 A:Residues: 1-14 <ROC>
 A:Experimental source: endosperm
 C:Superfamily: gliadin
 C:Keywords: prolamin; seed

Query Match 21.9%; Score 21; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 3e+03;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TTVOASYSKK 10
 | | | : | : |
 Db 2 TTVOYNPSEQ 11

Search completed: December 21, 2000, 08:30:07
 Job time: 271 sec

RESULT 8
S39049
cytotoxin-binding protein - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 18-Feb-1994 #sequence_revision 19-Apr-1996 #text_change 16-Feb-1997
C:Accession: S39049
R:Lutz, F.; Mohr, M.; Grimmig, M.; Leidolf, R.; Linder, D.
Eur. J. Biochem. 217, 1123-1128, 1993
A:Title: Pseudomonas aeruginosa cytotoxin-binding protein in rabbit erythrocyte membrane
A:Reference number: S39049; MUID:94039134
A:Accession: S39049
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <LUT>
C:Superfamily: Lens fiber membrane major intrinsic protein

Query Match 24.0%; Score 23; DB 2; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 KKKLF 13
|||:
Db 5 KKKIF 9

RESULT 9
PH0786
T-cell receptor alpha chain (IT) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0786
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-T
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846
A:Accession: PH0786
A:Molecule type: mRNA
A:Residues: 1-13 <CAS>
A:Cross-references: EMBL:X60889
A:Experimental source: T lymphocyte
A:Keywords: T-cell receptor

Query Match 22.9%; Score 22; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 ASYSKKLIF 13
::|:|:|
Db 4 SAYANKMIF 12

RESULT 10
S65717
prostaglandin D-synthase - rat (fragment)
N:Alternate names: prostaglandin-H2 D-isomerase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 31-Oct-1997
C:Accession: S65717
R:Giacomelli, S.; Leone, M.G.; Grima, J.; Silvestrini, B.; Cheng, C.Y.
Biochim. Biophys. Acta 1310, 269-276, 1996
A:Title: Astrocytes synthesize and secrete prostaglandin D synthetase in vitro.
A:Reference number: S65716; MUID:9617373
A:Accession: S65717
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <GTA>
C:Superfamily: lipocalin; lipocalin homology

Query Match 22.9%; Score 22; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 TVQASYSKKK 11
|||::|
Db 3 TVQPNFOODK 12

RESULT 11
PA0046
protein QA100044 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0046; PA0042
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensi
A:Reference number: PA0001
A:Accession: PA0046
A:Molecule type: protein
A:Residues: 1-15 <KAM>
A:Experimental source: stem

Query Match 22.9%; Score 22; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 KKLFLSLID 18
|||::|
Db 4 KKGFLAVSD 12

RESULT 12
S34444
blaz protein - Staphylococcus aureus plasmid p1258 (fragment)
C:Species: Staphylococcus aureus
C:Date: 22-Nov-1993 #sequence_revision 09-Mar-1996 #text_change 07-May-1999
C:Accession: S34444
R:Wang, P.Z.; Projan, S.J.; Novick, R.P.
Nucleic Acids Res. 19, 4000, 1991
A:Title: Nucleotide sequence of beta-lactamase regulatory genes from staphylococcal p
A:Reference number: S34444; MUID:91319567
A:Accession: S34444
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-16 <WAN>
A:Cross-references: EMBL:M62650
A:Experimental source: strain RN11
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
C:Genetics:
A:Gene: blaz
A:Genome: plasmid p1258

Query Match 22.9%; Score 22; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.4e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 KKLFLSLDF 19
|||::|
Db 6 KOLQKLKLF 15

RESULT 13
S54272
Circ 75 protein - human
C:Species: Homo sapiens (man)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C:Accession: S54272
R:Gensersch, E.; Eckerskorn, C.; Lottspeich, F.; Herzog, C.; Kuehn, K.; Poeschl, E.
EMBO J. 14, 791-800, 1995

Db 3 EKKLFLKAL 11

RESULT 3

152618 hemoglobin beta chain thalassemia mutant Portuguese - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 11-Jul-1996 #text_change 20-Apr-2000
C:Accession: I52618
R:One, R.; One, C.; Wilson, J.B.; Tamagnini, G.P.; Ribeiro, L.M.; Huisman, T.H.
Br. J. Haematol. 79, 306-310, 1991
A:Title: Dominant beta-thalassemia trait in a Portuguese family is caused by a deletion
A:Reference number: I52618; MUID:92068764
A:Accession: I52618
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14 <ONE>
A:Cross-references: GB:S68042; NID:9239717; PIDN:AA820440.1; PID:9239718
C:Genetics:
A:Gene: GDB:HHB
A:Cross-references: GDB:119297; OMIM:141900
A:Map position: 11p15.4-11p15.4

Query Match 27.1% Score 26; DB 4; Length 14;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 VOASYSK 9
|||:|
Db 3 VOAAVOK 9

RESULT 4
A61411
amelanin - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
C:Accession: A61411
R:Buzynski, S.R.
Anal. Biochem. 70, 359-365, 1976
A:Title: Sequential analysis in subnanomolar amounts of peptides. Determination of the
A:Reference number: A61411; MUID:76182447
A:Accession: A61411
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-6 <BUR>
C:Keywords: pyroglutamic acid
F:1/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 26.0% Score 25; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 QASYSK 9
|||:|
Db 1 QAGYSK 6

RESULT 5
149593
cystic fibrosis transmembrane conductance regulator - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C:Accession: I49593
R:Denamur, E.; Chehab, F.F.
Hum. Mol. Genet. 3, 1089-1094, 1994
A:Title: Analysis of the mouse and rat CFTR promoter regions.
A:Reference number: I49593; MUID:95072572
A:Accession: I49593
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-17 <RES>
A:Cross-references: GB:L04873; NID:9414726; PIDN:AAA73562.1; PID:9553892
C:Genetics:
A:Gene: CFTR
C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding casse

Query Match 25.0% Score 24; DB 2; Length 17;
Best Local Similarity 41.2%; Pred. No. 1.2e+03;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 3 VOASYSKKKFLSLDP 19
:|:|:|:|:|:|
Db 1 MOKSPLKASFISKLFP 17

RESULT 6
184733
gene CFTR protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C:Accession: I84733
R:Denamur, E.; Chehab, F.F.
Hum. Mol. Genet. 3, 1089-1094, 1994
A:Title: Analysis of the mouse and rat CFTR promoter regions.
A:Reference number: I49593; MUID:95072572
A:Accession: I84733
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-17 <RES>
A:Cross-references: GB:L26098; NID:9425185; PIDN:AAA73561.1; PID:9915270
C:Genetics:
A:Gene: CFTR
C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding casse

Query Match 25.0% Score 24; DB 2; Length 17;
Best Local Similarity 41.2%; Pred. No. 1.2e+03;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 3 VOASYSKKKFLSLDP 19
:|:|:|:|:|:|
Db 1 MOKSPLKASFISKLFP 17

RESULT 7
A49192
transhyretin - bullfrog (fragment)
N:Alternate names: 3,5,3'-L-triiodothyronine-specific binding protein
C:Species: Rana catesbeiana (bullfrog)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
C:Accession: A49192
R:Yamuchi, K.; Kasahara, T.; Hayashi, H.; Horiuchi, R.
Endocrinology 132, 2254-2261, 1993
A:Title: Purification and characterization of a 3,5,3'-L-triiodothyronine-specific bi
A:Reference number: A49192; MUID:93238653
A:Accession: A49192
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <YAM>
A:Experimental source: tadpole plasma
A>Note: sequence extracted from NCBI backbone (NCBIP:130235)

Query Match 24.0% Score 23; DB 2; Length 19;
Best Local Similarity 45.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 8 SKKKLPLSLD 18
|||:|:|:|
Db 7 SKKPLMKVLD 17

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:30:06 ; Search time 112.59 Seconds
(without alignments)
11.273 Million cell updates/sec

Title: US-08-934-367-11

Perfect score: 96

Sequence: 1 TTVQASYSKKLFLSLDLRQ 20

Scoring table: BLOSUM62

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR:51:
2: PIR:2:
3: PIR:3:
4: PIR:4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	31.2	18	2	S14560 probable heme-bind
2	28	29.2	14	2	S13864 methyl coenzyme M
3	26	27.1	14	4	I52618 hemoglobin beta ch
4	25	26.0	6	2	A61411 amelelin - rat
5	24	25.0	17	2	I49593 cystic fibrosis tr
6	24	25.0	17	2	I84733 gene CFTR protein
7	23	24.0	19	2	A49192 cytochrome-binding
8	23	24.0	20	2	S39049 T-cell receptor al
9	22	22.9	13	2	PH0786 prostaglandin D-sy
10	22	22.9	15	2	S65717 protein QA100044
11	22	22.9	15	2	PA0046 blaz protein - Sta
12	22	22.9	16	2	S34444 CTC 75 protein - h
13	22	22.9	18	2	G25272 R-phycocerythrin ga
14	21	21.9	13	2	S29209 2-halobenzoate 1,2
15	21	21.9	14	2	A4920 dystrophin-associa
16	21	21.9	14	2	PN0662 t-cell surface gly
17	21	21.9	15	2	B45895 L-ascorbate peroxi
18	21	21.9	16	2	S32587 adrenocortical cel
19	21	21.9	17	2	A35550 hypothetical prote
20	21	21.9	19	2	S59717 nuclear antigen EB
21	21	21.9	20	2	H49034 acid fibroblast
22	21	21.9	19	2	S03955 rRNA N-glycosidase
23	20	20.8	15	2	S01669 coat protein VP1 -
24	20	20.8	16	2	S02473 endosperm protein,
25	20	20.8	16	2	S70331 translation elonga
26	20	20.8	18	2	S45373 glutathione transf
27	20	20.8	18	2	S29108 glutathione S-tran
28	20	20.8	20	2	S63602
29	20	20.8	20	2	

30	20	20.8	20	2	PL0192 Ig lambda 2 chain
31	20	20.8	20	2	A44921 hydroxypruvate re
32	20	20.8	20	2	S46479 retinoid-X-recepto
33	19	19.8	9	3	PC7076 spectrin alpha cha
34	19	19.8	10	2	A13687 caerulain-like pep
35	19	19.8	12	2	S26536 T-cell receptor be
36	19	19.8	13	2	S47365 mastoparan B - hor
37	19	19.8	14	2	S14336 leukotriene B-4 12
38	19	19.8	15	2	S36890 ribosomal protein
39	19	19.8	15	2	S36890 hypothetical prote
40	19	19.8	17	2	S61451 Ig heavy chain DJ
41	19	19.8	17	2	PH1331 neurofibromatosis-
42	19	19.8	18	2	B35910 cyclin C mouse (
43	19	19.8	18	2	S48663 serpin W52CI - whe
44	19	19.8	19	2	S43652 flagellar sheath p
45	19	19.8	19	2	A47689

ALIGNMENTS

RESULT 1
S14560
probable heme-binding protein - garden pea chloroplast (fragment)
C:Species: Chloroplast Pisum sativum (garden pea)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 11-Jan-2000
C:Accession: S14560
R:Smith, A.G.; Wilson, R.J.; Kaethner, T.M.; Willey, D.L.; Gray, J.C.
submitted to the EMBL data library, October 1990
A:Reference number: S14557
A:Accession: S14560
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18 <SMI>
A:Cross-references: EMBL:X54750; NID:912194; PID:912198
A:Genetics:
A:Genome: chloroplast
C:Superfamily: maize chloroplast protein cema
C:Keywords: chloroplast; heme; transmembrane protein

Query Match 31.2%; Score 30; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 8 SKKKLFLSL 17
DB 2 AKKKAFLPL 11
RESULT 2
S13864
methyl coenzyme M reductase (EC 1.8.-.-) II alpha chain - Methanobacterium thermoauto
C:Species: Methanobacterium thermoautotrophicum
A:Variety: strain Marburg
C:Date: 19-Mar-1997 #sequence_revision 13-Sep-1998 #ext_change 30-Oct-1998
C:Accession: S13864
R:Rospert, S.; Linder, D.; Ellermann, J.; Thauer, R.K.
Eur. J. Biochem. 194, 871-877, 1990
A:Title: Two genetically distinct methyl-coenzyme M reductases in Methanobacterium th
A:Reference number: S13864; MUID:9109370
A:Accession: S13864
A:Molecule type: protein
A:Residues: 1-14 <ROS>
A:Experimental source: strain Marburg
C:Keywords: methanogenesis; oxidoreductase

Query Match 29.2%; Score 28; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 9 KKKLFLSL 17


```

: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-305-871A-9
    
```

```

Query Match      27.1%; Score 26; DB 1; Length 16;
Best Local Similarity 55.6%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
    
```

```

QY      3 VQASYSKKK 11
      ::| | | | |
Db       8 LKAIVKKKK 16
    
```

```

Search completed: December 21, 2000, 08:31:49
Job time: 372 sec
    
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APPLICANT: Kourilsky, Phillippe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION: 148
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-985B-26

Query Match 27.1%; Score 26; DB 3; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VQASYSKK 11
: : | | | |
DB 7 LKA1YEKK 15

RESULT 14
PCT-US95-01671-2
Sequence 2, Application PC/TUS9501671
GENERAL INFORMATION:
APPLICANT: University of Rochester
TITLE OF INVENTION: Inducing Tolerance With Tolerogenic
TITLE OF INVENTION: Fusion Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: Minnesota
COUNTRY: United States of America
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01671
FILING DATE: 10-FEB-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kevin W. Raasch
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 850.114W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-01671-2

Query Match 27.1%; Score 26; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VQASYSKK 11
: : | | | |
DB 7 LKA1YEKK 15

RESULT 15
US-08-305-871A-9
Sequence 9, Application US/08305871A
Patent No. 5736142
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Gaeta, Federico
APPLICANT: Grey, Howard M.
APPLICANT: Sidney, John
APPLICANT: Alexander, Jeffrey L.
TITLE OF INVENTION: Alteration of Immune Response Using Pan
TITLE OF INVENTION: DR-Blinding Peptides
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/305,871A
FILING DATE: 14-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,101
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-0062-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid

ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IR144PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-06077-5

Query Match 27.1%; Score 26; DB 4; Length 14;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 SYSKKK 11
11111
Db 1 SYKKK 6

RESULT 11

US-08-195-874-2
Sequence 2, Application US/08195874
Patent No. 5817308

GENERAL INFORMATION:
APPLICANT: Scott, David W.
APPLICANT: Zambidis, Elias T.
TITLE OF INVENTION: Tolerogenic Fusion Proteins of
TITLE OF INVENTION: Tolerogenic Fusion Proteins of
TITLE OF INVENTION: Tolerance
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,874
FILING DATE: 02-FEB-1994
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Mueling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 850,14-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-195-874-2

Query Match 27.1%; Score 26; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 VOASYSKKK 11
::11111
Db 7 LKAIYEKKK 15

RESULT 12

US-08-484-905-26
Sequence 26, Application US/08484905
Patent No. 5976551

GENERAL INFORMATION:
APPLICANT: Motiez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495,0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-905-26

Query Match 27.1%; Score 26; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 VOASYSKKK 11
::11111
Db 7 LKAIYEKKK 15

RESULT 13

US-08-481-985B-26
Sequence 26, Application US/08481985B
Patent No. 6011146

GENERAL INFORMATION:
APPLICANT: Motiez, Estelle
APPLICANT: Abastado, Jean-Pierre

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 SKKKFLSL 16
1 SKKKLALCT 9

RESULT 8

US-08-454-207A-41

Sequence 41, Application US/08454207A

Patent No. 5710123

GENERAL INFORMATION:

APPLICANT: Heavner, George A.

APPLICANT: Kruszyński, Marian

TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING

NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123r1s LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 1.44 MB

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/454,207A

FILING DATE: 09-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION NUMBER:

FILING DATE: 13-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/997,771

FILING DATE: 18-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Dianne B. Elderkin

REGISTRATION NUMBER: 28,598

REFERENCE/DOCKET NUMBER: CCOR-0183

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-454-207A-41

Query Match 27.1%; Score 26; DB 1; Length 9;

Best Local Similarity 75.0%; Pred. No. 1.2e+05;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 SKKKFLSL 15
1 SKKKLALCT 8

Db 1 SKKKLALCT 8

RESULT 9

US-08-454-207A-44

Sequence 44, Application US/08454207A

Patent No. 5710123

GENERAL INFORMATION:

APPLICANT: Heavner, George A.

APPLICANT: Kruszyński, Marian

TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING

NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123r1s LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 1.44 MB

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/454,207A

FILING DATE: 09-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/12110

FILING DATE: 13-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/997,771

FILING DATE: 18-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Dianne B. Elderkin

REGISTRATION NUMBER: 28,598

REFERENCE/DOCKET NUMBER: CCOR-0183

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-454-207A-44

Query Match 27.1%; Score 26; DB 1; Length 9;

Best Local Similarity 85.7%; Pred. No. 1.2e+05;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 SKKKFL 14
1 SKKKLHL 7

Db 1 SKKKLHL 7

RESULT 10

PCT-US95-06077-5

Sequence 5, Application PC/TUS9506077

GENERAL INFORMATION:

APPLICANT: Immunobiology Research, Institute Inc.

TITLE OF INVENTION: Vaccine Interdiction of Extracellular

TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus

TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, PO Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06077

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/247,991

FILING DATE: 23-MAY-1994

COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/654,839
FILING DATE: 19910213
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,753
FILING DATE: 03-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/415,029
FILING DATE: 29-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Bingham, Douglas A
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: SC90367P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-07-654-839-5

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Query Match          29.2%   Score 28; DB 1; Length 19;
Best Local Similarity 38.5%   Pred. No. 1.3e+02;
Matches      5;  Conservative      3;  Mismatches      5;  Indels      0;  Gaps      0;

Oy      7  YSKKRLFLSLDF 19
      1 1 1 : : : 1
Db      1  YSMKRTMKRIKF 13

RESULT      6
US-08-454-207A-45
; Sequence 45. Application US/08454207A
; Patent No. 5710123
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kuszynski, Marian
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 57101237ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 MB
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454, 207A
; FILING DATE: 09-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12110
; FILING DATE: 13-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/997,771

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Query Match	28.1%	Score 27	DB 1	Length 9
Best Local Similarity	85.7%	Pred. No. 1.2e+05		
Matches	6	Conservative	0	Mismatches 1
				Indels 0
				Gaps 0

RESULT 7
US-08-454-207A-30
; Sequence 30, Application US/08454207A

```

1 APPLICANT: Heavner, George A.
2 APPLICANT: Kruzynski, Marian
3 TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
4 NUMBER OF SEQUENCES: 70
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123r1s LLP
7 STREET: One Liberty Place - 46th Floor
8 CITY: Philadelphia
9 STATE: PA
10 COUNTRY: U.S.A.
11 ZIP: 19103
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: 3.5 inch disk, 1.44 MB
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Wordperfect 6.1
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/454,207A
19 FILING DATE: 09-JUN-1995
20 CLASSIFICATION: 514
21 PRIOR APPLICATION NUMBER:
22 APPLICATION NUMBER: PCT/US93/12110
23 FILING DATE: 13-DEC-1993
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 07/997,771
26 FILING DATE: 18-DEC-1992
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Dianne B. Elderkin
29 REGISTRATION NUMBER: 28,598
30 REFERENCE/DOCKET NUMBER: CCOR-0183
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 215-568-3100
33 TELEFAX: 215-568-3439
34 INFORMATION FOR SEQ ID NO: 30:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 9 amino acids
37 TYPE: amino acid
38 TOPOLOGY: linear
39
40 US-08-454-207A-30

```

Db 1 SKKKLFL 7

RESULT 2

5266328-11
; Patent No. 5266328
; APPLICANT: SKUBITZ, AMY P.N.; FURCHT, LEO T.
; TITLE OF INVENTION: LAMININ CHAIN POLYPEPTIDES FROM
; THE CARBOXY TERMINAL GLOBULAR DOMAIN
; NUMBER OF SEQUENCES: 14
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/573,672
; FILING DATE: 27-AUG-1990
; SEQ ID NO:11:
; LENGTH: 17
5266328-11

Query Match 33.3%; Score 32; DB 5; Length 17;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 TWOASYSKKLFL 13
11: 11:11
DB 6 TVTVEYIKKRAAF 17

RESULT 3

US-09-100-414B-26
; Sequence 26, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Mang, Chang YI
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Flinnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-26

Query Match 30.2%; Score 29; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KKKLFL 14
111111
DB 1 KKKLFL 6

RESULT 4

US-09-100-414B-30
; Sequence 30, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Mang, Chang YI
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Flinnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-30

Query Match 30.2%; Score 29; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KKKLFL 14
111111
DB 1 KKKLFL 6

RESULT 5

US-07-654-839-5
; Sequence 5, Application US/07654839
; Patent No. 5372933
; GENERAL INFORMATION:
; APPLICANT: Zamarron, Concepcion
; APPLICANT: Plov, Edward F
; APPLICANT: Ginsberg, Mark H
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST
; RECEPTOR-INDUCED BINDING SITES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESS: Patent Counsel
; STREET: 10666 No. 5372933th Torrey Pines Road., Suite 220,
; CITY: La Jolla
; STATE: CA

Query Match 30.2%; Score 29; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:31:49 ; Search time 99.91 Seconds
(without alignments)
3.355 Million cell updates/sec

Title: US-08-934-367-11
Perfect score: 96
Sequence: 1 TTVOASYSKKLLFLSLDFQ 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues
Total number of hits satisfying chosen parameters: 87906

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	34.4	9	1	US-08-454-207A-43
2	32	33.3	17	5	5266328-11
3	29	30.2	18	3	US-09-100-414B-26
4	29	30.2	18	3	US-09-100-414B-30
5	28	29.2	19	1	US-07-654-839-5
6	27	28.1	9	1	US-08-454-207A-45
7	26	27.1	9	1	US-08-454-207A-30
8	26	27.1	9	1	US-08-454-207A-41
9	26	27.1	9	1	US-08-454-207A-44
10	26	27.1	14	4	PCT-US95-06077-5
11	26	27.1	15	2	US-08-195-874-2
12	26	27.1	15	3	US-08-484-905-26
13	26	27.1	15	2	US-08-481-9858-26
14	26	27.1	15	4	PCT-US95-01671-2
15	26	27.1	16	1	US-08-305-871A-9
16	26	27.1	20	1	US-08-218-025A-81
17	25	26.0	9	1	US-08-454-207A-29
18	25	26.0	9	1	US-08-454-207A-31
19	25	26.0	9	1	US-08-454-207A-32
20	25	26.0	9	1	US-08-454-207A-33
21	25	26.0	9	1	US-08-454-207A-34
22	25	26.0	9	1	US-08-454-207A-35
23	25	26.0	9	1	US-08-454-207A-36
24	25	26.0	9	1	US-08-454-207A-37
25	25	26.0	9	1	US-08-454-207A-38
26	25	26.0	9	1	US-08-454-207A-39
27	25	26.0	9	1	US-08-454-207A-40
28	25	26.0	9	3	US-08-159-339A-78

29	25	26.0	10	1	US-08-454-207A-2	Sequence 2, Appl
30	25	26.0	10	1	US-08-454-207A-5	Sequence 5, Appl
31	25	26.0	10	2	US-08-456-112B-42	Sequence 42, Appl
32	25	26.0	10	3	US-08-159-339A-77	Sequence 77, Appl
33	25	26.0	11	2	US-08-310-912A-117	Sequence 117, App
34	25	26.0	11	4	PCT-US95-04589-117	Sequence 47, App
35	25	26.0	13	4	PCT-US94-01234-47	Sequence 9, Appl
36	25	26.0	14	2	US-09-133-774-9	Sequence 9, Appl
37	25	26.0	14	3	US-09-303-862-9	Sequence 9, Appl
38	25	26.0	17	1	US-07-992-288-4	Sequence 4, Appl
39	25	26.0	17	1	US-07-989-764-4	Sequence 10, Appl
40	25	26.0	18	1	US-08-233-203-10	Sequence 25, Appl
41	25	26.0	18	1	US-08-182-483A-25	Sequence 24, Appl
42	25	26.0	18	1	US-08-243-879A-24	Sequence 45, Appl
43	25	26.0	18	1	US-08-499-523-45	Sequence 24, Appl
44	25	26.0	18	3	US-09-100-414B-24	Sequence 20, Appl
45	25	26.0	20	2	US-08-564-972-20	

ALIGNMENTS

RESULT 1
US-08-454-207A-43
; Sequence 43, Application US/08454207A
; Patent No. 5710123
; GENERAL INFORMATION:
; APPLICANT: Kruszynski, Marian
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5710123rls LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 MB
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454, 207A
; FILING DATE: 09-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12110
; FILING DATE: 13-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/997, 771
; FILING DATE: 18-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28, 598
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-454-207A-43

Query Match 34.4%; Score 33; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 SKKRLFL 14

APPLICATION NUMBER: US/08/596,257A
FILING DATE: 08-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4327165.0
FILING DATE: 09-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mellman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: P/951-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 382-0700
TELEFAX: (212) 382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptid
ORIGINAL SOURCE:
ORGANISM: solanum tuberosum
US-08-596-257A-10

Query Match 24.3%; Score 27; DB 3; Length 15;
Best Local Similarity 30.8%; Pred. No. 1.4e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 LIQMDFGPEPHLL 14
| | : : | : : :
Db 1 LEQTYNGLPQOVI 13

RESULT 15
US-08-860-339-10
; Sequence 10. Application US/08860339
; Patent No. 6117665
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; APPLICANT: Emmermann, Michael
; APPLICANT: Virgilo, Ivar
; APPLICANT: Renz, Andreas
; TITLE OF INVENTION: DNA MOLECULES CODING FOR DEBRANCHING ENZYMES DERIVED
; FILE REFERENCE: AGREVO-6
; CURRENT APPLICATION NUMBER: US/08/860,339
; CURRENT FILING DATE: 1997-11-25
; EARLIER APPLICATION NUMBER: DE P4447387.7
; EARLIER FILING DATE: 1994-12-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-08-860-339-10

Query Match 24.3%; Score 27; DB 3; Length 15;
Best Local Similarity 30.8%; Pred. No. 1.4e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 LIQMDFGPEPHLL 14
| | : : | : : :
Db 1 LEQTYNGLPQOVI 13

Search completed: December 21, 2000, 08:36:43
Job time: 387 sec

Db 7 ERLEDLKALN 18

RESULT 12

US-08-940-096-134

; Sequence 134, Application US/08940096

; Patent No. 6046166

; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Butner, Klaus

; APPLICANT: Cornu, Isabelle

; APPLICANT: Melz, Gunther

; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

; NUMBER OF SEQUENCES: 258

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ Version 2.0

; CURRENT APPLICATION DATA:

; FILING DATE: 29-SEP-1997

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 009196-0005-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELETYPE: 66141 PENNTE

; INFORMATION FOR SEQ ID NO: 134:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 22 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 60461666

US-08-940-096-134

Query Match 25.2%; Score 28; DB 3; Length 22;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 7 ERLEDLKALN 18

RESULT 13

US-08-765-783A-83

; Sequence 83, Application US/08765783A

; Patent No. 5994524

; GENERAL INFORMATION:

; APPLICANT: Matsushima, Kouji

; APPLICANT: Matsumoto, Yoshihiro

; APPLICANT: Yamada, Yoshiaki

; APPLICANT: Sato, Koh

; APPLICANT: Tsuchiya, Masayuki

; APPLICANT: Yamazaki, Tatsumi

; TITLE OF INVENTION: Reshaped Human Antibody to

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 2000 Pennsylvania Avenue, NW, suite 5500

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1888

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/765,783A

; FILING DATE: 07-MAR-1997

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Murashige, Kate H

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 35029-20001.20

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-887-1500

; TELEFAX: 202-822-0168

; TELETYPE:

; INFORMATION FOR SEQ ID NO: 83:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-765-783A-83

Query Match 24.3%; Score 27; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 QHMFEP 7

RESULT 14

US-08-596-257A-10

; Sequence 10, Application US/08596257A

; Patent No. 6001628

; GENERAL INFORMATION:

; APPLICANT: KOSSMAN, Jens

; APPLICANT: EMERMAN, Michael

; APPLICANT: VIRGIN, Ivar

; TITLE OF INVENTION: DEBRANCHING ENZYMES AND DNA SEQUENCES

; TITLE OF INVENTION: CODING THEM, SUITABLE FOR CHANGING THE DEGREE OF BRANCHING

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ostrolenk, Faber, Gerb & Sofien

; STREET: 1180 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-8403

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-00503005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 401:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-401

Query Match 25.2%; Score 28; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. NO. 61;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPEHL 14
:||||
Db 2 YPEHLV 7

RESULT 10
US-08-940-095-134
Sequence 134, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6004925e
US-08-940-095-134

Query Match 25.2%; Score 28; DB 3; Length 22;
Best Local Similarity 50.0%; Pred. NO. 1.5e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 EHLVDLQSL 22
:|||||
Db 7 ERLLEDLKLALN 18

RESULT 11
US-08-940-093-134
Sequence 134, Application US/08940093
Patent No. 6037323
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,093
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6037323e
US-08-940-093-134

Query Match 25.2%; Score 28; DB 3; Length 22;
Best Local Similarity 50.0%; Pred. NO. 1.5e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 11 EHLVDLQSL 22
:|||||

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,618A
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,725
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-12/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-618A-22

Query Match 26.1%; Score 29; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 MDEGFPEHL 14
:11:1111
Db 9 IDFHYPNELL 18

RESULT 8
US-08-483-952A-22
Sequence 22, Application US/08483952A
Patent No. 6011139
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Erlander, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,952A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,859
FILING DATE: 17-SEP-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-7/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-952A-22

Query Match 26.1%; Score 29; DB 3; Length 20;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 MDEGFPEHL 14
:11:1111
Db 9 IDFHYPNELL 18

RESULT 9
US-08-159-339A-401
Sequence 401, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and their
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746

COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,508
FILING DATE: February 18, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,536
FILING DATE: February 23, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 571/058ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 121 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3322
TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
TOPOLOGY: unknown to applicant
MOLECULE TYPE: peptide
HYPOTHETICAL: yes
US-08-199-508-2

Query Match 27.0%; Score 30; DB 1; Length 20;
Best Local Similarity 38.5%; Pred. No. 63;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 7 FGPEHLVDFLQ 19
11:1::1:1
DB 1 FGPEVVEGDCVQ 13

RESULT 5
US-08-399-696-85
Sequence 85, Application US/08399696
Patent No. 5756669
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: P53-BINDING POLYPEPTIDES AND
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME
NUMBER OF SEQUENCES: 126
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,696
FILING DATE: 02-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/156,671
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15522-000710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-399-696-85

Query Match 26.1%; Score 29; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 87;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 EHLVDFL 18
111:1:1
DB 12 EHLIDGL 19

RESULT 6
US-08-484-530-22
Sequence 22, Application US/08484530
Patent No. 5846740
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J.
APPLICANT: Erlander, Mark G.
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,530
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-8/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-530-22

Query Match 26.1%; Score 29; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 MDGPEPEHL 14
11:1:1:1
DB 9 IDFHYPNELL 18

RESULT 7
US-08-827-618A-22
Sequence 22, Application US/08827618A
Patent No. 5998366
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J.
APPLICANT: Erlander, Mark G.
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:

Query Match 28.8%; Score 32; DB 3; Length 22;
Best Local Similarity 58.3%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 11 EHLVDPLQSL 22
| | | | | | | |
DB 7 ERLEDDLQALN 18

RESULT 2
US-08-940-093-133
; Sequence 133, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6037323e
US-08-940-093-133

Query Match 28.8%; Score 32; DB 3; Length 22;
Best Local Similarity 58.3%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 11 EHLVDPLQSL 22
| | | | | | | |
DB 7 ERLEDDLQALN 18

RESULT 3
US-08-940-096-133
; Sequence 133, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046166e
US-08-940-096-133

APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046166e
US-08-940-096-133

Query Match 28.8%; Score 32; DB 3; Length 22;
Best Local Similarity 58.3%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 11 EHLVDPLQSL 22
| | | | | | | |
DB 7 ERLEDDLQALN 18

RESULT 4
US-08-199-508-2
; Sequence 2, Application US/08199508
; Patent No. 5717058
; GENERAL INFORMATION:
; APPLICANT: Mathews, Maura-Ann H.
; APPLICANT: Stetler, Gary L.
; APPLICANT: Anthony-Cahill, Spencer J.
; APPLICANT: Anderson, David C.
; TITLE OF INVENTION: Modulators of Gene Expression
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 5797 Central Avenue
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:36:43 ; Search time 25.87 Seconds
(without alignments)
14.254 Million cell updates/sec

Title: US-08-934-367-10

Perfect score: 111

Sequence: 1 LLLQMDPFFPHLLVDFLOSLS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 92835

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	28.8	22	3	US-08-940-095-133 Sequence 133, App
2	32	28.8	22	3	US-08-940-095-133 Sequence 133, App
3	32	28.8	22	3	US-08-940-095-133 Sequence 133, App
4	30	27.0	20	1	US-08-199-508-2 Sequence 2, Appl
5	29	26.1	19	1	US-08-399-696-85 Sequence 85, Appl
6	29	26.1	20	2	US-08-484-530-22 Sequence 22, Appl
7	29	26.1	20	2	US-08-827-618A-22 Sequence 22, Appl
8	29	26.1	20	3	US-08-483-952A-22 Sequence 22, Appl
9	28	25.2	10	3	US-08-159-339A-401 Sequence 401, App
10	28	25.2	22	3	US-08-940-095-134 Sequence 134, App
11	28	25.2	22	3	US-08-940-095-134 Sequence 134, App
12	28	25.2	22	3	US-08-940-095-134 Sequence 134, App
13	27	24.3	9	2	US-08-765-783A-83 Sequence 83, Appl
14	27	24.3	15	3	US-08-596-257A-10 Sequence 10, Appl
15	27	24.3	15	3	US-08-860-339-10 Sequence 10, Appl
16	27	24.3	20	1	US-07-678-974D-8 Sequence 8, Appl
17	27	24.3	20	2	US-08-162-149-10 Sequence 10, Appl
18	27	24.3	20	2	US-08-945-168-13 Sequence 13, Appl
19	27	24.3	22	2	US-08-559-524A-12 Sequence 12, Appl
20	27	24.3	22	3	US-08-749-707-12 Sequence 12, Appl
21	26	23.4	7	1	US-07-923-724-47 Sequence 47, Appl
22	26	23.4	7	2	US-08-609-426A-47 Sequence 47, Appl
23	26	23.4	7	2	US-08-374-652C-37 Sequence 37, Appl
24	26	23.4	11	1	US-08-039-778B-6 Sequence 6, Appl
25	26	23.4	12	1	US-08-555-394-13 Sequence 13, Appl
26	26	23.4	12	3	US-08-745-892-13 Sequence 3, Appl
27	26	23.4	13	1	US-08-620-213-3 Sequence 3, Appl
28	26	23.4	16	1	US-08-346-455B-52 Sequence 52, Appl

ALIGNMENTS

29	26	23.4	16	3	US-08-977-221-52	Sequence 52, Appl
30	26	23.4	16	4	PCT-US95-06613-52	Sequence 52, Appl
31	26	23.4	17	1	US-08-620-213-1	Sequence 1, Appl
32	26	23.4	19	1	US-08-238-163-20	Sequence 20, Appl
33	26	23.4	19	1	US-07-977-696C-36	Sequence 36, Appl
34	26	23.4	19	1	US-08-129-930B-36	Sequence 36, Appl
35	26	23.4	22	1	US-08-039-778B-5	Sequence 5, Appl
36	25	22.5	6	1	US-08-487-006-76	Sequence 76, Appl
37	25	22.5	6	2	US-08-488-659A-76	Sequence 76, Appl
38	25	22.5	8	3	US-08-582-776C-29	Sequence 29, Appl
39	25	22.5	8	3	US-08-434-631B-29	Sequence 29, Appl
40	25	22.5	10	2	US-08-318-157B-25	Sequence 25, Appl
41	25	22.5	11	1	US-08-039-778B-3	Sequence 3, Appl
42	25	22.5	13	3	US-09-140-149-21	Sequence 21, Appl
43	25	22.5	15	1	US-07-918-181A-17	Sequence 17, Appl
44	25	22.5	15	1	US-07-918-181A-21	Sequence 21, Appl
45	25	22.5	15	1	US-08-080-073-21	Sequence 21, Appl

RESULT 1
US-08-940-095-133
; Sequence 133, Application US/08940095
; Patent No. 6004925
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennile & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940.095
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cornuzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNILE
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6004925e
; US-08-940-095-133

C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 31-Mar-2000
C:Accession: S36662
R:Minogawa, G.; Severin, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Krell, G.
FEBS Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of t
A:Reference number: S21152; MUID:92339502
A:Accession: S36662
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MG>

Query Match 20.7%; Score 23; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. NO. 1.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 FGPE 11
||:|:
Db 3 FGYPK 7

RESULT 15

PA0015
seed storage protein 12S 2 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 11-Jul-1997
C:Accession: PA0015
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JRPD, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional
A:Reference number: PA0001
A:Accession: PA0015
A:Molecule type: protein
A:Residues: 1-14 <KAM>
A:Experimental source: seed
C:Keywords: pyroglutamic acid; seed; storage protein
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.7%; Score 23; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. NO. 1e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 QMDGPEHL 13
| | | | |
Db 1 QGYLGVPEDL 10

Search completed: December 21, 2000, 08:37:13
Job time: 317 sec

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Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 PEHLTV 15
| | | | |
Db 7 PFHLTV 12

RESULT 9
A:Accession: A60834
A:Title: angiotensin I precursor - dog (fragment)
M:Alternate names: angiotensinogen I
N:Contains: angiotensin I
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1998
C:Accession: A60834
R:Oliver, J.A.
Hypertension 11, 21-27, 1988
A:Title: Purification and partial characterization of canine angiotensinogen.
A:Reference number: A60834; MUID:88113996
A:Accession: A60834
A:Molecule type: protein
A:Residues: 1-15 <OLI>
C:Superfamily: antithrombin III
C:Keywords: glycoprotein, plasma
F:1-10/Product: angiotensin I #status predicted <MAT>

Query Match 21.6%; Score 24; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 PEHLTV 15
| | | | |
Db 7 PFHLTV 12

RESULT 10
B31769
T-cell receptor delta-2 chain J region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 05-Nov-1999
C:Accession: B31769
R:Loth, E.Y.; Cwirla, S.; Serafini, A.T.; Phillips, J.H.; Lanier, L.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 9714-9718, 1988
A:Title: Human T-cell-receptor delta chain: genomic organization, diversity, and express
A:Reference number: A94221; MUID:89071766
A:Accession: B31769
A:Molecule type: DNA
A:Residues: 1-17 <LOH>
A:Cross-references: GB:L36386; NID:9540455; PIDN:AAA61108.1; PID:9540456
C:Keywords: T-cell receptor

Query Match 21.6%; Score 24; DB 2; Length 17;
Best Local Similarity 37.5%; Pred. No. 8.6e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 LLIQMDFGPEHLTV 16
| | | | |
Db 1 LTAQLFFGKTOLIVE 16

RESULT 11
PN0175
glutathione transferase (EC 2.5.1.18) 1 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 22-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 15-Jun-1996
C:Accession: PN0175
R:Tsuigita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
Submitted to JIPID, December 1995
A:Description: Two dimensional electrophoresis of plant proteins and standardization of
A:Reference number: PN0173

```

```

A:Accession: PN0175
A:Molecule type: protein
A:Residues: 1-18 <TSU>
A:Experimental source: leaf
C:Keywords: transferase

Query Match 21.6%; Score 24; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 DFGHP 10
| | | | |
Db 5 DFGHP 9

RESULT 12
H75063
hypothetical protein PAB7382 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: H75063
R:Anonymous; Genoscope
Submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: Insights into archaeal chromosome s
A:Reference number: A75061
A:Accession: H75063
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-18 <KAW>
A:Cross-references: GB:A0248287; GB:A1096836; NID:95458657; PIDN:CAB50405.1; PID:e151
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB7382

Query Match 21.6%; Score 24; DB 2; Length 16;
Best Local Similarity 35.7%; Pred. No. 9.2e+02;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 LQMDFGPEHLTV 16
| | | | |
Db 3 LRVETGCDRLVLD 16

RESULT 13
A37984
ADP/ATP carrier protein - yeast (Candida parapsilosis) (fragment)
C:Species: Candida parapsilosis
C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 07-Jun-1996
C:Accession: A37984
R:Querlin, B.; Bukusoglu, C.; Rakotomanana, F.; Wohlrab, H.
J. Biol. Chem. 265, 19736-19741, 1990
A:Title: Mitochondrial phosphate transport. N-ethylmaleimide insensitivity correlates
A:Reference number: A37984; MUID:91060585
A:Accession: A37984
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <GUE>

Query Match 21.6%; Score 24; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 HLVDPL 18
| | | | |
Db 5 NPLVDPL 11

RESULT 14
S36662
dermorphin (lys-7) [validated] - two-colored leaf frog

```

S59492
formate dehydrogenase alpha chain - Alcaigenes eutrophus (fragment)
C:Species: Alcaigenes eutrophus
C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C:Accession: S59492
R:Riedelbold, J.; Mayer, F.; Bill, E.; Trautwein, A.X.; Bowlen, B.
Bio1. Chem. Hoppe-Seyler 376, 561-568, 1995
A>Title: Structural and immunological studies on the soluble formate dehydrogenase from
A:Reference number: S59492; MUID:96145736
A:Accession: S59492
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <PRI>

Query Match 23.4%; Score 26; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 3.5e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 OMDFGFP 10
DB 6 EIDFGFP 12

RESULT 4
S71306
heat shock protein 90 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C:Accession: S71306
R:Comont, M.; Szweda, L.I.; Levine, R.L.; Stadman, E.R.; Friquet, B.
Arch. Biochem. Biophys. 331, 232-240, 1996
A>Title: Age-related decline of rat liver multicatalytic proteinase activity and protect
A:Reference number: S71306; MUID:96299287
A:Accession: S71306
A:Molecule type: protein
A:Residues: 1-15 <CON>
A:Experimental source: liver
C:Keywords: heat shock; phosphoprotein; stress-induced protein

Query Match 22.5%; Score 25; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 10 PEHLVDLQ 19
DB 6 PDHPIVETLR 15

RESULT 5
T44936
calmodulin kinase 2 - fission yeast (Schizosaccharomyces pombe) (fragment)
C:Species: Schizosaccharomyces pombe
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T44936
R:Alleman, V.; Alique, R.
submitted to the EMBL Data Library, May 1996
A:Reference number: 222873
A:Accession: T44936
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-16 <ALE>
A:Cross-references: EMBL:U57982; PIDN:AAD09466.1

Query Match 22.5%; Score 25; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FGFP 10
DB 5 FGFP 8

RESULT 6
B61597
cytochrome P450 AL-2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: B61597
R:Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.
Drug Metab. Dispos. 19, 291-297, 1991
A>Title: Purification and aminopyrine monooxygenase activity of liver microsomal cyto
A:Reference number: A61597; MUID:91292910
A:Accession: B61597
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SHI>

Query Match 22.1%; Score 24.5; DB 2; Length 14;
Best Local Similarity 47.1%; Pred. No. 5.7e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 5; Gaps 1;

OY 1 LLLQMDGFPPEHLVDL 17
DB 3 LLTSLSF-----LLVGF 14

RESULT 7
S03879
6-phosphofructokinase (EC 2.7.1.11) B - rabbit (fragment)
N:Alternate names: phosphofructo-1-kinase B
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 28-Apr-1993
C:Accession: S03879
R:Valaitis, A.P.; Foe, L.G.; Kwiatkowska, D.; Latschaw, S.P.; Kemp, R.G.
Biochim. Biophys. Acta 995, 187-194, 1989
A>Title: The sites of phosphorylation of rabbit brain phosphofructo-1-kinase by cycl
A:Reference number: S03879; MUID:89194250
A:Accession: S03879
A:Molecule type: protein
A:Residues: 1-13 <VAL>
A:Note: the sequence from the summary is inconsistent with that from table I and fig.
C:Keywords: glycolysis; phosphotransferase

Query Match 21.6%; Score 24; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LQMDFGF 9
DB 7 LSMDKGF 13

RESULT 8
A01250
angiotensin precursor - horse (fragment)
C:Species: Equus caballus (domestic horse)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 20-Mar-1998
C:Accession: A92775; A01250
R:Skeggis Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.
J. Exp. Med. 106, 439-453, 1957
A:Reference number: A92775
A:Accession: A92775
A:Molecule type: protein
A:Residues: 1-14 <SKK>
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; hormone; vasoconstrictor
F:1-10/Product: angiotensin I #status experimental <ANI>
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 21.6%; Score 24; DB 2; Length 14;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:37:13 ; Search time 26.84 Seconds
(Without alignments)
57.017 Million cell updates/sec

Title: us-08-934-367-10
Perfect score: 111
Sequence: 1 LLLQMDFGPEHLLVDFLOSLIS 22

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 4315

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	25.2	19	2	A39504 octamer-binding pr
2	27	24.3	21	2	A32521 hexokinase (EC 2.7
3	26	23.4	15	2	S59492 formate dehydrogen
4	25	22.5	15	2	S71306 heat shock protein
5	25	22.5	16	2	T44936 calmodulin kinase
6	24.5	22.1	14	2	B61597 cytochrome P450 AL
7	24	21.6	13	2	S03879 6-phosphofructokin
8	24	21.6	14	2	A01250 angiotensin precur
9	24	21.6	15	2	A60834 angiotensin I prec
10	24	21.6	17	2	B31769 T-cell receptor de
11	24	21.6	18	2	PM0175 glutathione transf
12	24	21.6	18	2	H75063 hypothetical prote
13	24	21.6	20	2	A37984 ADP,ATP carrier pr
14	23	20.7	7	2	S36662 seed storage prote
15	23	20.7	19	2	I46654 T-cell receptor de
16	23	20.7	14	2	I46654 proteinase inhibit
17	23	20.7	21	2	T07683 dermorphin - konde
18	22	19.8	7	1	A61324 I9 heavy chain CRD
19	22	19.8	11	2	PM0250 1-aminocyclopropan
20	22	19.8	12	2	C36201 photosystem II oxy
21	22	19.8	14	2	A61002 protein kinase C i
22	22	19.8	20	2	S72501 calsequestrin, fas
23	22	19.8	20	2	A31049 cytochrome-c oxida
24	22	19.8	20	2	S77989 dystroglycan - chl
25	22	19.8	20	2	A47105 zona pellucida gly
26	22	19.8	20	2	S50203 alanine dehydrogen
27	22	19.8	21	2	PX0078 dihydrolipamide S
28	21	18.9	9	2	B45796 serum amyloid P-co
29	21	18.9	9	2	B20569

30	21	18.9	14	2	PA0104 protein QP200070 -
31	21	18.9	15	2	PH1788 T cell receptor al
32	21	18.9	15	2	S72432 epoxycopropan isomer
33	21	18.9	17	2	A60743 ornithine carboxamoy
34	21	18.9	18	2	I49408 cytochrome-c oxida
35	21	18.9	19	2	B60822 cytochrome P450 ur
36	21	18.9	19	2	D32071 T-cell receptor de
37	21	18.9	20	2	S07232 cytochrome P450 PB
38	21	18.9	20	2	A60822 nuclear antigen EB
39	21	18.9	20	2	H49034 T-cell receptor ga
40	21	18.9	20	2	S35921 cytochrome b558 -
41	21	18.9	20	2	A54077 ubiquitin-carrier
42	21	18.9	22	2	B54397 collagen alpha 1(I
43	21	18.9	22	2	D56978 growth hormone rec
44	9	18.0	2	2	I46023 type I DNA methylit
45	20	18.0	12	2	S56122

ALIGNMENTS

RESULT 1
A39504 octamer-binding protein, Ku-like, 72K chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: A39504
R:May, G.; Sutton, C.; Gould, H.
J. Biol. Chem. 266, 3052-3059, 1991
A:Title: Purification and characterization of Ku-2, an octamer-binding protein relate
A:Reference number: A39504; MUID:91131605
A:Accession: A39504
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <MAY>

Query Match 25.2% Score 28; DB 2; Length 19;
Best Local Similarity 71.4% Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LQMDFGP 9
DB 11 LEMDVGF 17

RESULT 2
A32521 hexokinase (EC 2.7.1.1) I peptide III - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 12-Apr-1995
R:Schlirch, D.M.; Wilson, J.E.
Arch. Biochem. Biophys. 257, 1-12, 1987
A:Title: Rat brain hexokinase: amino acid sequence at the substrate hexose binding si
A:Reference number: A90080; MUID:87324917
A:Accession: A32521
A:Molecule type: protein
A:Residues: 1-21 <SCH>
C:Superfamily: human hexokinase I; hexokinase homology
C:Keywords: ATP; glycolysis; phosphotransferase

Query Match 24.3% Score 27; DB 2; Length 21;
Best Local Similarity 50.0% Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 LQMDFGPEH 12
DB 3 LGFTFSFPKH 12

RESULT 3

Query Match 17.18; Score 19; DB 1; Length 21;
 Best Local Similarity 44.48; Pred. No. 4.3e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Caps 0;

QY 8 GPPHLLVD 16
 DB 12 GHPVEALVE 20

Search completed: December 21, 2000, 08:38:16
 Job time: 149 sec

ID UP21_UPEIN STANDARD: PRT: 19 AA.
AC P82027;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE UPERIN 2.1.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Uperoleia.
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE-SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
Adams G.W., Severini C.;
RT "Novel upeirin peptides from the dorsal glands of the Australian
floodplain toadlet Uperoleia inundata.";
RL Aust. J. Chem. 49:475-484(1996).
CC -1- FUNCTION: SHOWS A MEDIUM ANTIBACTERIAL ACTIVITY AGAINST
L. MESENERIODES, M. LUTEUS AND S. UBERIS.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MM-1926; METHOD-FAB.
KW Amphibian skin; Antibiotic.
SQ SEQUENCE 19 AA; 1927 MW; 328834D77BA353D2 CRC64;

Query Match 17.1%; Score 19; DB 1; Length 19;
Best Local Similarity 37.5%; Pred. No. 3.9e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 14 LVDFLOSL 21
: : : :
Db 2 IVDFAKKV 9

RESULT 13
UP25_UPEIN STANDARD: PRT: 19 AA.
AC P82031;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE UPERIN 2.5.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Uperoleia.
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE-SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
Adams G.W., Severini C.;
RT "Novel upeirin peptides from the dorsal glands of the Australian
floodplain toadlet Uperoleia inundata.";
RL Aust. J. Chem. 49:475-484(1996).
CC -1- FUNCTION: SHOWS A MEDIUM ANTIBACTERIAL ACTIVITY AGAINST M. LUTEUS,
L. MESENERIODES AND S. UBERIS.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MM-1940; METHOD-FAB.
KW Amphibian skin; Antibiotic.
SQ SEQUENCE 19 AA; 1941 MW; 5E94C6C757B463D9 CRC64;

Query Match 17.1%; Score 19; DB 1; Length 19;
Best Local Similarity 37.5%; Pred. No. 3.9e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 14 LVDFLOSL 21
: : : :
Db 2 IVDFAKKV 9

RESULT 14

SUCB_CANFA STANDARD: PRT: 20 AA.
AC P99507;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE PUTATIVE SUCCINYL-COA LIGASE (GDP-FORMING) BETA-CHAIN (EC 6.2.1.4)
DE (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA) (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE.
RC TISSUE-HEART;
RX MEDLINE: 98163340.
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- CATALYTIC ACTIVITY: SUCCINATE + COA + GTP = SUCCINYL-COA + GDP +
ORTHOPHOSPHATE.
CC -1- PATHWAY: SUBSTRATE LEVEL PHOSPHORYLATION STEP OF THE TRICARBOXYLIC
ACID CYCLE.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER BETA SUBUNITS OF SUCCINYL-COA SYNTHETASE,
OF MALATE-COA LIGASE AND TO ATP CITRATE-LYASE.
DR HSC-2DPAGE: P99507; DOG.
DR INTERPRO: IPR000303; .
DR PROSITE: PS01217; SUCCINYL-COA_LIG_3; PARTIAL.
KW Ligase; Glycolysis; Tricarboxylic acid cycle; Mitochondrion.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2248 MW; BE8AEFD54BDAC2E CRC64;

Query Match 17.1%; Score 19; DB 1; Length 20;
Best Local Similarity 33.3%; Pred. No. 4.1e+03;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 11 EHLVDFIQ 19
: : : :
Db 5 EYSMELLQ 13

RESULT 15
DCMS_PSECA STANDARD: PRT: 21 AA.
AC P19921;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE CARBON MONOXIDE OXYGENASE (CYTOCHROME B-561) SMALL CHAIN (EC 1.2.2.4)
DE (FRAGMENT).
OS Pseudomonas carboxydovorans.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Oligotropa.
RN [1]
RP SEQUENCE.
RC STRAIN-OM5;
RX MEDLINE: 90055678.
RA Kraut M., Hengedieck I., Herwig S., Meyer O.;
RT "Homology and distribution of Co dehydrogenase structural genes in
carboxydotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + FERROCYTOCHROME B-561 = CO(2) +
2 H(+)+ FERRICCYTOCHROME B-561.
CC -1- COFACTOR: MOLYBDENUM.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
SMALL.
DR PIR: PLO144; PLO144.
KW Oxidoreductase; Molybdenum.
FT NON_TER 21
SQ SEQUENCE 21 AA; 2270 MW; 68DA380629401B9C CRC64;

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OG Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
OC Funariidae; Funariales; Funariaceae; Physcomitrella.
RN [1]
RP SEQUENCE.
RC TISSUE=PROTONEMA;
RA MEDLINE: 97275459.
RX Kasten B., Buck F., Nuske J., Reski R.;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
  plastid enzymes."
RL Planta 201;261-272(1997)
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
  GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
  SUBUNIT.
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
  CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
  SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
  HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
DR MENDEL: 13023; PHYPA:atpb;1.
DR INTERPRO: IPR000194; -.
DR PROSITE: PS00152; ATPASE_ALPHA_BETA: PARTIAL.
KM ATP synthetase; Chloroplast; Thylakoid membrane; CF(1);
KW Hydrolyase; ATP-binding; Hydrogen ion transport.
FT NON_TER 21
SQ SEQUENCE 21 AA; 2298 MM; 9558E4F5AC89D81A CRC64;

Query Match 18.0%; Score 20; DB 1; Length 21;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 MDPGFP 10
   1 11
Db 16 LDIXFP 21

RESULT 10
ID DP4_BOVIN STANDARD; PRT; 20 AA.
AC P81425;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (ADENOSINE DEAMINASE
  DE COMPLEXING PROTEIN) (ADCP-I) (FRAGMENTS).
GN DP4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RC TISSUE=KIDNEY;
RA MEDLINE: 98293306.
RX Ben-Shoshan I., Parola A.H.;
RT "The CP-I subunit of adenosine deaminase complexing protein from calf
  kidney is identical to human, mouse, and rat dipeptidyl peptidase
  IV."
RL Comp. Biochem. Physiol. 119B:289-292(1998).
CC -1- FUNCTION: REMOVES N-TERMINAL DIPEPTIDES SEQUENTIALLY FROM
  POLYPEPTIDES HAVING UNSUBSTITUTED N-TERMINI PROVIDED THAT THE
  PENULTIMATE RESIDUE IS PROLINE. BINDS AND REGULATES THE ACTIVITY
  OF ADA.
CC -1- CATALYTIC ACTIVITY: DIPEPTIDYL-POLYPEPTIDE + H(2)O = DIPEPTIDE +
  POLYPEPTIDE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS IN
  A SOLUBLE FORM (BY SIMILARITY).
CC -1- PTM: THE SOLUBLE FORM (SDP) DERIVES FROM THE MEMBRANE FORM (MDPP)
  BY PROTEOLYTIC PROCESSING.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B, ALSO KNOWN AS THE

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CC PROLYL OLIGOPEPTIDASE FAMILY.
DR INTERPRO: IPR002471; -.
DR PROSITE: PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolyase; Dipeptidase; Serine protease; Transmembrane; Glycoprotein;
  KW Signal-anchor.
FT NON_TER 1 1
FT NON_CONS 10 11
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2356 MM; 28B78E62639F7276 CRC64;

Query Match 17.6%; Score 19.5; DB 1; Length 20;
Best Local Similarity 33.3%; Pred. No. 3.4e+03;
Matches 5; Conservative 6; Mismatches 1; Indels 3; Gaps 1;

OY 1 LLLQMDGFPPEHLV 15
   11111111111111111111
Db 5 LLLLEV---YVENIIV 16

RESULT 11
ID OXLA_OPHHA STANDARD; PRT; 19 AA.
AC P81383;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE L-AMINO ACID OXIDASE (EC 1.4.3.2) (LAO) (LAO) (FRAGMENT).
DE Ophiophagus hannah (King cobra) (Naja hannah).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubridae;
OC Elapidae; Elapinae; Ophiophagus.
RN [1]
RP SEQUENCE.
RC TISSUE=VENOM;
RA MEDLINE: 94361525.
RX Pennudurai G., Chung M.C.M., Tan N.-H.;
RT "Purification and properties of the L-amino acid oxidase from Malayan
  pit viper (Calloselasma rhodostoma) venom."
RL Arch. Biochem. Biophys. 313:373-378(1994).
RN [2]
RP SEQUENCE OF 1-15.
RC TISSUE=VENOM;
RX MEDLINE: 97449790.
RA Ahn M.Y., Lee B.M., Kim Y.S.;
RT "Characterization and cytotoxicity of L-amino acid oxidase from the
  venom of King cobra (Ophiophagus hannah)."
RL Int. J. Biochem. Cell Biol. 29:911-919(1997).
CC -1- FUNCTION: HAS CYTOTOXIC ACTIVITY (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: A L-AMINO ACID + H(2)O + O(2) -> A 2-OXO ACID +
  NH(3) + H(2)O(2).
CC -1- COFACTOR: FAD.
CC -1- SUBUNIT: HOMODIMER (PROBABLE).
CC -1- PTM: GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
CC -1- STRONG, TO MOUSE FIG-1.
KW Oxidoreductase; Flavoprotein; FAD; Glycoprotein; Venom.
FT CONFICT 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2298 MM; DD911A5B414F1427 CRC64;

Query Match 17.1%; Score 19; DB 1; Length 19;
Best Local Similarity 40.0%; Pred. No. 3.9e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 3 LQMDGFPPEH 12
   11111111111111111111
Db 5 LRESEFQPEPY 14

RESULT 12
UP21_UPEIN

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MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE REFOOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL MATRIX (BY SIMILARITY)

-1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

DR FLVBASE; FB9n0010375; Mmp-P1.

DR INTERPRO; IPR001844; -.

DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.

KW Chaperone; ATP-binding; Mitochondrion.

FT NON_TER 1 1

FT NON_TER 11 11

SEQUENCE 11 AA; 1243 MW; 78501A36365A6DB CRC64;

Query Match 18.0%; Score 20; DB 1; Length 11;
Best Local Similarity 18.2%; Pred. No. 1.5e+03;
Matches 2; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 1 LLLQMDFGFPE 11
Db 1 VITEQSWGSPK 11

RESULT 6
ID TEML_RANTE STANDARD; PRT; 11 AA.
AC P56923;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TEMPORIN L.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
RN [1]
RP SEQUENCE.
RC TISSUE-SKIN.
RX MEDLINE; 97175050.
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RT "Temporins, antimicrobial peptides from the European red frog Rana
temporaria."
RL Eur. J Biochem. 242:788-792(1996).
CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
GRAM-POSITIVE BACTERIA.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAECURIN/RUGOSIN
FAMILY.
KW Amphibian skin; Antibiotic; Amidation; Multigene family.
FT MOD_RES 11 11
FT MOD_RES 11 AA; 1194 MW; 1E990549B372724 CRC64;
SEQUENCE 11 AA; 1194 MW; 1E990549B372724 CRC64;

Query Match 18.0%; Score 20; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 13 LLVDFLQSL 21
Db 1 LLPMLKSL 9

RESULT 7
ID DCMK_PSECF STANDARD; PRT; 14 AA.
AC P19914;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARBON MONOXIDE DEHYDROGENASE MEDIUM CHAIN (EC 1.2.99.2) (FRAGMENT).
OS Pseudomonas carboxydoflava.

Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
OC Hydrogenophaga.
RN [1]
RP SEQUENCE.
RX MEDLINE; 90055678.
RA Kraut M., Hengedieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydrotrophic bacteria."
RL Arch. Microbiol. 152:335-341(1989).
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
ACCEPTOR.
CC -1- COFACTOR: MOLYBDENUM.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
SMALL.
DR PIR; P10142; P10142.
KW Oxidoreductase; Molybdenum.
FT NON_TER 14 14
FT NON_TER 14 14
SEQUENCE 14 AA; 1756 MW; 65583C6D1FB7C25B CRC64;

Query Match 18.0%; Score 20; DB 1; Length 14;
Best Local Similarity 15.4%; Pred. No. 2e+03;
Matches 2; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

OY 1 LLLQMDFGFPEHL 13
Db 2 MIPREYHAPKHV 14

RESULT 8
ID MDH_SYNY4 STANDARD; PRT; 16 AA.
AC P80460;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MALATE DEHYDROGENASE (EC 1.1.1.37) (FRAGMENT).
GN MDH.
OS Synechocystis sp. (strain PCC 6714).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
RN [1]
RP SEQUENCE.
RA Naterstad K., Synstad B., Sirevag R.;
RL Submitted (SEP-1996) to the SWISS-PROT data bank.
CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE + NADH.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
DR INTERPRO; IPR001252; -.
DR PROSITE; PS00068; MDH; PARTIAL.
KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT NON_TER 16 16
FT NON_TER 16 16
SEQUENCE 16 AA; 1780 MW; 61D1896F14E81984 CRC64;

Query Match 18.0%; Score 20; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LQMDFG 8
Db 9 LTTDFG 14

RESULT 9
ID ATPB_PHYPA STANDARD; PRT; 21 AA.
AC P80658;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) (FRAGMENT).
GN ATPB.
OS Physcomitrella patens (Moss).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 88331073.
 RA Hall D.E., Frazer K.A., Hann B.C., Reichardt L.F.;
 RT Isolation and characterization of a laminin-binding protein from rat
 RT and chick muscle.";
 RL J. Cell Biol. 107:687-697(1988).
 CC -1- FUNCTION: CALSEQUESTRIN IS A HIGH-CAPACITY, MODERATE AFFINITY,
 CC CALCIUM-BINDING PROTEIN AND THUS ACTS AS AN INTERNAL CALCIUM STORE
 CC IN MUSCLE. THE RELEASE OF CALCIUM BOUND TO CALSEQUESTRIN THROUGH
 CC A CALCIUM RELEASE CHANNEL TRIGGERS MUSCLE CONTRACTION. BINDS 40
 CC TO 50 MOLES OF CALCIUM. ALSO BINDS LAMININ.
 CC -1- SUBCELLULAR LOCATION: THIS ISOFORM OF CALSEQUESTRIN OCCURS IN THE
 CC SARCOPLASMIC RETICULUM'S TERMINAL CISTERNAE LUMINAL SPACES OF
 CC FAST SKELETAL MUSCLE CELLS. ASPARTACTIN IS FOUND IN THE BASAL
 CC LAMINA SURROUNDING INDIVIDUAL MUSCLE FIBERS.
 CC -1- TISSUE SPECIFICITY: SKELETAL AND HEART MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE CALSEQUESTRIN FAMILY.
 DR PIR: A31049; A31049.
 DR INTERPRO: IPR001393.
 DR PROSITE: PS00864; CALSEQUESTRIN_2; PARTIAL.
 DR PROSITE: PS00863; CALSEQUESTRIN_1; 1.
 KW Muscle; Glycoprotein; Calcium-binding.
 FT NON_TER 20
 SO SEQUENCE 20 AA; 2238 MW; 92ADE04FC2A69280 CRC64;

Query Match 19.8%; Score 22; DB 1; Length 20;
 Best Local Similarity 62.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 9 GPEHLLVD 16
 ||| ||
 DB 6 PPEIDGVD 13

RESULT 3
 COXN_THUOB
 ID COXN_THUOB STANDARD: PRT: 20 AA.
 AC P80980;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE VIIb-HEART (EC 1.9.3.1) (FRAGMENT).
 OS Thunnus obesus (Bigeye tuna).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=HEART;
 RX MEDLINE: 97454291.
 RA Arnold S., Lee I., Kim M., Song E., Lindér D., Lottspeich F.,
 RA Kadanebach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver".
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
 CC 4 FERRICYTOCHROME C.
 CC Oxidoreductase; Mitochondrion.
 KW NON_TER 20
 SO SEQUENCE 20 AA; 2303 MW; 0A33BD34006E5AA6 CRC64;

Query Match 19.8%; Score 22; DB 1; Length 20;
 Best Local Similarity 57.1%; Pred. No. 1.4e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 DPGPEH 12
 ||| ||
 DB 14 DNGMPVH 20

RESULT 4
 SAMP_MUSCA
 ID SAMP_MUSCA STANDARD: PRT: 9 AA.
 AC P19095;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SERUM AMYLOID P-COMPONENT (SAP) (FRAGMENT).
 OS Musculus canis (Smooth dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes; Triakidae;
 OC Mustelus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 83160932.
 RA Robey F.A., Tanaka T., Liu T.-Y.;
 RT Isolation and characterization of two major serum proteins from the
 RT dogfish, Mustelus canis, C-reactive protein and amyloid P
 RT component.";
 RL J. Biol. Chem. 258:3889-3894(1983).
 CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
 CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
 CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
 DR PIR: B20569; B20569.
 DR INTERPRO: IPR001759.
 DR PROSITE: PS00289; PENTAXIN; PARTIAL.
 KW Amyloid; Glycoprotein; Plasma; Pentaxin.
 FT DOMAIN 1
 FT NON_TER 9
 SO SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match 18.9%; Score 21; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 8.8e+04;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 8 GPEHLLV 15
 ||| ||
 DB 1 GPEGSLI 8

RESULT 5
 CH60_DROME
 ID CH60_DROME STANDARD: PRT: 11 AA.
 AC P35380;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MITOCHONDRIAL MATRIX PROTEIN P1 (60 KDA CHAPERONIN) (HEAT SHOCK
 DE PROTEIN 60) (HSP-60) (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).
 GN MMP-P1 OR HSP60.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=VALLECAS; TISSUE=WING IMAGINAL DISK;
 RX MEDLINE: 93272852.
 RA Santaren J.F., van Damme J., Puype M., Vandekerckhove J.,
 RA Garcia-Bellido A.;
 RT Identification of Drosophila wing imaginal disc proteins by two-
 RT dimensional gel analysis and microsequencing.";
 RL Exp. Cell Res. 206:220-226(1993).
 CC -1- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:38:16 ; Search time 18.39 Seconds
(Without alignments)
38.219 Million cell updates/sec

Title: US-08-934-367-10

Perfect score: 111
Sequence: 1 LLLQMDFGPEHLVDFLQSLIS 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 1213

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	21.6	14	1	ANGT_HORSE
2	22	19.8	20	1	CAOS_RAT
3	22	19.8	20	1	COXN_THUOB
4	21	18.9	9	1	SAMP_MUSCA
5	20	18.0	11	1	CH60_DROME
6	20	18.0	11	1	TEML_RANTE
7	20	18.0	14	1	DCNM_PSECF
8	20	18.0	21	1	MDH_SYNY4
9	20	18.0	16	1	ATPB_PHYPA
10	19.5	17.6	20	1	DP4_BOVIN
11	19	17.1	19	1	OXIA_OPHHA
12	19	17.1	19	1	UP21_UPEIN
13	19	17.1	19	1	UP25_UPEIN
14	19	17.1	20	1	SUCB_CANFA
15	19	17.1	21	1	DCMS_PSECA
16	19	17.1	21	1	YD90_HAEIN
17	18	16.2	7	1	ALL7_CYDPO
18	18	16.2	8	1	ALL5_CALVO
19	18	16.2	8	1	ALL5_CYDPO
20	18	16.2	12	1	GRAR_RANRU
21	18	16.2	13	1	ORCK_ORCLI
22	18	16.2	13	1	PSBP_PINPS
23	18	16.2	15	1	LM42_LOCMI
24	18	16.2	17	1	FLA2_BARBA
25	18	16.2	18	1	NS4_PSEAR
26	18	16.2	19	1	HB82_UREHA
27	18	16.2	19	1	NUO6_SOLRU
28	18	16.2	20	1	THIO_CANFA
29	18	16.2	20	1	UN05_PINPS
30	18	16.2	21	1	CSPS_STRPR
31	18	16.2	21	1	OMP4_PASHA
32	17	15.3	8	1	CCRN_MACRU
33	17	15.3	9	1	FAR1_CALVO

34	17	15.3	10	1	CAER_LITXA
35	17	15.3	12	1	OPS3_DPROI
36	17	15.3	13	1	BSP3_PHYPA
37	17	15.3	13	1	SODM_CANFA
38	17	15.3	14	1	HCYA_MEGCR
39	17	15.3	15	1	LFP_ECOLI
40	17	15.3	16	1	LEK1_LOCMI
41	17	15.3	17	1	GAST_MACMU
42	17	15.3	19	1	TRBP_CAVPO
43	17	15.3	19	1	UP24_UPEIN
44	17	15.3	20	1	CPA7_PASEP
45	17	15.3	20	1	LFP3_HUMAN

ALIGNMENTS

RESULT	1	STANDARD	PRT	14 AA
ANGT_HORSE				
ID	ANGT_HORSE			
AC	P01016:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-FEB-1996 (Rel. 33, Last annotation update)			
DE	ANGIOTENSINOGEN (FRAGMENT).			
GN	ACT.			
OS	Equus caballus (Horse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.			
RN	[1]			
RP	SEQUENCE.			
RA	Skeggs L.T., Jr., Kahn J.R., Lentz K., Shumway N.P.;			
RT	"The preparation, purification, and amino acid sequence of a			
RT	polypeptide renin substrate.";			
RL	J. Exp. Med. 106:439-453(1957).			
CC	-1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN			
CC	CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN			
CC	CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE			
CC	PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT			
CC	PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL			
CC	BALANCE OF BODY FLUIDS.			
CC	-1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.			
CC	-1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.			
CC	PIR: A01250; A01250.			
DR	INTERPRO: IPR000215; -			
DR	PROSITE: PS00284; SERPIN; PARTIAL.			
KW	Vasocostrictor; Plasma; Serpin.			
FT	PEPTIDE 1 10			
FT	NON_TER 14 14			
FT	SEQUENCE 14 AA; 1759 MW; 2E9921F8EEFBDD7 CRC64;			
Query Match	21.6%; Score 24; DB 1; Length 14;			
Best Local Similarity	83.3%; Pred. NO. 4.6e+02;			
Matches	5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
OY	10 PEHLV 15			
DB	7 PEHLV 12			
RESULT	2			
CAOS_RAT				
ID	CAOS_RAT	STANDARD:	PRT:	20 AA.
AC	P19633:			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	CALDSQUESTRIN, SKELETAL MUSCLE ISOFORM (ASPARTACTIN) (LAMININ-BINDING			
DE	PROTEIN) (FRAGMENT).			
GN	CASQ1.			
OS	Rattus norvegicus (Rat).			

DR EMBL: U04282; AAC45541.1; -
FT NON TER 13 13
SO SEQUENCE 13 AA; 1407 MW; 08FAB3930E0BC720 CRC64;

Query Match 21.6%; Score 24; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 LIQMDFG 8
: 1:111
Db 6 ILVLDVG 12

Search completed: December 21, 2000, 08:37:55
Job time: 288 sec

RA Menting J.C., Cornish E., Scopes R.K.;
 RT "Purification and partial characterization of NADPH-cytochrome c
 RL reducease from Petunia hybrida flowers.";
 RL Plant Physiol. 106:643-650(1994).
 SQ SEQUENCE 20 AA: 2390 MW: 8BCDA6F8CF7EEDC CRC64;

Query Match
 Best Local Similarity 50.0%; Score 25; DB 10; Length 20;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 QMDGFEHL 13
 :|||:|
 Db 1 RMDFTVEEEL 10

RESULT 12

O9PS42 PRELIMINARY; PRT; 22 AA.
 AC O9PS42;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE PHENOBARBITAL-INDUCED 48 KDA CYTOCHROME P-450 (FRAGMENT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN [1]
 RP SEQUENCE.
 RA MEDLINE: 92406903.
 RA Nakai K., Ward A.M., Gannon M., Rifkind A.B.;
 RT "Beta-naphthoflavone induction of a cytochrome P-450 arachidonic acid
 RT epoxidegenase in chick embryo liver distinct from the aryl hydrocarbon
 RT hydroxylase and from phenobarbital-induced arachidonate epoxidegenase.";
 RL J. Biol. Chem. 267:19503-19512(1992).
 SQ SEQUENCE 22 AA: 2377 MW: 6BA9C990EE33E9C1 CRC64;

Query Match
 Best Local Similarity 58.3%; Score 24.5; DB 13; Length 22;
 Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

OY 5 MDF-GPEHLV 15
 |||||
 Db 1 MDPLGLPTILL 12

RESULT 13

ID O31364 PRELIMINARY; PRT; 13 AA.
 AC O31364;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE GUAA (FRAGMENT).
 GN Borrelia garinii.
 OS Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-G25;
 RX MEDLINE: 97426044.
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
 RA Rosa P.;
 RT "The Borrelia burgdorferi circular plasmid cp26: conservation of
 RT plasmid structure and targeted inactivation of the ospC gene.";
 RL Mol. Microbiol. 25:361-374(1997).
 DR EMBL: U93700; AAC45534.1; -;
 FT NON_TER 13
 SQ SEQUENCE 13 AA: 1449 MW: 08FAB9B0E0BC720 CRC64;

Query Match
 Best Local Similarity 57.1%; Score 24; DB 2; Length 13;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 LLOMDFG 8
 :|:|
 Db 6 ILVLDG 12

RESULT 14

ID O31365 PRELIMINARY; PRT; 13 AA.
 AC O31365;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE GUAA (FRAGMENT).
 GN Borrelia garinii.
 OS Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-IP90;
 RX MEDLINE: 97426044.
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
 RA Rosa P.;
 RT "The Borrelia burgdorferi circular plasmid cp26: conservation of
 RT plasmid structure and targeted inactivation of the ospC gene.";
 RL Mol. Microbiol. 25:361-374(1997).
 DR EMBL: U93701; AAC45536.1; -;
 FT NON_TER 13
 SQ SEQUENCE 13 AA: 1382 MW: 08FBA180E0BC720 CRC64;

Query Match
 Best Local Similarity 57.1%; Score 24; DB 2; Length 13;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 LLOMDFG 8
 :|:|
 Db 6 ILVLDG 12

RESULT 15

ID O34622 PRELIMINARY; PRT; 13 AA.
 AC O34622;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE GUAA (FRAGMENT).
 GN Borrelia burgdorferi (Lyme disease spirochete).
 OS Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CT39 (ILL-1), DNI27C19-2, AND 25015;
 RX MEDLINE: 97426044.
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
 RA Rosa P.;
 RT "The Borrelia burgdorferi circular plasmid cp26: conservation of
 RT plasmid structure and targeted inactivation of the ospC gene.";
 RL Mol. Microbiol. 25:361-374(1997).
 DR EMBL: U93694; AAC45522.1; -;
 FT NON_TER 13
 SQ SEQUENCE FROM N.A.
 RC STRAIN-DNI27C19-2, AND 25015;
 RX MEDLINE: 95154673.
 RA Stevenson B., Barthold S.W.;
 RT "Expression and sequence of outer surface protein C among North
 RT American isolates of Borrelia burgdorferi.";
 RL FEMS Microbiol. Lett. 124:367-372(1994).
 DR EMBL: U93694; AAC45522.1; -;
 FT NON_TER 13
 SQ SEQUENCE 13 AA: 1449 MW: 08FAB9B0E0BC720 CRC64;

RESULT 7
 092655 PRELIMINARY; PRT; 21 AA.
 AC 092655;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE ATP-BINDING PROTEIN (FRAGMENT).
 GN RECF.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-L2 434B;
 RA Wang L., Steenburgh S.D., Zheng Y., Larsen S.H.;
 RT "Gene identification of Chlamydia trachomatis by random DNA
 sequencing."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF087306; AAD04082.1; -.
 KW ATP-binding.
 FT NON_TER 1 1
 FT SEQUENCE 21 AA; 2336 MW; 0185D9AC428276D9 CRC64;
 SQ

Query Match 23.9%; Score 26.5; DB 2; Length 21;
 Best Local Similarity 41.7%; Pred. No. 9.2e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Oy 2 LMDGFGPEHL 13
 :||: ||:|
 Db 8 ILQL-ISPKHI 18

RESULT 8
 002830 PRELIMINARY; PRT; 22 AA.
 AC 002830;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE PRO ALPHAI TYPE II COLLAGEN (FRAGMENT).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96377339.
 RA Metsaranta M., Kujala U.M., Pellinleml L., Osterman H., Aho H.,
 RA Vuorio E.;
 RT "Evidence for insufficient chondrocytic differentiation during repair
 of full-thickness defects of articular cartilage."
 RL Matrix Biol. 15:39-47(1996).
 DR EMBL: S83370; AAB50773.1; -.
 DR INTERPRO: IPR000885; -.
 DR PRAM: PF01410; COFI; 1.
 FT NON_TER 1 1
 FT SEQUENCE 22 AA; 2292 MW; 2E05FE169844236D CRC64;
 SQ

Query Match 23.4%; Score 26; DB 6; Length 22;
 Best Local Similarity 71.4%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5 MDFGPE 11
 ||| |||
 Db 3 MDIGPE 9

RESULT 9
 094554 PRELIMINARY; PRT; 16 AA.
 AC 094554;
 AC 094554;

DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE CALMODULIN KINASE 2 (FRAGMENT).
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
 OC Schizosaccharomycetaceae; Schizosaccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Alemany V., Alique R.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U57982; AAD09466.1; -.
 KW Kinase.
 FT NON_TER 1 1
 FT SEQUENCE 16 AA; 1846 MW; 4A673B1F4C328BD9 CRC64;
 SQ

Query Match 22.5%; Score 25; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 FGFP 10
 ||||
 Db 5 FGFP 8

RESULT 10
 09PS70 PRELIMINARY; PRT; 19 AA.
 ID 09PS70;
 AC 09PS70;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 92011685.
 RA Stifant S., Barber D.L., Aebersold R., Steyrer E., Shen X., Nimpf J.,
 RA Schneider W.J.;
 RT "The laying hen expresses two different low density lipoprotein
 receptor-related proteins."
 RL J. Biol. Chem. 266:19079-19087(1991).
 SQ SEQUENCE 19 AA; 1861 MW; 4EEC931205620608 CRC64;

Query Match 22.5%; Score 25; DB 13; Length 19;
 Best Local Similarity 40.0%; Pred. No. 1.4e+03;
 Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Oy 2 LMDGFGPEHLVD 16
 ||| ||| |||
 Db 1 LLAQGLGPTALAD 15

RESULT 11
 09S878 PRELIMINARY; PRT; 20 AA.
 ID 09S878;
 AC 09S878;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE NADPH-CYTOCROME P450 REDUCTASE (EC 1.6.2.4) (FRAGMENT).
 OS Petunia hybrida (Petunia).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
 OC Solanaceae; Petunia.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 95083756.

RP SEQUENCE FROM N.A.
RC STRAIN-212:
RX MEDLINE: 97312006.
RA Ge Y., Old I.G., Girons I.S., Charon N.W.:
RT "The flk motility operon of *Borrelia burgdorferi* is initiated by a
RL sigma 70-like promoter."
DR Microbiology 143:1681-1690(1997).
EMBL: U62901; AAB62742.1; -.
FT NON_TER 21 21
SO SEQUENCE 21 AA; 2432 MW; F33EEC548BD5B33 CRC64;

Query Match 27.0%; Score 30; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 5 MDCFPPEHL 14
: | | | | |
Db 7 IEFDPEGL 16

RESULT 3
O9TWH5 PRELIMINARY; PRT; 20 AA.
AC O9TWH5;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE 40 KDA GAP JUNCTION PROTEIN (FRAGMENT).
OS *Heliothis virescens* (Noctuid moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Dliaryta;
OC Noctuoidea; Noctuidae; Heliothinae; Heliothis.
RN [1]
RP SEQUENCE.
RX MEDLINE: 95347000.
RA Ryerse J.S.:
RT "Immunocytochemical, electrophoresis, and immunoblot analysis of
RT *Heliothis virescens* gap junctions isolated in the presence and absence
RL of protease inhibitors."
Cell Tissue Res. 281:179-186(1995).
SO SEQUENCE 20 AA; 2304 MW; A298D5E3B89586B CRC64;

Query Match 26.1%; Score 29; DB 5; Length 20;
Best Local Similarity 35.3%; Pred. No. 3.5e+02;
Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 LLLQMDGPEHLVDF 17
: | | | | |
Db 3 VVINDGGYLFELTRDF 19

RESULT 4
O9UGS1 PRELIMINARY; PRT; 12 AA.
AC O9UGS1;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE DJ796117.4 (NOVEL PROTEIN SIMILAR TO GS2) (FRAGMENT).
GN DJ796117.4.
OS *Homo sapiens* (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.:
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AL035398; CAB63074.1; -.
FT NON_TER 1 1
SO SEQUENCE 12 AA; 1430 MW; AF7740ABECB69AA6 CRC64;

Query Match 24.3%; Score 27; DB 4; Length 12;
Best Local Similarity 44.4%; Pred. No. 4.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LLLQMDGPF 9
: | | | | |
Db 1 MILEDMSF 9

RESULT 5
O9TRO7 PRELIMINARY; PRT; 14 AA.
AC O9TRO7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE CALCYCLIN-ASSOCIATED PROTEIN PEPTIDE L-8, CAP-50-ANNEXIN.
OS *Bos taurus* (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RX MEDLINE: 92317074.
RA Mizutani A., Usuda N., Tokumitsu H., Minami H., Yasui K.,
RA Kobayashi R., Hida H.:
RT "CAP-50, a newly identified annexin, localizes in nuclei of cultured
RT fibroblast 3Y1 cells."
J. Biol. Chem. 267:13498-13504(1992).
SO SEQUENCE 14 AA; 1446 MW; C8322EB96DD9C6C6 CRC64;

Query Match 24.3%; Score 27; DB 6; Length 14;
Best Local Similarity 41.7%; Pred. No. 4.9e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 7 FGPEHLVDFL 18
: | | | | |
Db 2 FGDEQATIDXL 13

RESULT 6
O9SBE1 PRELIMINARY; PRT; 22 AA.
AC O9SBE1;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE ANNEXIN (FRAGMENT).
OS Capsicum annuum (bell pepper).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
OC Solanaceae; Capsicum.
RN [1]
RP SEQUENCE.
RX MEDLINE: 95353219.
RA Hoshino T., Mizutani A., Chida M., Hida H., Mizutani J.:
RT "Plant annexin form homodimer during Ca(2+)-dependent liposome
RT aggregation."
RL Biochem. Mol. Biol. Int. 35:749-755(1995).
SO SEQUENCE 22 AA; 2465 MW; A36D1A1FE311F0F CRC64;

Query Match 24.3%; Score 27; DB 10; Length 22;
Best Local Similarity 41.7%; Pred. No. 8e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 7 FGPEHLVDFL 18
: | | | | |
Db 3 WGTDEKLIDIL 14

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:37:54 ; Search time 37.32 Seconds
(without alignments)
\$5.044 Million cell updates/sec

Title: US-08-934-367-10
111
Perfect score: 1 LLLQMDFGPEHLVDFLQSL 22
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4962

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_14:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.invertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	27.9	19	6	Q9RR6
2	30	27.0	21	2	P70861
3	29	26.1	20	5	Q9TWH5
4	27	24.3	12	4	Q9UGS1
5	27	24.3	14	6	Q9TRC7
6	27	24.3	22	10	Q9SBE1
7	26.5	23.9	21	2	Q9ZGS5
8	26	23.4	22	6	002830
9	25	22.5	16	3	094554
10	25	22.5	19	13	Q9PS70
11	25	22.5	20	10	Q9S878
12	24.5	22.1	22	13	Q9PS42
13	24	21.6	13	2	031365
14	24	21.6	13	2	031365
15	24	21.6	13	2	034622
16	24	21.6	18	1	Q9UYK7
17	24	21.6	19	5	Q9W508
18	24	21.6	20	6	Q9TIG3
19	24	21.6	21	2	Q9X3D0

20	23	20.7	8	2	085406
21	23	20.7	9	5	096417
22	23	20.7	10	2	09X534
23	23	20.7	10	2	09X533
24	23	20.7	13	2	031296
25	23	20.7	13	2	034770
26	23	20.7	13	11	035758
27	23	20.7	17	2	09X313
28	23	20.7	18	13	P82068
29	23	20.7	19	11	090VE3
30	23	20.7	20	13	Q9PRN5
31	23	20.7	21	4	016575
32	23	20.7	21	8	Q9ZYB7
33	23	20.7	21	10	Q41496
34	23	20.7	21	12	080817
35	23	20.7	22	1	P71537
36	22.5	20.3	17	6	Q9TR11
37	22	19.8	13	4	Q9UDE7
38	22	19.8	14	2	056945
39	22	19.8	15	10	Q41526
40	22	19.8	17	8	Q9T2S2
41	22	19.8	17	11	Q9QU74
42	22	19.8	19	9	Q38371
43	22	19.8	20	5	Q9TWI4
44	22	19.8	20	6	Q9TR41
45	22	19.8	20	13	Q9PRM4

ALIGNMENTS

RESULT 1
Q9TRR6 PRELIMINARY: PRT: 19 AA.
AC Q9TRR6: 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CALCYCLIN-ASSOCIATED PROTEIN, CAP50-CA2+/PHOSPHOLIPID-BINDING PROTEIN
DE L-14 FRAGMENT.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP MEDLINE: 92250478.
RX Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;
RA "A calyculin-associated protein is a newly identified member of the
RT Ca2+/phospholipid-binding proteins, annexin family.";
J. Biol. Chem. 267:8919-8924(1992).
SQ SEQUENCE 19 AA: 2018 MW: 9A54062504B8322E CRC64;

Query Match 27.9%; Score 31; DB 6; Length 19;
Best local Similarity 43.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 7 FGPEHLVDFLQSL 22
Db 2 FGDEQALIDLSRS 17
RESULT 2
P70861 PRELIMINARY: PRT: 21 AA.
AC P70861: 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE TMDF (FRAGMENT).
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
RN [1]


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RT Immunodeficiency virus type 1-infected patients."?
RN J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RP [2]
RC SEQUENCE FROM N.A.
RA STRAIN-PATIENT P74;
RX Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U45043; AAB04194.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2219 MW; B36910F4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 MVKFLPPRPOQH 14
DB 2 LLRWGFTTPDKKH 14

RESULT 14
ID 073479 PRELIMINARY; PRT; 18 AA.
AC 073479;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBlrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U45045; AAB04196.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2219 MW; B36910F4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 MVKFLPPRPOQH 14
DB 2 LLRWGFTTPDKKH 14

RESULT 15
ID 073481 PRELIMINARY; PRT; 18 AA.
AC 073481;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBlrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.

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OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE: 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RL "Evolution of zidovudine resistance-associated genotypes in human
RT immunodeficiency virus type 1-infected patients."?
RN J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U45047; AAB04198.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2219 MW; B36910F4583BBFFE CRC64;

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Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 MVKFLPPRPOQH 14
DB 2 LLRWGFTTPDKKH 14

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Search completed: December 21, 2000, 08:35:39
 Job time: 602 sec

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MYKFLPPDOOH 14
DB 2 LIRMGFTTPDKKH 14

RESULT 10

073471 PRELIMINARY; PRT: 18 AA.
AC 073471;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE: 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE: 96242958.
RA Leigh Brown A.J.;
RT Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
RW RNA-directed DNA polymerase.
FT NON_TER 1 18
SQ SEQUENCE 18 AA: 2219 MW: B36138D4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MYKFLPPDOOH 14
DB 2 LIRMGFTTPDKKH 14

RESULT 11

073473 PRELIMINARY; PRT: 18 AA.
AC 073473;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE: 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE: 96242958.
RA Leigh Brown A.J.;
RT Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.

DR EMBL: U45039; AAB04190.1; -
KW RNA-directed DNA polymerase.
FT NON_TER 1 18
SQ SEQUENCE 18 AA: 2219 MW: B36138D4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MYKFLPPDOOH 14
DB 2 LIRMGFTTPDKKH 14

RESULT 12

073475 PRELIMINARY; PRT: 18 AA.
AC 073475;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE: 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE: 96242958.
RA Leigh Brown A.J.;
RT Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
RW RNA-directed DNA polymerase.
FT NON_TER 1 18
SQ SEQUENCE 18 AA: 2219 MW: B36138D4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MYKFLPPDOOH 14
DB 2 LIRMGFTTPDKKH 14

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MYKFLPPDOOH 14
DB 2 LIRMGFTTPDKKH 14

RESULT 13

073477 PRELIMINARY; PRT: 18 AA.
AC 073477;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE: 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human

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DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RL immunodeficiency virus type 1-infected patients.";
RN J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45029; AAB04180.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2219 MW; B36138D4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 MWKFLPPRDOQH 14
Db 2 LLRWGFTTPDKKH 14

RESULT 7
ID 073465 PRELIMINARY; PRT; 18 AA.
AC 073465;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RL immunodeficiency virus type 1-infected patients.";
RN J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45031; AAB04182.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2219 MW; B36138D4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 MWKFLPPRDOQH 14
Db 2 LLRWGFTTPDKKH 14
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RESULT 8
ID 073467 PRELIMINARY; PRT; 18 AA.
AC 073467;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RL immunodeficiency virus type 1-infected patients.";
RN J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45033; AAB04184.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2219 MW; B36138D4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 MWKFLPPRDOQH 14
Db 2 LLRWGFTTPDKKH 14

RESULT 9
ID 073469 PRELIMINARY; PRT; 18 AA.
AC 073469;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RL immunodeficiency virus type 1-infected patients.";
RN J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45035; AAB04186.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2219 MW; B36138D4583BBFFE CRC64;
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GN POL.
OS Human Immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RA MEDLINE: 96242958.
RX Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovir. 12:6-13(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RA Leigh Brown A.J.;
RX Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U5053; AAB04204.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
FT SEQUENCE 18 AA; 2191 MW; B36910F4583BA0C3 CRC64;

Query Match 29.9%; Score 32; DB 12; Length 18;
Best Local Similarity 38.5%; Pred. No. 63;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 MVKFLPPRDOOH 14
DB 2 LKMGFTTPDKH 14

RESULT 3
ID 09W9U1 PRELIMINARY; PRT; 19 AA.
AC 09W9U1;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE GLYCOPROTEIN G (FRAGMENT).
GN USA.
OS Simian herpes B virus (Cercopithecoid herpesvirus 1) (Shbv).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-20620, 9400371, 7709642, 7709609;
RA Eberle R., Smith A., Black D.;
RT "Molecular evidence for distinct genotypes of monkey B virus
(Herpesvirus simiae) which are related to the Macaque host species."
RL J. Virol. 0:0-0(1998).
DR EMBL: AF082804; AAC34447.1; -.
DR EMBL: AF082812; AAC34111.1; -.
DR EMBL: AF082813; AAC34114.1; -.
DR EMBL: AF082814; AAC34117.1; -.
FT NON_TER 1 1
FT SEQUENCE 19 AA; 2220 MW; E585178F064B278B CRC64;

Query Match 28.0%; Score 30; DB 12; Length 19;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 9 RPDQHSVAVT 19
DB 2 LKMGFTTPDKH 12

RESULT 4
ID 09WLD2 PRELIMINARY; PRT; 20 AA.
AC 09WLD2;
DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GLYCOPROTEIN G (FRAGMENT).
GN USA.
OS Simian herpes B virus (Cercopithecoid herpesvirus 1) (Shbv).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-12930;
RA Eberle R., Smith A., Black D.;
RT "Molecular evidence for distinct genotypes of monkey B virus
(Herpesvirus simiae) which are related to the Macaque host species."
RL J. Virol. 0:0-0(1998).
DR EMBL: AF082808; AAC34459.1; -.
FT NON_TER 1 1
FT SEQUENCE 20 AA; 2377 MW; E58517E7DBAB278B CRC64;

Query Match 28.0%; Score 30; DB 12; Length 20;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 9 RPDQHSVAVT 19
DB 3 RSPQSHRVRT 13

RESULT 5
ID 073461 PRELIMINARY; PRT; 18 AA.
AC 073461;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBlrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE: 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovir. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RA Leigh Brown A.J.;
RX Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U5027; AAB04178.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
FT SEQUENCE 18 AA; 2219 MW; B36918D4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MVKFLPPRDOOH 14
DB 2 LKMGFTTPDKH 14

RESULT 6
ID 073463 PRELIMINARY; PRT; 18 AA.
AC 073463;
DT 01-NOV-1996 (TREMBlrel. 01, Created)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:35:38 ; Search time 157.2 Seconds
(without alignments)
11.880 Million cell updates/sec

Title: US-08-934-367-9

Perfect score: 107
Sequence: 1 VMVKLFPPRDQHSVAYTF 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_14:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	31.8	17	3 Q06800	Q06800 saccharomyc
2	32	29.9	18	12 Q73487	Q73487 human immun
3	30	28.0	19	12 Q9W9U1	Q9W9U1 simian hep
4	30	28.0	20	12 Q9WLD2	Q9WLD2 simian hep
5	29	27.1	18	12 Q73461	Q73461 human immun
6	29	27.1	18	12 Q73463	Q73463 human immun
7	29	27.1	18	12 Q73465	Q73465 human immun
8	29	27.1	18	12 Q73467	Q73467 human immun
9	29	27.1	18	12 Q73469	Q73469 human immun
10	29	27.1	18	12 Q73471	Q73471 human immun
11	29	27.1	18	12 Q73473	Q73473 human immun
12	29	27.1	18	12 Q73475	Q73475 human immun
13	29	27.1	18	12 Q73477	Q73477 human immun
14	29	27.1	18	12 Q73479	Q73479 human immun
15	29	27.1	18	12 Q73481	Q73481 human immun
16	29	27.1	18	12 Q73483	Q73483 human immun
17	29	27.1	18	12 Q73485	Q73485 human immun
18	29	27.1	18	12 Q73489	Q73489 human immun
19	29	27.1	18	12 Q73491	Q73491 human immun

20	29	27.1	18	12 Q73493	Q73493 human immun
21	29	27.1	18	12 Q73495	Q73495 human immun
22	29	27.1	18	12 Q73497	Q73497 human immun
23	29	27.1	18	12 Q73499	Q73499 human immun
24	29	27.1	18	12 Q73501	Q73501 human immun
25	29	27.1	18	12 Q73503	Q73503 human immun
26	29	27.1	18	12 Q73505	Q73505 human immun
27	29	27.1	18	12 Q73507	Q73507 human immun
28	29	27.1	18	12 Q73509	Q73509 human immun
29	29	27.1	18	12 Q73511	Q73511 human immun
30	29	27.1	18	12 Q73513	Q73513 human immun
31	29	27.1	18	12 Q73515	Q73515 human immun
32	29	27.1	18	12 Q73519	Q73519 human immun
33	29	27.1	18	12 Q73521	Q73521 human immun
34	29	27.1	18	12 Q73525	Q73525 human immun
35	29	27.1	18	12 Q73527	Q73527 human immun
36	29	27.1	18	12 Q73529	Q73529 human immun
37	29	27.1	18	12 Q73529	Q73529 human immun
38	28	26.2	16	12 Q79458	Q79458 murine mlu
39	28	26.2	19	12 Q90625	Q90625 simian hep
40	27	25.2	17	12 Q73531	Q73531 human immun
41	27	25.2	17	12 Q73533	Q73533 human immun
42	27	25.2	17	12 Q73535	Q73535 human immun
43	27	25.2	17	12 Q73537	Q73537 human immun
44	27	25.2	17	12 Q73539	Q73539 human immun
45	27	25.2	17	12 Q73541	Q73541 human immun

ALIGNMENTS

RESULT	ID	Q06800	PRELIMINARY:	PRT:	17 AA.
AC	Q06800	Q06800	Q06800	Q06800	Q06800
DT	01-NOV-1996	(TREMBlrel. 01, Created)			
DT	01-NOV-1996	(TREMBlrel. 01, Last sequence update)			
DT	01-NOV-1998	(TREMBlrel. 08, Last annotation update)			
DE	N1780.				
GN	N1780.				
OS	Saccharomyces cerevisiae (Baker's yeast).				
OC	Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;				
OC	Saccharomycetales; Saccharomycetes.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 96287653.				
RA	Nast F., Becam A.M., Herbert C.J.:				
RT	"The sequence of 36.8 kb from the left arm of chromosome XIV reveals				
RT	24 complete open reading frames: 18 correspond to new genes, one of				
RT	RT which encodes a protein similar to the human myotonic dystrophy				
RT	kinase."				
RL	Yeast 12:169-175(1996).				
DR	EMBL: X92517; CAA63292.1; -				
SQ	SEQUENCE 17 AA: 2139 MW: BD7E9AFAADF754AF CRC64;				
Query Match 31.8%; Score 34; DB 3; Length 17;					
Best Local Similarity 75.0%; Pred. No. 27;					
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;					
QY	12 Q0HSVAYT 19				
DB	3 Q0HSVCF 10				
RESULT 2					
ID	Q73487	PRELIMINARY:	PRT:	18 AA.	
AC	Q73487	Q73487	Q73487	Q73487	Q73487
DT	01-NOV-1996	(TREMBlrel. 01, Created)			
DT	01-NOV-1996	(TREMBlrel. 01, Last sequence update)			
DT	01-NOV-1998	(TREMBlrel. 08, Last annotation update)			
DE	REVERSE TRANSCRIPTASE (FRAGMENT).				


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CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR PIR; A35704; A35704.
DR INTERPRO; IPR001128; -.
DR PROSITE; PS00086; CYTOCHROME_P450: PARTIAL.
KM Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum; Olfaction.
FT NON_TER 1 1
FT VARIANT 6 6 G -> D.
FT VARIANT 11 11 A -> E.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2058 MW; F80746F76CCD77FF CRC64;

Query Match
Best Local Similarity 66.7%; Score 22; DB 1; Length 18;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 PRPDQ 13
   1 1 1
   5 PGPDQ 10
Db

RESULT 13
UPA3_HUMAN STANDARD; PRT; 9 AA.
ID UPA3_HUMAN
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 11) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE.
RC TISSUE=PLASMA;
RX MEDLINE; 93092937.
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquall C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.6, ITS MW IS: 46 KDA.
DR SWISS-2DPAGE; P30089; HUMAN.
FT NON_TER 1 1
FT NON_TER 9 9
FT SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match
Best Local Similarity 19.6%; Score 21; DB 1; Length 9;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 LFPPD 11
   1 1 1
   3 LFPPXD 8
Db

RESULT 14
TKNA_HORSE STANDARD; PRT; 11 AA.
ID TKNA_HORSE
AC P01290;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
GN TAC1 OR NK1A OR TAC2 OR NKA.
OS Equus caballus (Horse), and Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
RN [1]
RP SEQUENCE.

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RC SPECIES=HORSE;
RA Studer R.O., Trzeciak A., Lergier W.;
RT "Isolation and amino-acid sequence of substance P from horse
RT intestine.";
RL Helv. Chim. Acta 56:860-866(1973).
RN [2]
RP SEQUENCE.
RC SPECIES=C.PORCELLUS;
RX MEDLINE; 90044685.
RA Murphy R.;
RT "Primary amino acid sequence of guinea-pig substance P.";
RL Neuropeptides 14:105-110(1989).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; A01558; SPPO.
DR PIR; A60654; A60654.
DR INTERPRO; IPR002040; -.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11
FT SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C67 CRC64;

Query Match
Best Local Similarity 19.6%; Score 21; DB 1; Length 11;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PRPDQ 12
   1 1 1
   2 PKPDQ 6
Db

RESULT 15
ECDE_LYMDI STANDARD; PRT; 13 AA.
ID ECDE_LYMDI
AC P80941;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE TESTIS ECDYSTOTROPIN PEPTIDE E (TE).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuidae; Lymantriidae; Lymantria.
RN [1]
RP SEQUENCE.
RC TISSUE=BRAIN;
RX MEDLINE; 97387807.
RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
RA Bell R.A.;
RT "Naturally occurring analogs of Lymantria testis ecdystotropin, a
RT gonadotropin isolated from brains of Lymantria dispar pupae.";
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
CC -1- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
CC OF LARVAE AND PUPAE.
SQ SEQUENCE 13 AA; 1357 MW; 1841B4CA3275B764 CRC64;

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Query Match
Best Local Similarity 19.6%; Score 21; DB 1; Length 13;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 PRPDQHS 15
   1 1 1
   5 PNPDPDS 12
Db

```

Search completed: December 21, 2000, 08:32:59
 Job time: 442 sec

RP SEQUENCE.
 RC TISSUE-SKIN;
 RX MEDLINE: 90287814.
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 the Australian frog *Pseudophryne guntheri*."
 RL Peptides 11:299-304(1990).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 MUSCLES.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: B60409; B60409.
 DR INTERPRO: IPR002040; -.
 DR PROSITE: PS00267; TACHYKININ: 1.
 KW Tachykinin: Neuropeptide: Amidation.
 FT MOD.RES 1 11 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD.RES 1 11 AMIDATION.
 SQ SEQUENCE 11 AA: 1269 MW: 30847C37C9CB1AB7 CRC64;

Query Match 20.6%; Score 22; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 4.5e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 PRPDQ 12
 1 11:
 2 PNPDE 6

RESULT 10
 TKN2_PSEGU STANDARD: PRT; 11 AA.
 AC P42987;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE KASSININ-LIKE PEPTIDE K-II (PG-KII).
 OS Pseudophryne guntheri (Frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 CC Pseudophryne.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-SKIN;
 RX MEDLINE: 90287814.
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 the Australian frog *Pseudophryne guntheri*."
 RL Peptides 11:299-304(1990).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 MUSCLES.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: C60409; C60409.
 DR INTERPRO: IPR002040; -.
 DR PROSITE: PS00267; TACHYKININ: 1.
 KW Tachykinin: Neuropeptide: Amidation.
 FT MOD.RES 1 11 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD.RES 1 11 AMIDATION.
 SQ SEQUENCE 11 AA: 1246 MW: 3A247C37C9CB1AB7 CRC64;

Query Match 20.6%; Score 22; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 4.5e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 PRPDQ 12
 1 11:
 2 PNPDE 6

RESULT 11
 TKN4_PSEGU STANDARD: PRT; 11 AA.
 AC P42989;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P-LIKE PEPTIDE I (PG-SP1).
 OS Pseudophryne guntheri (Frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 CC Pseudophryne.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-SKIN;
 RX MEDLINE: 90287814.
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 the Australian frog *Pseudophryne guntheri*."
 RL Peptides 11:299-304(1990).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 MUSCLES.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: E60409; E60409.
 DR INTERPRO: IPR002040; -.
 DR PROSITE: PS00267; TACHYKININ: 1.
 KW Tachykinin: Neuropeptide: Amidation.
 FT MOD.RES 1 11 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD.RES 1 11 AMIDATION.
 SQ SEQUENCE 11 AA: 1294 MW: 3A247C2CC9CB1AB7 CRC64;

Query Match 20.6%; Score 22; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 4.5e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 PRPDQ 12
 1 11:
 2 PNPDE 6

RESULT 12
 CPAX_BOVIN STANDARD: PRT; 18 AA.
 AC P22779;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CYTOCHROME P450 2A (OLF2) (OLFACTIVE) (P52) (EC 1.14.14.1) (FRAGMENT).
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 91027757.
 RA Lazar D., Tal N., Rubinstein M., Khen M., Lancet D., Zupko K.;
 RT "Identification and biochemical analysis of novel olfactory-specific
 cytochrome P-4501A and UDP-glucuronosyl transferase."
 RL Biochemistry 29:7433-7440(1990).
 CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
 MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
 NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
 OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
 ACIDS, AND XENOBIOTICS.
 CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) -> ROH +
 OXIDIZED FLAVOPROTEIN + H(2)O.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.

Best Local Similarity 57.1%; Pred. No. 3.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 12 QOHSVAY 18
:||||:
Db 3 RRHSVAV 9

RESULT 6
HELT_HELHO STANDARD; PRT; 20 AA.
ID HELT_HELHO
AC P46693;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE HELOTHERMINE (FRAGMENT).
OS Heloderma horridum horridum (Mexican beaded lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Scleroglossa; Anguilliformes; Helodermatidae;
OC Heloderma.
CC [1]
RN SEQUENCE.
RP TISSUE=VENOM.
RC MEDLINE: 90260878.
RX Mochica-Morales J., Martin B.M., Possani L.D.;
RT "Isolation and characterization of heloethermine, a novel toxin from
RT Heloderma horridum horridum (Mexican beaded lizard) venom."
RT Toxicon 28:299-309(1990).
CC -1- FUNCTION: TOXIC TO MICE; INDUCES LETHARGY, PARTIAL PARALYSIS OF
CC REAR LIMBS AND LOWERING OF BODY TEMPERATURE, SUGGESTING THAT IT
CC MIGHT BE A HYPOTHERMIC TOXIN
CC -1- MISCELLANEOUS: THE COMPLETE PROTEIN HAS AN APPARENT MW OF 25 KDA
CC AND A PI OF 6.8.
CC DR PIR: A34859; A34859.
KM Toxin.
FT NON_TER 20 20
SQ SEQUENCE 20 AA: 2156 MW: 91D62B36F7B4F940 CRC64;

Query Match 22.4%; Score 24; DB 1; Length 20;
Best Local Similarity 57.1%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PDQHSV 16
:||||:
Db 14 PDQTEI 20

RESULT 7
TKNA_ONCMY STANDARD; PRT; 11 AA.
ID TKNA_ONCMY
AC P28499;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
RN [1]
RP TISSUE=BRAIN.
RC MEDLINE: 92298992.
RX Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
RT of the cod and trout."
RT Eur. J. Biochem. 206:659-664(1992).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR PIR: S23307; S23307.
DR PIR: S23308; S23308.
DR INTERPRO: IPR002040; -.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11
SQ SEQUENCE 11 AA: 1358 MW: 214860DEC9D6D1F7 CRC64;

Query Match 21.5%; Score 23; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PRPDQ 12
:||||:
Db 2 PRPDQ 6

RESULT 8
TKNA_SCYCA STANDARD; PRT; 11 AA.
ID TKNA_SCYCA
AC P41333;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeidae; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE=BRAIN.
RX MEDLINE: 93292508.
RA Maugh D., Wang Y., Hazon N., Baiment R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
RT peptides from the brain of the dogfish, Scyliorhinus canicula."
RT Eur. J. Biochem. 214:469-474(1993).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC CC PIR: S33300; S33300.
DR INTERPRO: IPR002040; -.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11
SQ SEQUENCE 11 AA: 1278 MW: 214860DEC9D6D867 CRC64;

Query Match 21.5%; Score 23; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PRPDQ 12
:||||:
Db 2 PRPDQ 6

RESULT 9
TKN1_PSEGU STANDARD; PRT; 11 AA.
ID TKN1_PSEGU
AC P42986;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE KASSTININ-LIKE PEPTIDE K-1 (PG-KI).
OS pseudophryne guentheri (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Pseudophryninae.
RN [1]

RT "Purification and partial amino acid sequences of two distinct
 RT albumins from turtle plasma."
 RL Comp. Biochem. Physiol. 118B:367-374(1997).
 CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
 CC BINDING CAPACITY FOR WATER, CA⁺⁺, NA⁺, K⁺, FATTY ACIDS, HORMONES,
 CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
 CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- MISCELLANEOUS: IN THE RED-EARED SLIDER TURTLE, THERE ARE TWO FORMS
 CC OF ALBUMIN, ALB-1 AND ALB-2.
 CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/YDB FAMILY.
 DR INTERPRO: IPR000264; -
 DR PROSITE: PS00212; ALBUMIN: PARTIAL.
 KW Plasma: Metal-binding; Lipid-binding; Albumin.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA: 1733 MW: 4B7422B89FE73223 CRC64;

Query Match 23.4%; Score 24; DB 1; Length 15;
 Best Local Similarity 30.0%; Pred. No. 1.9e+02;
 Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 11 DQHSVAYTF 20
 I: : : : :
 DB 3 DETHLGHXF 12

RESULT 3
 TKNA_CHICK STANDARD; PRT; 11 AA.
 AC P19850;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=INTESTINE;
 RX MEDLINE: 88204263.
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
 RT "[Arg3]substance P and neurokinin A from chicken small intestine."
 RL Regul. Pept. 20:171-180(1988).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR INTERPRO: IPR002040; -
 DR PROSITE: PS00267; TACHYKININ: 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11
 SQ SEQUENCE 11 AA: 1377 MW: 21487FE3C9DC6C7 CRC64;

Query Match 22.4%; Score 24; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 PRPDQ 12
 I: I: I: I:
 DB 2 PRPDQ 6

RESULT 4
 TKNA_GADMO STANDARD; PRT; 11 AA.
 ID TKNA_GADMO
 AC P28498;

DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 OS GADUS MORHUA (Atlantic cod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidae; Gadidae;
 OC Gadus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=BRAIN;
 RX MEDLINE: 92298992.
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout."
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR INTERPRO: IPR002040; -
 DR PROSITE: PS00267; TACHYKININ: 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11
 SQ SEQUENCE 11 AA: 1315 MW: 214860D759DC6C7 CRC64;

Query Match 22.4%; Score 24; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 PRPDQ 12
 I: I: I: I:
 DB 2 PRPDQ 6

RESULT 5
 GALS_SALTY STANDARD; PRT; 18 AA.
 ID GALS_SALTY
 AC P41030;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE MGL REPRESSOR AND GALACTOSE ULTRAINDUCTION FACTOR (FRAGMENT).
 GN GALS.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RX MEDLINE: 89112167.
 RA Benner-Luger D., Boos W.;
 RT "The mglB sequence of Salmonella typhimurium LT2: promoter analysis
 RT by gene fusions and evidence for a divergently oriented gene coding
 RT for the mgl repressor."
 RL Mol. Gen. Genet. 214:579-587(1988).
 CC -1- FUNCTION: REPRESSOR OF THE MGL OPERON. BINDS GALACTOSE AND
 CC D-FUCULOSE AS INDUCERS. GALS BINDS TO AN OPERATOR DNA SEQUENCE
 CC WITHIN ITS OWN CODING SEQUENCE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE LACI FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR STYGENE: SG10521; GALS.
 DR INTERPRO: IPR000843; -
 DR PROSITE: PS00356; HTL_LACI_FAMILY: PARTIAL.
 KW Transcription regulation; DNA-binding; Repressor.
 FT NON_TER 1 1
 SQ SEQUENCE 18 AA: 2133 MW: 74A77150FA9FB8B CRC64;

Query Match 22.4%; Score 24; DB 1; Length 18;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:32:58 : Search time 62.7 Seconds
(without alignments)
10.191 Million cell updates/sec

Title: us-08-934-367-9

Perfect score: 107
Sequence: 1 VMVKFLFRRPDQHSVATNF 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25.2	12	1	TKN1_KASMA	P08613 kassina mac
2	25.2	15	1	ALB2_TRASC	P81189 tirachemys s
3	23.4	11	1	TKNA_CHICK	P19850 gallus gall
4	22.4	11	1	TKNA_GADMO	P28498 gadus morhu
5	22.4	18	1	GALS_SALTY	P41030 salmoneilla
6	22.4	20	1	HELT_HELHO	P46693 heloderma h
7	21.5	11	1	TKNA_ONCMY	P28499 oncorhynch
8	21.5	11	1	TKNA_SCYCA	P41333 scyllorhinu
9	20.6	11	1	TKNA_PSEGU	P42986 pseudophryn
10	20.6	11	1	TKNA_PSEGU	P42987 pseudophryn
11	20.6	11	1	TKNA_PSEGU	P42989 pseudophryn
12	20.6	18	1	CPAX_BOVIN	P22779 bos tauris
13	19.6	9	1	UPA3_HUMAN	P30089 homo sapien
14	19.6	11	1	TKNA_HORSE	P01290 equus caball
15	19.6	13	1	ECDE_LYMDI	P80941 lymantria d
16	19.6	15	1	MK2A_PALPR	P80409 palomena pr
17	19.6	16	1	MK3_PALPR	P80411 palomena pr
18	19.6	17	1	PSBL_SYNVU	P12241 synchococc
19	18.7	9	1	FAR9_ASCSU	P43172 ascaris suu
20	18.7	10	1	BPP2_BOVJA	P01022 bothrops ja
21	18.7	11	1	TKNA_RANCA	P22688 rana catesb
22	18.7	13	1	BPP1_BOVJA	P01020 bothrops ja
23	18.7	13	1	GER1_HORVU	P28525 hordeum vul
24	18.7	17	1	SRY_URSAR	P81383 ursus arcto
25	18.7	19	1	OXLA_OPHHA	P80227 bos taurus
26	18.7	20	1	ACPH_BOVIN	P18673 artocarpus
27	18.7	20	1	LEC3_ARTIN	P81864 pardachirus
28	17.8	5	1	PAP2_PARMA	P38553 locusta mig
29	17.8	10	1	FARP_LOCOMI	P30423 bothrops in
30	17.8	11	1	BPP3_BOVIN	P30424 bothrops in
31	17.8	11	1	BPP4_BOVIN	P01021 agkistrodon
32	17.8	11	1	BPPB_AKSHA	P08614 kassina mac
33	17.8	12	1	TKN2_KASMA	

34	19	17.8	12	1	TKN_KASSE	P08611 kassina sen
35	19	17.8	13	1	GER2_HORVU	P28526 hordeum vul
36	19	17.8	13	1	YCTA_SALTY	P25944 salmoneilla
37	19	17.8	15	1	MK1_PALPR	P80408 palomena pr
38	19	17.8	16	1	MK2B_PALPR	P80410 palomena pr
39	19	17.8	17	1	APID_BOMPA	P81454 bombus pasc
40	19	17.8	17	1	VALA_TRYBB	P17961 trypanosoma
41	19	17.8	20	1	ALAT_PIG	P13191 sus scrofa
42	19	17.8	20	1	PIRR_PIRAP	P37362 pyrrhocoris
43	18.5	17.3	18	1	HEMH_THETS	P80155 thermozon
44	18	16.8	10	1	UPA2_HUMAN	P30088 homo sapien
45	18	16.8	13	1	CRBL_ICASP	P17237 icaria sp.

ALIGNMENTS

RESULT 1
TKN1_KASMA STANDARD: PRT: 12 AA.
ID TKN1_KASMA
AC P08613;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HYLAMBATES KASSININ (Glu(2)-Pro(5) KASSININ).
OS KASSINA MACULATA (African rhacophorid frog) (Hylambates maculatus).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Hyperoliidae;
OC KASSINA.
RN [1]
RA YASUHARA T., NAKAJIMA T., ERSPAMER G.F., ERSPAMER V.;
RT "New tachykinnins, Glu2, Pro5-kassinin (hylambates-kassinin) and
RT hylambatin, in the skin of the African rhacophorid frog Hylambates
RT maculatus.";
RL Biomed. Res. 2:613-617(1981).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC PIR: S10059, S10059.
DR INTERPRO: IPR002040;
DR PROSITE: PS00267; TACHYKININ: 1.
KW Tachykinnin; Neuropeptide; Amidation; Amphibian skin.
FT MOD_RES 12
FT SEQUENCE 12 AA: 1376 MW: 3E756D279DD6DAB7 CRC64;

Query Match 25.2%; Score 27; DB 1; Length 12;
Best local similarity 80.0%; Pred. No. 69;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PRPDQ 12
Db 3 PKPDQ 7
RESULT 2
ALB2_TRASC STANDARD: PRT: 15 AA.
ID ALB2_TRASC
AC P81189;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 68 KDA SERUM ALBUMIN (ALB-2) (FRAGMENT).
OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidae; Emydidae; Trachemys.
RN [1]
RP SEQUENCE: 98103404.
RX MEDLINE: 98103404.
RA Brown M.A., Chambers G.K., Licht P.;

Query Match 22.4%; Score 24; DB 2; Length 19;
 Best Local Similarity 71.4%; Pred. No. 7.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 QOHSAVY 18
 11 1:11
 DB 12 QOWSMAY 18

RESULT 14

S69166
 ferredoxin b - Japanese radish (fragments)
 C:Species: Kaiware daikon (Japanese radish)
 C:Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
 C:Accession: S69166
 R:Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
 Arch. Biochem. Biophys. 316, 797-802, 1995
 A:Title: Four ferredoxins from Japanese radish leaves.
 A:Reference number: S69164; MUID:95168867
 A:Accession: S69166
 A:Molecule type: protein
 A:Residues: 1-19 <OBA>
 C:Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match 22.4%; Score 24; DB 2; Length 19;
 Best Local Similarity 28.6%; Pred. No. 7.6e+02;
 Matches 4; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 3 VKFLFPPRPOQHSV 16
 111:1 : : :
 DB 5 VKFTPTPTTKREDM 18

RESULT 15

JP0055
 ribosomal protein L30 - Bacillus polymyxa (fragment)
 C:Species: Bacillus polymyxa
 C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
 C:Accession: JP0055
 R:Oehl, K.
 submitted to JPIB, February 1994
 A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pr
 A:Reference number: JP0042
 A:Accession: JP0055
 A:Molecule type: protein
 A:Residues: 1-20 <OCII>
 C:Keywords: protein biosynthesis; ribosome

Query Match 22.4%; Score 24; DB 2; Length 20;
 Best Local Similarity 35.7%; Pred. No. 8.1e+02;
 Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 2 WVKFLFPPRPOQHS 15
 : : 1 1 1 : :
 DB 7 LVRSILGRPGTQRT 20

Search completed: December 21, 2000, 08:30:06
 Job time: 270 sec

A:Residues: 1-11 <JEN>
 A:Experimental source: brain
 C:Function:
 A:Description: may play a physiological role in the regulation of cardiovascular and gas
 A:Note: Substance P is derived by post-translational processing of preprotachykinin A
 C:Keywords: neuropeptide; amidated carboxyl end; tachykinin
 F:11/Modified site: amidated carboxyl end (met) #status predicted

Query Match 22.4%; Score 24; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 PRPDQ 12
 |||
 Db 2 PRPDQ 6

RESULT 9
 S47395
 T-cell antigen receptor VJ junction beta chain - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S47395
 R:Lehner, P.J.
 Submitted to the EMBL Data Library, August 1994
 A:Description: Human HLA-A0201 restricted recognition of Influenza A is dominated by T
 A:Reference number: S47355
 A:Accession: S47395
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-12 <LEH>
 A:Cross-references: EMBL:Z35715; NID:9527525; PIDN:CA04784.1; PID:9527526
 C:Keywords: T-cell receptor

Query Match 22.4%; Score 24; DB 2; Length 12;
 Best Local Similarity 62.5%; Pred. No. 4.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 13 QHSVAYTF 20
 |||
 Db 5 QGSYGYTF 12

RESULT 10
 S29207
 avenin gamma-4 - oat (fragment)
 N:Alternate names: CIP-1; coeliac immunoreactive protein 1
 C:Species: Avena sativa (oat)
 C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
 C:Accession: S29207
 R:Hoehner, A.; Collilla, F.; Ortiz, M.L.; Mendez, E.
 FEBS Lett. 310, 37-40, 1992
 A:Title: Identification of the three major coeliac immunoreactive proteins and one alpha
 A:Reference number: S29207; MUID:92405739

A:Accession: S29207
 A:Molecule type: protein
 A:Residues: 1-15 <ROC>
 A:Experimental source: endosperm
 C:Superfamily: gliadin
 C:Keywords: prolamin; seed

Query Match 22.4%; Score 24; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 5.9e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 PRPDQ 13
 |||
 Db 7 PRPDQ 12

RESULT 11

A28965
 ribulose-bisphosphate carboxylase (PC 4.1.1.39) large chain - spinach (fragments)
 C:Species: Spinacia oleracea (spinach)
 C:Date: 22-Dec-1988 #sequence_revision 22-Dec-1988 #text_change 23-Feb-1997
 C:Accession: A28965
 R:Milligan, R.M.; Houtz, R.L.; Tolbert, N.E.
 Proc. Natl. Acad. Sci. U.S.A. 85, 1513-1517, 1988
 A:Title: Reaction-intermediate analogue binding by ribulose biphosphate carboxylase/
 acetylated protein.
 A:Reference number: A28965; MUID:88144466
 A:Accession: A28965
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <MUL>
 C:Keywords: carbon-carbon lyase; carboxy-lyase; chloroplast

Query Match 22.4%; Score 24; DB 2; Length 15;
 Best Local Similarity 62.5%; Pred. No. 5.9e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 KELEPRPD 11
 |||
 Db 6 KELEPRPD 13

RESULT 12
 B25348
 UDPglucose--glycogen glucosyltransferase (EC 2.4.1.11) P-2 peptide - rabbit (fragment)
 N:Alternate names: UDPglucose-glycogen glucosyltransferase
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 06-Dec-1996
 C:Accession: B25348
 R:Wang, Y.; Bell, A.W.; Hermodson, M.A.; Roach, P.J.
 J. Biol. Chem. 261, 16909-16915, 1986
 A:Title: Liver isozyme of rabbit glycogen synthase. Amino acid sequences surrounding
 A:Reference number: A92570; MUID:87057401
 A:Accession: B25348
 A:Molecule type: protein
 A:Residues: 1-17 <WAN>
 C:Function:
 A:Description: catalyzes the alpha-1,4-glucosylation of glycogen by UDPglucose produc
 C:Keywords: glycogen/starch biosynthesis; glucosyltransferase; hexosyltransferase

Query Match 22.4%; Score 24; DB 2; Length 17;
 Best Local Similarity 60.0%; Pred. No. 6.7e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 LEPRP 10
 ::|||
 Db 1 MYPRP 5

RESULT 13
 S19613
 globin - polychaete (Eudistylia vancouveri) (fragment)
 C:Species: Eudistylia vancouveri
 C:Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998
 C:Accession: S19613
 R:Qabar, A.N.; Stern, M.S.; Walt, D.A.; Chiu, J.T.; Tinkovitch, R.; Wall, J.S.; Kapp,
 J. Mol. Biol. 222, 1109-1129, 1991
 A:Title: Hierarchy of globin complexes. The quaternary structure of the extracellular
 A:Reference number: S19532; MUID:92106333
 A:Accession: S19613
 A:Molecule type: protein
 A:Residues: 1-19 <QAB>
 A:Experimental source: plume
 C:Complex: dodecamers, each consisting of a trimer of tetramers of globin chains; dode
 C:Keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier

RESULT 3

A:Accession: A54083
p190/210, fatty acid synthase, p140ex02 strand exchange protein activator - fission yeast
C:Species: Schizosaccharomyces pombe
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
C:Accession: A54083
R:Kaslian, E.; Heyer, W.D.
J. Biol. Chem. 269, 14103-14110, 1994
A:Title: Schizosaccharomyces pombe fatty acid synthase mediates DNA strand exchange in vivo
A:Reference number: A54083; MUID:94245730
A:Accession: A54083
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <KAS>
A:Note: sequence extracted from NCBI backbone (NCBIP:148744)
C:Superfamily: yeast fatty-acid synthase

Query Match 24.3%; Score 26; DB 2; Length 20;
Best Local Similarity 36.4%; Pred. No. 3.7e+02;

Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 9 RPDOHSAVAT 19
||:|:|:|
DB 2 RPEVEBELAHT 12

RESULT 4

A:Accession: A60770
cell surface allantoigen gp60 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-Feb-1997
C:Accession: A60770
R:Schadenkopf, D.; Yamaguchi, H.; Old, L.J.; Srivastava, P.K.
J. Immunol. 142, 1621-1625, 1989
A:Title: A novel heteromorph human cell surface allantoigen, gp60, defined by a human
A:Reference number: A60770; MUID:89140552
A:Accession: A60770
A:Molecule type: protein
A:Residues: 1-14 <SCH>
C:Comment: This protein is an allantoigen in human populations but is not found on cells
C:Comment: This protein exists in both membrane bound and cytosolic forms.
C:Keywords: glycoprotein; polymorphism; surface antigen

Query Match 23.4%; Score 25; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 14 HSAVAT 19
|||:|:|
DB 3 HSAVAT 8

RESULT 5

A:Accession: PS0221
gastrin-releasing peptide - laughing frog (fragment)
C:Species: Rana ridibunda (laughing frog)
C>Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 03-Mar-1995
C:Accession: PS0221
R:Conlon, J.M.; O'Harte, F.; Vaudry, H.
Biochem. Biophys. Res. Commun. 178, 526-530, 1991
A:Title: Primary structures of the bombesin-like neuropeptides in frog brain show that
A:Reference number: P00177; MUID:91315477
A:Accession: PS0221
A:Molecule type: protein
A:Residues: 1-15 <CON>
A:Experimental source: brain
C:Keywords: neuropeptide

Query Match 23.4%; Score 25; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 PDQOH 14
|||:|:|
DB 2 PSQOH 6

RESULT 6

A:Accession: A41436
alpha-macroglobulin - green sea turtle (fragment)
C:Species: Chelonia mydas (green sea turtle)
C>Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 18-Jun-1993
C:Accession: A41436
R:Osada, T.; Sasaki, T.; Ikal, A.
J. Biochem. 103, 212-217, 1988
A:Title: Purification and characterization of alpha-macroglobulin and ovomacroglobulin
A:Reference number: A41436; MUID:88227890
A:Accession: A41436
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <OSA>

Query Match 23.4%; Score 25; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VMVKPLF 7
||:|:|:|
DB 8 VLVKPLF 14

RESULT 7

A:Accession: JN0023
substance P - chicken
C:Species: Gallus gallus (chicken)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997
C:Accession: JN0023
R:Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A:Title: [Arg3]substance P and neurokinin A from chicken small intestine.
A:Reference number: JN0023; MUID:88204263
A:Accession: JN0023
A:Molecule type: protein
A:Residues: 1-11 <CON>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; tachykinin
F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 22.4%; Score 24; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 PRPDQ 12
|||:|:|
DB 2 PRPDQ 6

RESULT 8

A:Accession: S23306
substance P - Atlantic cod
C:Species: Gadus morhua (Atlantic cod)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Feb-1999
C:Accession: S23306
R:Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A:Title: Substance-P-related and neurokinin-A-related peptides from the brain of the
A:Reference number: S23186; MUID:92289892
A:Accession: S23306
A:Molecule type: protein

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:30:06 ; Search time 112.59 Seconds
(without alignments)
11.273 Million cell updates/sec

Title: US-08-934-367-9
Perfect score: 107
Sequence: 1 VMWKLFPDPDOHSHVAYNF 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues
Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	27	25.2	12	2	SI0059
2	27	25.2	20	2	JP0053
3	26	24.3	20	2	A54083
4	25	23.4	14	2	A60770
5	25	23.4	15	2	PS0221
6	25	23.4	15	2	A41436
7	24	22.4	11	2	JN0023
8	24	22.4	11	2	S23306
9	24	22.4	12	2	S47395
10	24	22.4	15	2	S29207
11	24	22.4	15	2	A28965
12	24	22.4	17	2	B25348
13	24	22.4	19	2	S19613
14	24	22.4	19	2	S69166
15	24	22.4	20	2	JP0055
16	24	22.4	20	2	A34859
17	23	21.5	9	2	A60108
18	23	21.5	10	2	S19296
19	23	21.5	11	2	S78026
20	23	21.5	11	2	S33300
21	23	21.5	11	2	S23308
22	23	21.5	16	2	A60551
23	23	21.5	20	2	A47105
24	22	20.6	7	4	I56695
25	22	20.6	11	2	B60409
26	22	20.6	11	2	C60409
27	22	20.6	11	2	E60409
28	22	20.6	14	2	S60353
29	22	20.6	18	2	A35704

ALIGNMENTS

30	22	20.6	18	2	A42016	mammary-derived gr
31	22	20.6	19	2	JP0054	ribosomal protein
32	21	19.6	9	4	S15594	orf 1 rara 5'-regi
33	21	19.6	11	1	SPHO	substance P - hors
34	21	19.6	11	1	A60654	substance P - guin
35	21	19.6	12	2	S47391	T-cell antigen rec
36	21	19.6	15	2	S26515	T-cell receptor al
37	21	19.6	16	2	S57517	DNA-directed RNA p
38	21	19.6	17	2	JH0785	photosystem II pro
39	21	19.6	17	2	S05033	protein I - Legion
40	21	19.6	18	2	S55002	hypothetical prote
41	21	19.6	20	2	S18582	urinary tract ston
42	21	19.6	20	2	A56046	cardioacceleratory
43	20	18.7	8	2	S66646	angiotensin-conver
44	20	18.7	10	1	XAV16B	hementin (EC 3.4.-
45	20	18.7	10	2	A61007	

RESULT 1
SI0059
tachykinin - African tree frog (kassina maculata)
N:Alternate names: hylambates-kassinin
C:Species: Kassina maculata
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999
C:Accession: SI0059
R:Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.
Biomed. Res. 2, 613-617, 1981
A:Title: New tachykinins, Glu2, pro5-kassinin (hylambates-kassinin) and hylambatin, 1
A:Reference number: S07436
A:Accession: SI0059
A:Molecule type: protein
A:Residues: 1-12 <YAS>
A:Experimental source: skn
A>Note: The source is designated as Hylambates maculatus
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:1/2/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 25.2% Score 27; DB 2; Length 12;
Best Local Similarity 80.0% Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PRPDQ 12
1:111
DB 3 PKPDQ 7

RESULT 2
JP0053
ribosomal protein L30 - Bacillus macerans (fragment)
C:Species: Bacillus macerans
C>Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
C:Accession: JP0053
R:Ochi, K.
submitted to JPID, February 1994
A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal
A:Reference number: JP0042
A:Accession: JP0053
A:Molecule type: protein
A:Residues: 1-20 <OCH>
C:Keywords: protein biosynthesis; ribosome

Query Match 25.2% Score 27; DB 2; Length 20;
Best Local Similarity 35.7% Pred. No. 2.5e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 VMWKLFPDPDOHS 15
1:1111:
DB 7 LVRSLSIGRPEXQRT 20

TELEFAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-432-871C-73

Query Match 25.2%; Score 27; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

QY 5 FLFPRPDQHSVAY 18
1 1 1 1 1 1
Db 1 FTFDR---HPIAY 10

RESULT 15
US-07-678-974D-8
Sequence 8, Application US/07678974D
Patent No. 5629146
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN PAPILLOMAVIRUS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERMAN & AISENBERG
STREET: 1730 RHODE ISLAND AVENUE, N.W.,
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-3186
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/678,974D
FILING DATE: 25-JUN-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AISENBERG, Irwin M.
REGISTRATION NUMBER: 19,007
REFERENCE/DOCKET NUMBER: SG19171
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-293-1404
TELEFAX: 202-872-0493
TELEX: 440 069 AIS UI
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-07-678-974D-8

Query Match 24.8%; Score 26.5; DB 1; Length 20;
Best Local Similarity 44.4%; Pred. No. 1.8e+02;
Matches 8; Conservative 0; Mismatches 5; Indels 5; Gaps 1;

QY 4 KFLFP-----RPDQHSV 16
1 1 1 1 1 1
Db 2 KFGPPTSTFYNPDTQRLV 19

Search completed: December 21, 2000, 08:31:49
Job time: 372 sec

RESULT 12
US-08-221-580-7
; Sequence 7, Application US/08221580
; Patent No. 5519000
; GENERAL INFORMATION:
; APPLICANT: Heavenr, George A.
; APPLICANT: Kruszyński, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5519000FIS
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: United States of America
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,580
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; US-08-221-580-7

Query Match 25.2%; Score 27; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 12 OQHSVAYTF 20
DB 5 QSHSWPFTF 13

RESULT 13
PCT-US95-04018-69
; Sequence 69, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavenr, George A.
; APPLICANT: Kruszyński, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSER: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: peptide
PCT-US95-04018-69

Query Match 25.2%; Score 27; DB 4; Length 13;
Best Local Similarity 55.6%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 12 OQHSVAYTF 20
DB 5 QSHSWPFTF 13

RESULT 14
US-08-432-871C-73
; Sequence 73, Application US/08432871C
; Patent No. 5877010
; GENERAL INFORMATION:
; APPLICANT: Loeb, Lawrence A.
; APPLICANT: Black, Margaret E.
; TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,871C
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMASTERS, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 240052.409C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-11

Query Match 27.1%; Score 29; DB 3; Length 14;
Best Local Similarity 45.5%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 8 PRPDQHSVAY 18
| | | | |
Db 3 PYPGNHAY 13

RESULT 10
US-08-974-775-39
Sequence 39, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Walsh, F. Gary
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-974-775-39

Query Match 26.2%; Score 28; DB 3; Length 14;
Best Local Similarity 36.4%; Pred. No. 66;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 8 PRPDQHSVAY 18
| | | | |
Db 3 PYPGNHAY 13

RESULT 11
US-08-159-339A-558
Sequence 558, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esben
TITLE OF INVENTION: HLA Binding peptides and Their
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TEXT:
INFORMATION FOR SEQ ID NO: 558:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-558

Query Match 25.2%; Score 27; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 67;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 FPRPDQH 14
| | | | |
Db 1 FTTPDKH 8

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,639A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A-63005/PJS STAN-187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FMT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-606-639A-5

Query Match 28.0%; Score 30; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 9 RPDOOHSHVAY 18
| | | | |
DB 5 RPSORHGSKY 14

RESULT 7
US-08-297-395-14
Sequence 14, Application US/08297395A
Patent No. 6039947
GENERAL INFORMATION:
APPLICANT: Howard L. Weiner
TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
TITLE OF INVENTION: EPITOPES OF MYELIN BASIC PROTEIN
FILE REFERENCE: 1010/05723US3
CURRENT APPLICATION NUMBER: US/08/297,395A
CURRENT FILING DATE: 1994-08-11
EARLIER APPLICATION NUMBER: 08/059,189
EARLIER FILING DATE: 1993-05-06
EARLIER APPLICATION NUMBER: 07/502,559
EARLIER FILING DATE: 1990-03-30
EARLIER APPLICATION NUMBER: PC7/US88/02139
EARLIER FILING DATE: 1988-06-24
EARLIER APPLICATION NUMBER: 07/065,734
EARLIER FILING DATE: 1987-06-24
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Fastseq for Windows Version 3.0
SEQ ID NO 14
LENGTH: 20
TYPE: PPT
ORGANISM: Homo sapiens
US-08-297-395-14

Query Match 28.0%; Score 30; DB 3; Length 20;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 9 RPDOOHSHVAY 18
| | | | |
DB 5 RPSORHGSKY 14

RESULT 8
US-08-974-775-12
Sequence 12, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Clyffront
STREET: Plaza Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-12

Query Match 27.1%; Score 29; DB 3; Length 13;
Best Local Similarity 45.5%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 8 RPDOOHSHVAY 18
| | | | |
DB 3 PYPOGHEAVY 13

RESULT 9
US-08-974-775-11
Sequence 11, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Clyffront
STREET: Plaza Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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? COUNTRY: USA
? ZIP: 94105-1492
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/483,021
? FILING DATE: 07-JUN-1995
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/210,594
? FILING DATE: 23-JUN-1988
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/367,751
? FILING DATE: 21-JUN-1989
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/635,840
? FILING DATE: 12-DEC-1990
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/690,840
? FILING DATE: 23-APR-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/793,938
? FILING DATE: 19-NOV-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/978,946
? FILING DATE: 18-NOV-1992
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? APPLICATION NUMBER: US 08/208,072
? FILING DATE: 03-MAR-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/397,533
? FILING DATE: 02-MAR-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: Bastian, Kevin L.
? REGISTRATION NUMBER: 34,774
? REFERENCE/DOCKET INFORMATION:
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 543-9600
? TELEFAX: (415) 543-5043
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 14 amino acids
? TYPE: amino acid
? STRANDEDNESS:
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 1
? OTHER INFORMATION: /product= "Xaa = N-acetyl alanine"
? FEATURE:
? NAME/KEY: Peptide
? LOCATION: 1..14
? OTHER INFORMATION: /note= "rat myelin basic protein
? OTHER INFORMATION: peptide analog of MBP(1-14)4-A"
? US-08-483-021-3

Query Match 28.0%; Score 30; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 RPDQOHVAV 18
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   5 RPSQRHGSKY 14

RESULT 5
US-08-468-540B-1
; Sequence 1, Application US/08468540B
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; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafner, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H 32,140
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO. 5858980e
; US-08-468-540B-1

Query Match 28.0%; Score 30; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 RPDQOHVAV 18
   |||:|
   5 RPSQRHGSKY 14

RESULT 6
US-08-606-639A-5
; Sequence 5, Application US/08606639A
; Patent No. 5939400
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Weisman, Ari
; TITLE OF INVENTION: DNA VACCINATION FOR INDUCTION OF
; TITLE OF INVENTION: SUPPRESSIVE T CELL RESPONSE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
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Query Match 31.8%; Score 34; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 4;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 9 RPDQHSVAV 18
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DB 1 QPDQYDVAV 10

RESULT 2

US-08-440-861-11
; Sequence 11, Application US/08440861
; Patent No. 5710126
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.
; APPLICANT: Kuo, Mei-Chang
; APPLICANT: Lugman, Mohammad
; TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
; TITLE OF INVENTION: ALLERGEN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,861
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,016
; FILING DATE: 31-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-075 (IMI-040cp)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
US-08-440-861-11

Query Match 29.0%; Score 31; DB 1; Length 20;
Best Local Similarity 46.2%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 6 LPPRPDQHSVAV 18
:1111:111
DB 3 LIPKLDYAVAV 15

RESULT 3

US-08-159-339A-1076
; Sequence 1076, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.

APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 1076:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-1076

Query Match 28.0%; Score 30; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 RPDQHSVAV 18
:1111:111
DB 1 RPSQRHGSKY 10

RESULT 4

US-08-483-021-3
; Sequence 3, Application US/08483021
; Patent No. 5734023
; GENERAL INFORMATION:
; APPLICANT: Nag, Bishwajit
; APPLICANT: Clark, Brian R.
; APPLICANT: Sharma, Somesh
; APPLICANT: McConnell, Harden
; TITLE OF INVENTION: MHC Subunit Conjugates Useful in
; NUMBER OF SEQUENCES: 5
; TITLE OF INVENTION: Ameliorating Deleterious Immune Responses
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:31:48 ; Search time 99.91 Seconds
(without alignments)
3.355 Million cell updates/sec

Title: US-08-934-367-9
Perfect score: 107
Sequence: 1 VMVKFLPPRPOQHSVAYTF 20

Scoring table: BLOSUM62
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Searched: 164575 seqs, 1676186 residues

Total number of hits satisfying chosen parameters: 87906

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/plodata/2/1aa/PCITS_COMB.pep:*
5: /cgn2_6/plodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	31	29.0	20	1	US-08-440-861-11
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4	30	28.0	14	1	US-08-483-021-3
5	30	28.0	20	2	US-08-468-5408-1
6	30	28.0	20	2	US-08-606-639A-5
7	30	28.0	20	3	US-08-297-395-14
8	29	27.1	13	3	US-08-974-775-12
9	29	27.1	14	3	US-08-974-775-11
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11	27	25.2	10	3	US-08-159-339A-558
12	27	25.2	13	4	US-08-221-580-7
13	27	25.2	13	4	PCT-US95-04018-69
14	27	25.2	15	2	US-08-432-871C-73
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16	26.5	24.8	20	2	US-08-945-168-13
17	26	24.3	8	3	US-08-159-339A-1049
18	26	24.3	8	3	US-08-925-002-49
19	26	24.3	11	2	US-08-540-388-1
20	26	24.3	12	1	US-07-778-233B-23
21	26	24.3	12	1	US-07-963-321-23
22	26	24.3	12	1	US-08-290-641-23
23	26	24.3	12	1	US-08-548-540-23
24	26	24.3	12	4	PCT-US96-09809-23
25	26	24.3	13	1	US-08-469-005A-13
26	26	24.3	13	1	US-08-188-426-7
27	26	24.3	13	1	US-08-469-009-7
28	26	24.3	13	2	US-08-469-007-7

29	26	24.3	13	3	US-08-974-775-16
30	26	24.3	13	3	US-08-462-351-8
31	26	24.3	13	5	5194425-9
32	26	24.3	14	3	US-08-974-775-15
33	26	24.3	18	2	US-08-951-871-10
34	26	24.3	19	2	US-08-482-142-80
35	26	24.3	19	2	US-08-613-235-6
36	26	24.3	19	2	US-08-478-572-80
37	25.5	23.8	20	2	US-08-107-676-21
38	25	23.4	4	5	5425936-4
39	25	23.4	4	5	5433940-1
40	25	23.4	5	1	US-08-022-381A-12
41	25	23.4	5	1	US-08-475-827A-12
42	25	23.4	5	5	5196404-17
43	25	23.4	5	5	5433940-22
44	25	23.4	7	1	US-08-482-880-32
45	25	23.4	7	2	US-08-273-274-32

ALIGNMENTS

RESULT 1
US-08-159-339A-935
; Sequence 935, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esben
; TITLE OF INVENTION: HLA Binding peptides and their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELETYPE:
; INFORMATION FOR SEQ ID NO: 935:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-935

Sequence 16, Appl
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Patent No. 5194425
Sequence 15, Appl
Sequence 10, Appl
Sequence 80, Appl
Sequence 6, Appl
Sequence 21, Appl
Patent No. 5425936
Patent No. 5433940
Sequence 12, Appl
Sequence 12, Appl
Patent No. 5196404
Patent No. 5433940
Sequence 32, Appl
Sequence 32, Appl

Tu Dec 21 08:51:39 2000

us-08-934-367-8.rpt

Page 5

Search completed: December 21, 2000, 08:35:38
Job time: 601 sec

RT enzymatic specificity and amino acid sequence deduced from mRNA."
 RL Insect Mol. Biol. 3:201-211(1994).
 SQ SEQUENCE 18 AA; 1922 MW; 352EB0729B126B11 CRC64;

Query Match 24.5%; Score 25; DB 5; Length 18;
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 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 5 QEVYGGFSPQ 14
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 Db 6 EATVCGQFPYQ 15

RESULT 12

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 AC 006140:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DE MAJOR OUTER MEMBRANE PROTEIN P1.16 (PORIN)(FRAGMENT).
 GN POR.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93116032.
 RA Wedge E., Dalseg R., Caugant D.A., Poolman J.T., Froholm L.O.;
 RT "Expression of an inaccessible P1.7 subtype epitope on meningococcal
 RT class 1 proteins.";
 RL J. Med. Microbiol. 38:23-28(1993).
 CC -1 SUBUNIT: MONOMER.
 DE EMBL: S51901; AAB4741.1; -.
 KW Outer membrane: Antigen.
 FT NON_TER 1 1
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 1773 MW; AFAC572B037E0484 CRC64;

Query Match 24.5%; Score 25; DB 2; Length 19;
 Best Local Similarity 42.9%; Pred. No. 1.2e+03;
 Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 5 QEVYGGFSPQAVT 18
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 Db 2 QANCGASQGVKVT 15

RESULT 13

OC09511 PRELIMINARY; PRT: 19 AA.
 AC 09511:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DE 01-JUN-2000 (TREMBLrel. 14, last annotation update)
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 OS Brevibacterium.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Micrococcineae; Brevibacteriaceae.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 92407758.
 RA Duran R., Chlon C.K., Bigey F., Arnaud A., Galzy P.;
 RT "The N-terminal amino acid sequences of Brevibacterium sp. R312
 RT nitrile hydratase.";
 RL J. Basic Microbiol. 32:13-19(1992).
 SQ SEQUENCE 19 AA; 1923 MW; 84726D1A1282FB63 CRC64;

Query Match 24.5%; Score 25; DB 2; Length 19;
 Best Local Similarity 71.4%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 PSQAQVY 18
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 Db 13 PAQAQVY 19

RESULT 14

OC0908F7 PRELIMINARY; PRT: 18 AA.
 AC 0908F7:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DE PAIRED DOMAIN TRANSCRIPTIONAL FACTOR EY (FRAGMENT).
 GN EYELESS.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xu P.-X., Toon A., Heaney S., Zhang X., Michelson A., Maas R.L.;
 RT "The regulation of Pax6 is conserved between mice and flies.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DE EMBL: AF089733; AAD54001.1; -.
 FT NON_TER 1 1
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 1680 MW; 642A9C256071D610 CRC64;

Query Match 23.5%; Score 24; DB 5; Length 18;
 Best Local Similarity 66.7%; Pred. No. 1.6e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 VGGFPS 13
 : | | | | | | | |
 Db 12 VGGIPA 17

RESULT 15

OC062637 PRELIMINARY; PRT: 19 AA.
 AC 062637:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DE 01-NOV-1998 (TREMBLrel. 08, last annotation update)
 DE XANTHINE DEHYDROGENASE (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE DAWLEY;
 RX MEDLINE: 94268906.
 RA Chow C.W., Clark M., Rinaldo J., Chalkley R.;
 RT "Identification of the rat xanthine dehydrogenase/oxidase promoter.";
 RL Nucleic Acids Res. 22:1846-1854(1994).
 DE EMBL: U08123; AAB6044.1; -.
 FT NON_TER 1 1
 FT VARIANT 19 19
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2128 MW; A02841D686F50139 CRC64;

Query Match 23.5%; Score 24; DB 11; Length 19;
 Best Local Similarity 28.6%; Pred. No. 1.7e+03;
 Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 OEITFOEVGGFSPQ 14
 : | | | | | | | |
 Db 4 EELI0SVCGLAEE 17

Db "1 IVGCVKAOA 9

RESULT 7
ID 004817 PRELIMINARY; PRT; 19 AA.
AC 004817;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE HYPOTHEORETICAL 2.3 KDA PROTEIN (FRAGMENT).
OS Sporobolus stapfianus.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Sporobolus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RA Blomstedt C.K., Gianello R.D., Neale A.D., Hamill J.D., Gaff D.F.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y10781; CAA71753.1; -.
KM Hypothetical protein.1
FT NON_TER
SQ SEQUENCE 19 AA; 2270 MW; 4C644625813F244E CRC64;

Query Match 25.5%; Score 26; DB 10; Length 19;
Best Local Similarity 27.3%; Pred. No. 7.8e+02;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 QEIFQEVGCGF 11
| : : : : |
Db 1 OKLYDLDTSGF 11

RESULT 8
ID 09R4Z4 PRELIMINARY; PRT; 20 AA.
AC 09R4Z4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE AMBIENT-TEMPERATURE FIMBRIA; ATF.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Bacteria; Proteus.
RN [1]
RP SEQUENCE.
RX MEDLINE: 94222573.
RA Messad G., Bahrani F.K., Mobley H.L.;
RT "Proteus mirabilis fimbriae: identification, isolation, and
characterization of a new ambient-temperature fimbria.";
RL Infect. Immun. 62:1989-1994(1994).
SQ SEQUENCE 20 AA; 2017 MW; BZFC481003863AE2 CRC64;

Query Match 25.5%; Score 26; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 8.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFPSOAGVT 19
| : : : : |
Db 4 GTPAPTEVT 13

RESULT 9
ID 09UCA3 PRELIMINARY; PRT; 20 AA.
AC 09UCA3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE PROSTASIN (FRAGMENT).
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE: 94308140.
RA Yu J.X., Chao L., Chao J.;
RT "Prostasin is a novel human serine proteinase from seminal fluid.
purification, tissue distribution, and localization in prostate
gland.";
RL J. Biol. Chem. 269:18843-18848(1994).
DR INTERPRO: IPR001254; -.
PEAM: PF00089; trypsin; 1.
SQ SEQUENCE 20 AA; 2108 MW; EDF142A1F9E880FE CRC64;

Query Match 25.5%; Score 26; DB 4; Length 20;
Best Local Similarity 41.7%; Pred. No. 8.3e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VVGGFPSOAGVT 18
| : : : : |
Db 8 VAGQWQVSIT 19

RESULT 10
ID 09S8T0 PRELIMINARY; PRT; 20 AA.
AC 09S8T0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE JACALIN BETA-SUBUNIT.
OS Artocarpus Champeden.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Rosidae; eurosids 1; Rosales; Moraceae;
OC Artocarpus.
RN [1]
RP SEQUENCE.
RX MEDLINE: 93152601.
RA Ngoc L.D., Brillard M., Hoebeke J.;
RT "The alpha- and beta-subunits of the jacalins are cleavage products
from a 17-kda precursor.";
RL Biochim. Biophys. Acta 1156:219-222(1993).
SQ SEQUENCE 20 AA; 2071 MW; 8D5AE975F4D0E212 CRC64;

Query Match 25.0%; Score 25.5; DB 10; Length 20;
Best Local Similarity 56.2%; Pred. No. 1e+03;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 3 IFQEVVGFPSSOAGVT 18
| : : : : |
Db 6 ISQTVIVG-PMGAGVT 20

RESULT 11
ID 09TWL4 PRELIMINARY; PRT; 18 AA.
AC 09TWL4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 25 KDA CHYMOTRYPSIN-LIKE ENZYME (FRAGMENT).
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Calliphoridae; Lucilia.
RN [1]
RP SEQUENCE.
RX MEDLINE: 95219141.
RA Casu R.E., Pearson R.D., Jarney J.M., Cadogan L.C., Riding G.A.,
RA Tellam R.L.;
RT "Excretory/secretory chymotrypsin from Lucilia cuprina: purification,

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RN [1]
RP SEQUENCE.
RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
RT Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer aurein peptides from the Australian
RL bell frogs Litoria aurea and Litoria raniformis.";
CC Eur. J. Biochem. 0:0-0(2000).
CC -1- FUNCTION: AUREIN 2.1 HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
KM Amidation; Antibiotic.
FT PEPTIDE 3 16 AUREIN 2.1.1.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1616 MW; 1D9A5DADB4D240F9 CRC64;

Query Match
Best Local Similarity 28.4%; Score 29; DB 13; Length 16;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 EIFQEVVGFPSS 13
DB 4 DIVKKVVGAFGS 15

RESULT 3
P82392 PRELIMINARY; PRT; 16 AA.
ID P82392;
AC P82392;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE AUREIN 2.5.
OS Litoria raniformis, and Litoria aurea (Australian frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
RN [1]
RP SEQUENCE.
RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
RT Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer aurein peptides from the Australian
RL bell frogs Litoria aurea and Litoria raniformis.";
CC Eur. J. Biochem. 0:0-0(2000).
CC -1- FUNCTION: HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
KM Amidation; Antibiotic.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1650 MW; 1D9A5DADB4DAE2F9 CRC64;

Query Match
Best Local Similarity 28.4%; Score 29; DB 13; Length 16;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 EIFQEVVGFPSS 13
DB 4 DIVKKVVGAFGS 15

RESULT 4
O9TWK8 PRELIMINARY; PRT; 19 AA.
ID O9TWK8;
AC O9TWK8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE HAPTOGLOBIN-RELATED PROTEIN BETA SUBUNIT (FRAGMENT).
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
RN [1]
RP SEQUENCE.
RX MEDLINE: 95232503.
RA Smith A.B., Esko J.D., Hajduk S.L.;
RT "Killing of trypanosomes by the human haptoglobin-related protein.";
RL Science 268:284-286(1995).

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SQ SEQUENCE 19 AA; 2055 MW; 65BD135667C94056 CRC64;

Query Match
Best Local Similarity 26.5%; Score 27; DB 5; Length 19;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 9 GGFPQAQV 17
DB 10 GSPFQAQV 18

RESULT 5
O84274 PRELIMINARY; PRT; 19 AA.
ID O84274;
AC O84274;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE E6 PROTEIN (FRAGMENT).
OS Human papillomavirus type 25.
OC Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88089511.
RA Krubke J., Kraus J., Dellus H., Chow L., Broker T.R., Iftner T.,
RT Pfister H.;
RT "Genetic relationship among human papillomaviruses associated with
RT benign and malignant tumours of patients with epidermodysplasia
RT verruciformis.";
RL J. Gen. Virol. 68:3091-3103(1987).
DR EMBL: D00205; BAA00145.1; -.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 1955 MW; 5C820487F69A5ED1 CRC64;

Query Match
Best Local Similarity 26.5%; Score 27; DB 12; Length 19;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 10 GPPQAQV 17
DB 11 GPPQAQV 18

RESULT 6
O9TWB8 PRELIMINARY; PRT; 20 AA.
ID O9TWB8;
AC O9TWB8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE TRYPSIN-LIKE PROTEIN (DER F III ALLERGEN HOMOLOG) (FRAGMENT).
OS Dermaphagoides farinae (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptiformes; Astigmata; Analgoidea; Pyroglyphidae;
OC Dermaphagoides.
RN [1]
RP SEQUENCE.
RX MEDLINE: 93074427.
RA Ando T., Homma R., Ito G., Miyahara A., Yamakawa H., Iwaki M.,
RA Okumura Y., Suko M., Haida M.;
RT "Is a trypsin-like protease of mites a Der f III allergen?";
RL Jpn. J. Allergy 41:704-707(1992).
SQ SEQUENCE 20 AA; 2087 MW; 961537685DB36A2 CRC64;

Query Match
Best Local Similarity 26.5%; Score 27; DB 5; Length 20;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 7 VVGFPSQA 15
DB 7 VVGFPSQA 15

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DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUN-1998 (Rel. 36, Last annotation update)
 DE FERREDOXIN--NAD(+) REDUCTASE (EC 1.18.1.3) (FRAGMENT).
 OS Streptomyces griseus.
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 92041607.
 RA Ramachandra M., Seetharam R., Emplage M.H., Sarislaani F.S.;
 RT "Purification and characterization of a soybean flour-inducible
 ferredoxin reductase of Streptomyces griseus.";
 RL J. Bacteriol. 173:7106-7112(1991).
 CC -1- FUNCTION: COUPLE ELECTRON TRANSFER FROM NADH TO CYTOCHROME
 P450(SOY) IN THE PRESENCE OF FERREDOXIN.
 CC -1- CATALYTIC ACTIVITY: REDUCED FERREDOXIN + NAD(+) = OXIDIZED
 FERREDOXIN + NADH.
 CC -1- COFACTOR: FAD; REQUIRES MAGNESIUM.
 CC HSSP: P09063; 11VL.
 DR Oxidoreductase; Flavoprotein; NAD; FAD; Magnesium.
 KM NON_TER
 FT SEQUENCE 16 AA; 1485 MW; 27D11A7C37AC0510 CRC64;
 SQ

Query Match 21.6%; Score 22; DB 1; Length 16;
 Best Local Similarity 50.0%; Pred. No. 9.5e+02;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 VVGGRP 12
 : : : : :
 Db 5 IIGGGP 10

RESULT 14
 FIXA_RHILE STANDARD; PRT: 18 AA.
 ID P14313;
 AC 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE FIXA PROTEIN (FRAGMENT).
 GN Rhizobium leguminosarum.
 OS Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Rhizobiaceae; Rhizobium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 90066358.
 RA Hontelez J.G.J., Lankhorst R.K., Katinakis P., van den Bos R.C.,
 RA van Kammen A.;
 RT "Characterization and nucleotide sequence of a novel gene fixW
 upstream of the fixABC operon in Rhizobium leguminosarum.";
 RL Mol. Gen. Genet. 218:536-544(1989).
 CC -1- FUNCTION: MAY PLAY A ROLE IN A REDOX PROCESS INVOLVED IN NITROGEN
 FIXATION.
 CC -1- SUBUNIT: FIXA AND FIXB FORM A HETERODIMER (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE ETF BETA-SUBUNIT / FIXA FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation-
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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL: X16521; CAA34527.1; -
 DR PIR: P00022; P00022.
 DR INTERPRO: IPR000049; -
 DR PROSITE: PS01065; ETF_BETA; PARTIAL.
 KM Election transport; Nitrogen fixation.
 FT NON_TER
 SQ SEQUENCE 18 AA; 2036 MW; 74973C8BA2087663 CRC64;

Query Match 21.6%; Score 22; DB 1; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 12 PQSQAOVTV 19
 : : : : :
 Db 11 PQSAQIRV 18

RESULT 15
 TCBL_TRILIO STANDARD; PRT: 19 AA.
 ID P80070;
 AC 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE TRICHOLOGIN BI AND BII.
 OS Trichoderma longibrachiatum.
 CC Eukaryota; Fungi; Ascomycota; anamorphic Ascomycota; Trichoderma.
 RN [1]
 RP SEQUENCE, AND STRUCTURE BY NMR.
 RX MEDLINE; 92037622.
 RA Rebuffat S., Prigent Y., Auvin-Guette C., Bodo B.;
 RT "Tricholongs BI and BII, 19-residue peptaibols from Trichoderma
 longibrachiatum. Solution structure from two-dimensional NMR
 spectroscopy.";
 RL Eur. J. Biochem. 201:661-674(1991).
 CC -1- FUNCTION: TRICHOLONGINS ARE PEPTIDES WHICH DISPLAY ANTIFUNGAL
 AND ANTIBACTERIAL ACTIVITY. PROBABLY INTERACT WITH BIOLOGICAL
 MEMBRANES AND PROBABLY PRODUCES HOLES LEADING TO LEAKAGE.
 CC -1- PTM: AIB IS ALPHA-AMINO ISOBUTYRIC ACID.
 CC -1- PTM: IVA IS ISOVALINE.
 KM Antibiotic; Fungicide; Methylation; Acetylation; Hydroxylation;
 KM Membrane.
 KW MOD_RES 1 1 ACETYLATION (TO FORM AIB).
 FT MOD_RES 1 4 METHYLATION (TO FORM AIB).
 FT MOD_RES 4 4 METHYLATION (TO FORM AIB).
 FT MOD_RES 5 5 METHYLATION (TO FORM AIB).
 FT MOD_RES 7 7 METHYLATION (TO FORM AIB).
 FT MOD_RES 8 8 METHYLATION (TO FORM AIB).
 FT MOD_RES 9 9 METHYLATION (TO FORM AIB).
 FT MOD_RES 12 12 METHYLATION (TO FORM AIB).
 FT MOD_RES 15 15 METHYLATION (TO FORM AIB).
 FT MOD_RES 16 16 METHYLATION (TO FORM AIB).
 FT MOD_RES 16 16 ETHYLATION (TO FORM IVA; IN BII).
 FT MOD_RES 19 19 HYDROXYLATION.
 SQ SEQUENCE 19 AA; 1756 MW; B908C2DFE83D238 CRC64;

Query Match 21.6%; Score 22; DB 1; Length 19;
 Best Local Similarity 40.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 10 GPPSOAOVTV 19
 : : : : :
 Db 2 GFPAOAAASL 11

Search completed: December 21, 2000, 08:32:58
 Job time: 441 sec

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OC Amphibia: Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Uperoleia.
RN (1)
RP SEQUENCE, AND MASS SPECTROMETRY.
RA BRADFORD A.M., BOWLE J.H., TYLER M.J., WALLACE J.C.;
RT "New antibiotic uperin peptides from the dorsal glands of the
RT Australian toadlet Uperoleia mabergii."
RL Aust. J. Chem. 49:1325-1331(1996).
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=1948; METHOD=FAb.
KW Amphibian skin.
SQ SEQUENCE 19 AA; 1949 MW; 24E4F83ACBA35F21 CRC64;

Query Match 22.5%; Score 23; DB 1; Length 19;
Best Local Similarity 44.4%; Pred. No. 7.8e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 EIPQEVVG 10
DB 4 DIAKKLVG 12

RESULT 10
TRYL_STRXL
ID TRYL_STRXL STANDARD; PRT: 20 AA.
AC P80420;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE TRYPSIN-LIKE PROTEASE (EC 3.4.21.-) (FRAGMENT).
OS Streptomyces exfoliatus (Streptomyces hygroscopicus).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
RN (1)
RP SEQUENCE.
RX STRAIN-SMF13;
RX MEDLINE: 95291424.
RA Kim I.S., Lee K.J.;
RT "Physiological roles of leupeptin and extracellular proteases in
RT mycelium development of Streptomyces exfoliatus SMF13."
RL Mycobiology 141:1017-1025(1995).
CC -1- FUNCTION: INVOLVED IN MYCELIUM DIFFERENTIATION.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2A; ALSO KNOWN AS THE
CC ALPHA-LYTIC PROTEASE FAMILY.
CC HSP: P00775; 1SGT.
DR INTERPRO: IPR001254;
DR PROSITE: PS00134; TRYPsin_HIS; PARTIAL.
DR PROSITE: PS00135; TRYPsin_SER; PARTIAL.
KW Hydrolase; Serine protease.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2129 MW; 4568F56D0E7393AF CRC64;

Query Match 22.5%; Score 23; DB 1; Length 20;
Best Local Similarity 36.4%; Pred. No. 8.2e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 9 GGFPSQAOYTV 19
DB 10 GNFPEQOXLSM 20

RESULT 11
SAMP_MUSCA
ID SAMP_MUSCA STANDARD; PRT: 9 AA.
AC P19095;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SERUM AMYLOID P-COMPONENT (SAP) (FRAGMENT).
OS Musculus canis (Smooth dogfish).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
OC Mustelus.
RN (1)
RP SEQUENCE.
RX MEDLINE: 83160932.
RA Robey F.A., Tanaka T., Liu T.-Y.;
RT "Isolation and characterization of two major serum proteins from the
RT dogfish, Mustelus canis, C-reactive protein and amyloid P
RT component."
RL J. Biol. Chem. 258:3889-3894(1983).
CC -1- SUBUNIT: HOMOHEPTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
DR PIR: B20569; B20569.
DR INTERPRO: IPR001759;
DR PROSITE: PS00289; PENTAXIN; PARTIAL.
KW Amyloid; Glycoprotein; Plasma; Pentaxin.
FT DOMAIN 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match 21.6%; Score 22; DB 1; Length 9;
Best Local Similarity 37.5%; Pred. No. 8.8e+04;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 10 GPFPSQAOY 17
DB 1 GPFPSQSLI 8

RESULT 12
UN46_CLOPA
ID UN46_CLOPA STANDARD; PRT: 14 AA.
AC P81362;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE UNKNOWN PROTEIN CP 46 FROM 2D-PAGE (FRAGMENT).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
RN (1)
RP SEQUENCE.
RX STRAIN-W5;
RX MEDLINE: 98291870.
RA Flensburg R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5."
RL Electrophoresis 19:802-806(1998).
CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.4, ITS MW IS: 38.2 KDA.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1550 MW; 198078F4C0367170 CRC64;

Query Match 21.6%; Score 22; DB 1; Length 14;
Best Local Similarity 42.9%; Pred. No. 8.3e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 IFQEVVG 9
DB 2 IFNDLIG 8

RESULT 13
FENR_STRGR
ID FENR_STRGR STANDARD; PRT: 16 AA.
AC P24134;
DT 01-MAR-1992 (Rel. 21, Created)

```

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 EIFOEVVGG 10
: : : : :
Db 4 DLAKKVVGG 12

RESULT 6

UP23_UPEIN STANDARD; PRT; 19 AA.

AC P82029;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE UPERIN 2.3.

OS Uperoleia Inundata (Floodplain toadlet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;

OC Uperoleia.

RN [1]

SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE-SKIN SECRETION;

RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,

RT "Novel uperin peptides from the dorsal glands of the Australian

RT floodplain toadlet Uperoleia inundata."

RL Aust. J. Chem. 49:475-484(1996).

-1- FUNCTION: SHOWS A MEDIUM ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS,

CC L. MENSETERIOIDES AND S.UBERIS.

CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.

CC -1- MASS SPECTROMETRY: MW=1974; METHOD=FAV.

KW Amphibian skin; Antidiotic.

SEQUENCE 19 AA; 1975 MW; 2F34EF077BA35B70 CRC64;

Query Match 23.5%; Score 24; DB 1; Length 19;

Best local Similarity 44.4%; Pred. No. 5.2e+02;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 EIFOEVVGG 10
: : : : :
Db 4 DLAKKVVGG 12

RESULT 7

COG1_CHIOP STANDARD; PRT; 20 AA.

AC P34153;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE COLLAGENOLYTIC PROTEINASE 23 KDA II/III (EC 3.4.21.32) (FRAGMENT).

OS Chionoecetes opilio (Crab-beetle).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

OC Eubrachyura; Majoidae; Majidae; Chionoecetes.

RN [1]

SEQUENCE.

RC TISSUE=HEPATOPANCREAS;

RX MEDLINE; 92120073.

RA Klimova O.A., Vedishcheva V.V., Strongin A.Y.;

RT "Isolation and characteristics of collagenolytic enzymes from the

RT hepatopancreas of the crab Chionoecetes opilio."

RL Dokl. Akad. Nauk SSSR 317:482-484(1991).

-1- FUNCTION: THIS ENZYME IS A SERINE PROTEASE CAPABLE OF DEGRADING

CC THE NATIVE TRIPLE HELIX OF COLLAGEN.

CC -1- CATALYTIC ACTIVITY: BROAD SPECIFICITY; DEGRADATES NATIVE COLLAGEN.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE

CC TRYPSIN FAMILY.

DR HSSP; P00771.1A2Z.

DR INTERPRO; IPR001254.

DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.

DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.

KW Hydrolase; Serine protease; Collagen degradation.

FT NON_TER 20 20

SEQUENCE 20 AA; 2204 MW; CE0D7B996EF281A7 CRC64;

Query Match 23.5%; Score 24; DB 1; Length 20;

Best local Similarity 35.7%; Pred. No. 5.5e+02;

Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 7 VVGFPQAQVTVH 20
: : : : :
Db 1 IVGGQATPHTVWH 14

RESULT 8

CPAX_BOVIN STANDARD; PRT; 18 AA.

AC P22779;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE CYTOCHROME P450 2A (OLP2) (OLFACTIVE) (P52) (EC 1.14.14.1) (FRAGMENT).

OS Bos taurus (Bovine); Chordata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

RN [1]

SEQUENCE.

RA MEDLINE; 91027757.

RA Lazard D., Tal N., Rubinstein M., Khen M., Lancet D., Zupko K.;

RT "Identification and biochemical analysis of novel olfactory-specific

RT cytochrome P-45011A and UDP-glucuronosyl transferase."

RL Biochemistry 29:7433-7440(1990).

-1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE

CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN

CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY

CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATY

CC ACIDS, AND XENOBIOTICS.

CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +

CC OXIDIZED FLAVOPROTEIN + H(2)O.

CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

CC PIR; A35704; A35704.

DR INTERPRO; IPR001128; ..

DR PROSITE; PS00086; CYTOCHROME_P450; PARTIAL.

KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;

FT Microsome; Endoplasmic reticulum; Olfaction.

FT NON_TER 1 1

FT VARIANT 6 6 G -> D.

FT VARIANT 11 11 A -> E.

FT NON_TER 18 18

SEQUENCE 18 AA; 2058 MW; F80746F76CCD77FF CRC64;

Query Match 22.5%; Score 23; DB 1; Length 18;

Best local Similarity 44.4%; Pred. No. 7.3e+02;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 QEIFQEVG 9
: : : : :
Db 9 QQAQKEIAG 17

RESULT 9

UP27_UPEMJ STANDARD; PRT; 19 AA.

AC P82039;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE UPERIN 2.7.

OS Uperoleia mjobergii (Australian toadlet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RESULT 2

COCO_LIMPO STANDARD; PRT: 14 AA.
ID COCO_LIMPO
AC P35586;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE COCONASE (EC 3.4.21.-) (FRAGMENT).
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura; Limulidae; Limulus.
CC
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPsin FAMILY.
CC HSSP: P00760; 4TPI.
DR INTERPRO: IPR001254;
DR PROSITE: PS00134; TRYPsin_HIS; PARTIAL.
DR PROSITE: PS00135; TRYPsin_SER; PARTIAL.
KW Hydrolase; Serine protease.
FT NON_TER 14
FT SEQUENCE 14 AA; 1452 MW; 1615FB1073747570 CRC64;

Query Match 24.5%; Score 25; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YVGGF 11

Db 1 YVGGF 5

RESULT 3

TRYP_FELICA STANDARD; PRT: 16 AA.
ID TRYP_FELICA
AC P81071;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TRYPsin PRECURSOR (EC 3.4.21.4) (FRAGMENT).
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
CC
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPsin FAMILY.
CC INTERPRO: IPR001254;
DR PROSITE: PS00134; TRYPsin_HIS; PARTIAL.
DR PROSITE: PS00135; TRYPsin_SER; PARTIAL.
KW Hydrolase; Serine protease; Digestion; Pancreas; Zymogen.
FT PROPEP 1
FT CHAIN 9 >16
FT NON_TER 16
FT SEQUENCE 16 AA; 1825 MW; A6D751B58760A86 CRC64;

Query Match 23.5%; Score 24; DB 1; Length 16;
Best Local Similarity 33.3%; Pred. No. 4.4e+02;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 6 EVVGGFSSQ 14

Db 8 KIVGGYTNR 16

RESULT 4

ALL7_OLEEU STANDARD; PRT: 19 AA.
ID ALL7_OLEEU
AC P81430;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE POLLEN ALLERGEN OLE E 7 (OLE E VII) (FRAGMENT).
OS Olea europaea (Common olive).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterales; easterids I; Lamiales; Oleaceae; Olea.
CC
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPsin FAMILY.
CC HSSP: P00760; 4TPI.
DR INTERPRO: IPR001254;
DR PROSITE: PS00134; TRYPsin_HIS; PARTIAL.
DR PROSITE: PS00135; TRYPsin_SER; PARTIAL.
KW Hydrolase; Serine protease.
FT NON_TER 19
FT SEQUENCE 19 AA; 1986 MW; 999A5008C41A467E CRC64;

Query Match 23.5%; Score 24; DB 1; Length 19;
Best Local Similarity 71.4%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 PSQAQVT 18

Db 2 PSQGTVT 8

RESULT 5

UP22_UPEIN STANDARD; PRT: 19 AA.
ID UP22_UPEIN
AC P82028;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE UPERIN 2.2.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae; Uperoleia.
CC
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPsin FAMILY.
CC INTERPRO: IPR001254;
DR PROSITE: PS00134; TRYPsin_HIS; PARTIAL.
DR PROSITE: PS00135; TRYPsin_SER; PARTIAL.
KW Hydrolase; Serine protease; Digestion; Pancreas; Zymogen.
FT PROPEP 1
FT CHAIN 9 >16
FT NON_TER 16
FT SEQUENCE 19 AA; 1927 MW; 3283EF077BA35B70 CRC64;

Query Match 23.5%; Score 24; DB 1; Length 19;
Best Local Similarity 44.4%; Pred. No. 5.2e+02;

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: December 21, 2000, 08:32:57 ; Search time 62.7 Seconds
(without alignments)
10.191 Million cell updates/sec

Title: US-08-934-367-8

Perfect score: 102
Sequence: 1 QEIFQEVGSGFSPQAOVYH 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 segs, 31947931 residues
Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	25.5	15	1	GLN2_PINPS
2	25	24.5	14	1	COCO_LIMPO
3	24	23.5	16	1	TRYP_FELCA
4	24	23.5	19	1	ALIT_OUEIU
5	24	23.5	19	1	UP22_UPEIN
6	24	23.5	19	1	UP23_UPEIN
7	23	22.5	20	1	COG1_CHIOP
8	23	22.5	18	1	CPAX_BOVIN
9	23	22.5	19	1	UP27_UPEIM
10	23	22.5	20	1	TRVL_SPREX
11	22	21.6	9	1	SAMP_MUSCA
12	22	21.6	14	1	UN46_CLOPA
13	22	21.6	16	1	FENR_STRGR
14	22	21.6	18	1	FIXA_RHLE
15	22	21.6	19	1	TCBI_TRILO
16	22	21.6	19	1	UP21_UPEIN
17	22	21.6	20	1	COG2_CHIOP
18	21	20.6	17	1	UP37_UPEIM
19	21	20.6	18	1	AKOF_STRRM
20	21	20.6	19	1	OXLA_OPHHA
21	21	20.6	20	1	ATP4_SPIOI
22	21	20.6	20	1	ELAS_GADMO
23	21	20.6	20	1	TL18_SPIOI
24	20	19.6	13	1	BPPI_BORTA
25	20	19.6	13	1	UN12_CLOPA
26	20	19.6	13	1	CYSK_CLOPA
27	20	19.6	15	1	MILT_ONCKE
28	20	19.6	15	1	UC25_MAIZE
29	20	19.6	16	1	CP12_LITCI
30	20	19.6	16	1	LPK1_LOCOMI
31	20	19.6	17	1	ERC2_THEAO
32	20	19.6	19	1	UP24_UPEIN
33	20	19.6	20	1	ANCR_AGRBI

34	19	18.6	10	1	FARP_MANSE	P18523 manduca sex
35	19	18.6	13	1	CRBL_VESTR	P17231 vespa tropi
36	19	18.6	15	1	ATP2_PINPS	P81663 pinus pinas
37	19	18.6	15	1	COX1_THUOB	P80979 thunus obe
38	19	18.6	15	1	ESTY_MANSE	P19985 manduca sex
39	19	18.6	15	1	FIBA_ANAPL	P12801 anas platyr
40	19	18.6	16	1	CT11_LITCI	P81835 litorea cit
41	19	18.6	16	1	CT13_LITCI	P81846 litorea cit
42	19	18.6	19	1	HBR2_URCHA	P18992 utorastlyx h
43	19	18.6	20	1	ALAT_PIG	P13191 sus scrofa
44	19	18.6	20	1	COG1_PARC	P20731 paralithode
45	19	18.6	20	1	COG2_CHIOP	P34154 chionocete

ALIGNMENTS

RESULT	ID	GLN2_PINPS	STANDARD	PRT	15 AA.
1	GLN2_PINPS	STANDARD	PRT	15 AA.	
AC	P81107	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	PROBABLE GLUTAMINE SYNTHETASE LEAF ISOZYME (EC 6.3.1.2) (GLUTAMATE--				
DE	AMMONIA LIGASE) (S2205/S2287) (N47/N48) (FRAGMENT).				
OS	Pinus pinaster (Maritime pine).				
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;				
OC	Coniferopsida; Coniferales; Pinaceae; Pinus.				
RC	SEQUENCE.				
RC	TISSUE-NEEDLE;				
RA	Plomion C., Costa P., Bahman N., Frigerio J.-M.;				
RT	"Genetic analysis of needle proteins in maritime pine. 1. Mapping				
RT	dominant and codominant protein markers assayed on diploid tissue, in				
RT	a haploid-based genetic map."				
RL	SciValae Genetica 46:161-165(1997).				
RP	(2)				
RP	SEQUENCE.				
RC	TISSUE-NEEDLE;				
RC	MEDLINE: 99274088.				
RA	Costa P., Pionneau C., Bauw G., Dubos C., Bahman N., Kremer A.,				
RA	Frigerio J.-M., Plomion C.;				
RT	"Separation and characterization of needle and xylem maritime pine				
RT	proteins."				
RL	Electrophoresis 20:1098-1108(1999).				
CC	-1- FUNCTION: THE LIGHT-MODULATED CHLOROPLAST ENZYME, ENCODED BY A				
CC	NUCLEAR GENE AND EXPRESSED PRIMARILY IN LEAVES, IS RESPONSIBLE FOR				
CC	THE REASSIMILATION OF THE AMMONIA GENERATED BY PHOTORESPIRATION				
CC	(BY SIMILARITY).				
CC	-1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) -> ADP + GLUTAMINE +				
CC	ORTHOPOSPHATE.				
CC	-1- SUBUNIT: HOMOCYMER (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).				
CC	-1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:				
CC	5.7, ITS MW IS: 42 KDA.				
CC	-1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.				
DR	INTERPRO: IPR001691; -				
DR	PROSITE: PS00180; GLNA_1; PARTIAL.				
DR	PROSITE: PS00181; GLNA_ATP; PARTIAL.				
KW	ligase; Chloroplast.				
FT	NON_TER				
FT	NON_TER				
SO	SOURCE				
	15 AA; 1614 MW; 24A2420BFFD60D27 CRC64;				
Qy	8 VGFP 12				
Db	10 VGVP 14				

Query Match: 25.5%; Score 26; DB 1; Length 15;
Best Local Similarity: 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 3 VSGGFAS 9

RESULT 14

Protein QA30027 - Arabidopsis thaliana (fragment)
 PA0026
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C:Accession: PA0026
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional
 A:Reference number: PA0001
 A:Accession: PA0026
 A:Molecule type: protein
 A:Residues: 1-15 <KAM>
 A:Experimental source: leaf

Query Match 22.5% Score 23; DB 2; Length 15;

Best Local Similarity 45.5% Pred. No. 1.1e+03;

Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 8 VSGFPSQAQVT 18

Db 4 VVGXPFAXQIT 14

RESULT 15

A35704

Cytochrome P450 olf2 - bovine (fragment)

N:Contains: oxidoreductase (EC 1.-.-.-)

C:Species: Bos primigenius taurus (cattle)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 12-Mar-1999

C:Accession: A35704

R:Lazard, D.; Tal, N.; Rubinstein, M.; Khen, M.; Lancet, D.; Zupko, K.

Biochemistry 29, 7433-7440, 1990

A:Title: Identification and biochemical analysis of novel olfactory-specific cytochrome

A:Reference number: A35704; MUID:91027757

A:Accession: A35704

A:Molecule type: protein

A:Residues: 1-18 <LAZ>

C:Genetics:

A:Gene: CYP2A

C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C:Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane protein

Query Match 22.5% Score 23; DB 2; Length 18;

Best Local Similarity 44.4% Pred. No. 1.4e+03;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QETFEVVG 9

Db 9 QQAfKELOG 17

Search completed: December 21, 2000, 08:30:06
 Job time: 270 sec

A:Experimental source: cytolitic T-lymphocyte
C:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 24.5%; Score 25; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 VGGFSS 13
| | | | |
DB 5 VGGFAS 10

RESULT 9

A20190
hypodermin B - early cattle grub (fragment)
C:Species: Hypoderma lineatum (early cattle grub)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Jun-1993
C:Accession: A20190
R:Leclercq, A.; Tong, N.T.; Kell, B.
Eur. J. Biochem. 134, 261-267, 1983
A:Title: Hypodermin B, a trypsin-related enzyme from the insect Hypoderma lineatum.
A:Reference number: A20190; MUID:83261874
A:Accession: A20190
A:Molecule type: protein
A:Residues: 1-16 <LECG>

Query Match 24.5%; Score 25; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVGGF 11
| | | | |
DB 1 IVGGF 5

RESULT 10

A45806
T-cell receptor beta chain C region type 1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Jul-1999
C:Accession: A45806
R:Dent, A.L.; Fink, P.J.; Hedrick, S.M.
J. Immunol. 143, 322-328, 1989
A:Title: Characterization of an alternative exon of the murine T cell receptor beta-chain.
A:Reference number: A45806; MUID:89278666
A:Accession: A45806
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-20 <DEN>
A:Cross-references: GB:M27225; NID:g339373; PIDN:AA61099.1; PID:g553781
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 24.0%; Score 24.5; DB 2; Length 20;
Best Local Similarity 35.3%; Pred. No. 8.6e+02;
Matches 6; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 2 EIFQEVVGGF-PSQAQV 17
::: | | | | |
DB 4 KVFPEVAVFEPSEAFI 20

RESULT 11

I52698
hypothetical THR1/BTR mutant fusion protein, cell line BR474 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C:Accession: I52698
R:Futurel, P.A.; Cochran, C.; Marks, J.R.; Iglehart, J.D.; Zimmerman, W.; Barrett, J.C.;

Cancer Res. 54, 1791-1794, 1994
A:Title: Mutation analysis of the THR1 gene in breast cancer: deletion/fusion of the
A:Reference number: I52698; MUID:94185019
A:Accession: I52698

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-15 <FUT>
A:Cross-references: GB:S71020; NID:g546111; PIDN:AA630341.1; PID:g546112
C:Comment: This sequence is the chimeric product of a deletion or translocation mutat
C:Genetics:
A:Gene: THR1/BTR
A:Map position: 17q11.2
C:Keywords: fusion protein

Query Match 23.5%; Score 24; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 11 FPSQAQVTVH 20
| | | | |
DB 3 FSEQFRVQVH 12

RESULT 12

PC2241
heat shock protein 42A - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 17-Mar-1999
C:Accession: PC2241
R:Hayama, T.; Yasuda, K.; Nishiyama, E.
Biochem. Biophys. Res. Commun. 204, 357-365, 1994
A:Title: Characterization of high-molecular-mass heat shock proteins and 420C-specific
A:Reference number: PC2238; MUID:95032120
A:Accession: PC2241
A:Molecule type: protein
A:Residues: 1-17 <HAT>
C:Keywords: heat shock; stress-induced protein

Query Match 23.5%; Score 24; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 EYVGG 10
| | | | |
DB 8 EIVGG 12

RESULT 13

PH1448
T-cell receptor alpha chain (clone A24/PEG2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1448
R:Casanova, J.L.; Martison, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.;
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompa
A:Reference number: PH1430; MUID:93171821
A:Accession: PH1448
A:Molecule type: mRNA
A:Residues: 1-14 <CAS>
A:Experimental source: cytolitic T-lymphocyte
C:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 22.5%; Score 23; DB 2; Length 14;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 VVGGFSS 13
| | | | |

```
RESULT 3
S56122
Type I DNA methyltransferase M.EcoRI24 I chain HsdM - Escherichia coli (fragments)
C:Species: Escherichia coli
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
C:Accession: S56122
R:Webb, M.; Taylor, I.A.; Firman, K.; Kneale, G.G.
J. Mol. Biol. 250, 181-190, 1995
A:Title: Probing the domain structure of the type IC DNA methyltransferase M.EcoRI24I by
A:Reference number: S56121; MUID:95333175
A:Accession: S56122
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <MEB>

Query Match
Best Local Similarity 25.5%; Score 26; DB 2; Length 12;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPPSOA 15
DB 7 GYPSA 12

RESULT 4
A61392
brain-associated small cell lung cancer antigen - human (fragment)
M:Alternate names: BASCA
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Sep-1994
C:Accession: A61392
R:Umezawa, Y.; Kuge, S.; Kikyo, N.; Shirai, T.; Watanabe, J.; Fujiwara, M.; Okabe, T.
Jpn. J. Clin. Oncol. 21, 251-255, 1991
A:Title: Identity of brain-associated small cell lung cancer antigen and the CD56 (NKH-1
A:Reference number: A61392; MUID:92046737
A:Accession: A61392
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <UME>

Query Match
Best Local Similarity 25.5%; Score 26; DB 2; Length 16;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 PSOAOVT 19
DB 7 PSOGETSV 14

RESULT 5
C34917
catechol 1,2-dioxygenase (EC 1.13.11.1) beta chain - Pseudomonas sp. (fragment)
M:Alternate names: pyrocatechase beta chain
C:Species: Pseudomonas sp.
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 10-Feb-1995
C:Accession: C34917
R:Nakai, C.; Horike, K.; Kuramitsu, S.; Kagamiyama, H.; Nozaki, M.
J. Biol. Chem. 265, 660-665, 1990
A:Title: Three isozymes of catechol 1,2-dioxygenase (pyrocatechase), alphaalpha, alpha
A:Reference number: A34917; MUID:90110118
A:Accession: C34917
A:Molecule type: protein
A:Residues: 1-20 <NAK>
C:Keywords: heterodimer; homodimer; oxidoreductase

Query Match
Best Local Similarity 25.5%; Score 26; DB 2; Length 20;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QEIFEYWG 9

RESULT 6
S29636
jacalin beta-I chain - Artocarpus champedon (fragment)
C:Species: Artocarpus champedon
C:Date: 19-Mar-1997 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
C:Accession: S29636
R:Ngoc, L.D.; Brillard, M.; Hoebeke, J.
Biochim. Biophys. Acta 1156, 219-222, 1993
A:Title: The alpha- and beta subunits of the jacalins are cleavage products from a 17
A:Reference number: S29635; MUID:93152601
A:Accession: S29636
A:Molecule type: protein
A:Residues: 1-20 <NGO>
A:Experimental source: seed
C:Complex: heterotetramer; two alpha and two beta chains
C:Function:
A:Description: seed storage protein
A:Note: lectin for D-galactosyl-beta-1->3-N-acetylglucosamine, a tumor-associated T
C:Keywords: heterotetramer; lectin; seed; storage protein

Query Match
Best Local Similarity 25.0%; Score 25.5; DB 2; Length 20;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 3 IFQEWGPPSOAOVT 18
DB 6 ISQTVIVG-PMGQOVT 20

RESULT 7
B61168
cococonase (EC 3.4.21.-) - Chinese oak silkworm (fragment)
C:Species: Anthrenaea pernyi (Chinese oak silkworm)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C:Accession: B61168
R:Kramer, K.J.; Feilsted, R.L.; Law, J.H.
J. Biol. Chem. 248, 3021-3028, 1973
A:Title: Cococonase. V. Structural studies on an insect serine protease.
A:Reference number: A61168; MUID:73166540
A:Accession: B61168
A:Molecule type: protein
A:Residues: 1-5 <KRA>
C:Keywords: hydrolase; serine proteinase; zymogen
F:1-5/Product: cococonase (fragment) #status experimental <MNT>

Query Match
Best Local Similarity 24.5%; Score 25; DB 2; Length 5;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVGGF 11
DB 1 IVGGF 5

RESULT 8
PH1436
T-cell receptor alpha chain (clone A24/PEF5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1436
R:Casanova, J.L.; Martinon, F.; Gounnier, H.; Barra, C.; Pannetier, C.; Regnault, A.;
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompa
A:Reference number: PH1430; MUID:93171821
A:Accession: PH1436
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:30:06 ; Search time 112.59 seconds
(without alignments)

11.273 Million cell updates/sec

Title: US-08-934-367-8

Perfect score: 102

Sequence: 1 QEIFQEVVGFPSPQAQVTVH 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	28.4	16	2	A60551
2	27	26.5	17	2	A61557
3	26	25.5	12	2	S56122
4	26	25.5	18	2	A61392
5	26	25.5	20	2	C34917
6	25.5	25.0	20	2	S29636
7	25	24.5	5	2	B61168
8	25	24.5	15	2	PH1436
9	25	24.5	16	2	A20180
10	24.5	24.0	20	2	A45806
11	24	23.5	15	4	I52698
12	24	23.5	17	2	PC2241
13	23	22.5	14	2	PH1448
14	23	22.5	15	2	PA0026
15	23	22.5	18	2	A35704
16	23	22.5	20	2	S50022
17	23	22.5	20	2	P00033
18	22.5	22.1	20	2	A56900
19	22	21.6	9	2	B20569
20	22	21.6	12	2	PH1183
21	22	21.6	14	2	PH0747
22	22	21.6	15	2	S26527
23	22	21.6	16	2	C53113
24	22	21.6	16	2	A44897
25	22	21.6	17	2	B61334
26	22	21.6	18	2	P00022
27	22	21.6	19	2	S29167
28	22	21.6	19	2	S74087
29	22	21.6	20	2	S50023

ALIGNMENTS

30	22	21.6	20	2	S71601	recombination prot
31	21.5	21.1	20	2	S29108	glutathione transf
32	21.5	21.1	20	2	A61327	trypsin (EC 3.4.21
33	21.5	21.1	20	2	D34817	collagenolytic pro
34	21	20.6	12	2	PH1189	T-cell receptor al
35	21	20.6	12	2	PH1180	T-cell receptor al
36	21	20.6	12	2	PH1188	T-cell receptor al
37	21	20.6	12	2	PH1172	T-cell receptor al
38	21	20.6	13	2	PH1175	T-cell receptor al
39	21	20.6	13	2	A32734	enkephalin precurs
40	21	20.6	14	2	PA0015	seed storage prote
41	21	20.6	14	2	FS0278	ribulose-bisphosph
42	21	20.6	14	2	PH1450	T-cell receptor al
43	21	20.6	15	2	S26516	T-cell receptor al
44	21	20.6	15	2	S26524	T-cell receptor al
45	21	20.6	15	2	S26528	T-cell receptor al

RESULT 1
A60551
Leukocyte elastase (EC 3.4.21.37) - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 17-Mar-1999
C:Accession: A60551
R:Axelsson, L.; Bergenfelt, M.; Björk, P.; Olsson, R.; Ohlsson, K.
Scand. J. Clin. Lab. Invest. 50, 35-42, 1990
A:Title: Release of immunoreactive canine leukocyte elastase normally and in endotoxi
A:Reference number: A60551; MUID:90193608
A:Accession: A60551
A:Molecule type: Protein
A:Residues: 1-16 <AXE>
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; leukocyte; lysosome; serine proteinase

Query Match 28.4%; Score 29; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 VVGFPSPQ 14
:||| |:
DB 1 IVGGRPAQ 8

RESULT 2
A61557
major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (strain Fc
C:Species: Plasmodium falciparum
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C:Accession: A61557
R:Heidrich, H.G.
Biol. Cell 64, 205-214, 1988
A:Title: Isolation and functional characterization of Plasmodium falciparum merozoite
A:Reference number: A61557; MUID:89150734
A:Accession: A61557
A:Status: preliminary
A:Molecule type: Protein
A:Residues: 1-17 <HEI>
C:Keywords: surface antigen

Query Match 26.5%; Score 27; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 EIFFQEVVGFPSP 13
|:|:| |:
DB 4 ESYQELAVVTPS 15

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-286-889-15

Query Match 26.5%; Score 27; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 IFQEVVGGF 11
:11111
1 VFQEXGAGF 9
DB

RESULT 15
US-08-485-618-15
Sequence 15, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-485-618-15

Query Match 26.5%; Score 27; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 IFQEVVGGF 11
:11111
1 VFQEXGAGF 9
DB

Search completed: December 21, 2000, 08:31:48
Job time: 371 sec

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-666-473-114

Query Match 27.5%; Score 28; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 PQQAQTV 19
1 |||||
Db 1 PHMAQTV 8

RESULT 12
US-08-669-284B-26
; Sequence 26, Application US/08669284B
; Patent No. 5939534
; GENERAL INFORMATION:
; APPLICANT: Inoue, Makoto
; APPLICANT: Kikuchi, Kaoru
; APPLICANT: Ishige, Yoko
; APPLICANT: Ito, Akira
; APPLICANT: Kimura, Toru
; APPLICANT: Nakayama, Chikao
; APPLICANT: No. 5939534uchi, Hiroshi
; TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUROTROPHIC FACTORS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,284B
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/02269
; FILING DATE: 27-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 06-268281
; FILING DATE: 05-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 06-201504
; FILING DATE: 02-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 05-350934
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: O-42041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-669-284B-26

Query Match 26.5%; Score 27; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.2e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 FOEVVGG 10
11: |||
Db 2 FQGVVGG 8

RESULT 13
US-08-173-497-15
; Sequence 15, Application US/08173497
; Patent No. 5437958
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van Der Vieren, Monica
; TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,497
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5437958and, Greta E.
; REGISTRATION NUMBER: 35,302
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-173-497-15

Query Match 26.5%; Score 27; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 IFQEVVGGF 11
1: ||| 11
Db 1 VFQGVVGGF 9

RESULT 14
US-08-286-889-15
; Sequence 15, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Mich
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:

TITLE OF INVENTION: METHODS FOR THE TREATMENT OF
TITLE OF INVENTION: GASTROINTESTINAL TRACT DISORDERS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Delavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: U.S.A.
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622,720A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-396
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-622-720A-23

Query Match 29.4%; Score 30; DB 2; Length 17;
Best Local Similarity 53.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 7 VVGFPQAOVTV 19
||||| : ||
Db 1 VVGQPGNSPMV 13

RESULT 10
US-08-943-363-112
Sequence 112, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5837478 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-112

Query Match 28.4%; Score 29; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 IFQEVGG 10
||||| ||
Db 10 IFQEDAG 17

RESULT 11
US-08-666-473-114
Sequence 114, Application US/08666473
Patent No. 5843713
GENERAL INFORMATION:
APPLICANT: YOSHIDA, Aruto
TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,473
FILING DATE: 19-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP95/02238
FILING DATE: 01-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-22101
FILING DATE: 09-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-269111
FILING DATE: 01-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16887/837
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 114:

STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,348A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-466-348A-41

Query Match 30.4%; Score 31; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 9 GGFPQAQVTV 19
| 1:111: :
DB 1 GAMPNQAQMRI 11

RESULT 7
US-08-468-545B-41
Sequence 41, Application US/08468545B
Patent No. 5876712
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,545B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-468-545B-41

SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-466-680B-41

Query Match 30.4%; Score 31; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 9 GGFPQAQVTV 19
| 1:111: :
DB 1 GAMPNQAQMRI 11

RESULT 8
US-08-466-680B-41
Sequence 41, Application US/08466680B
Patent No. 6075122
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,680B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-466-680B-41

Query Match 30.4%; Score 31; DB 3; Length 15;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 9 GGFPQAQVTV 19
| 1:111: :
DB 1 GAMPNQAQMRI 11

RESULT 9
US-08-622-720A-23
Sequence 23, Application US/08622720A
Patent No. 5814308
GENERAL INFORMATION:
APPLICANT: Zhang, Ke

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:31:47 ; Search time 99.91 Seconds
(without alignments)
3.355 Million cell updates/sec

Title: US-08-934-367-8

Perfect score: 102

Sequence: 1 OEIPEVVGFPQAQVTVH 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 1676186 residues

Total number of hits satisfying chosen parameters: 87906

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

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4: /cgn2_6/ptodata/2/1aa/PCPUS.COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	35.3	14	3	US-09-120-365-87
2	34	33.3	19	5	Sequence 87, Appl 5219991-12
3	32	31.4	20	5	Patent No. 5219991
4	31	30.4	15	1	US-08-467-083-41
5	31	30.4	15	1	Sequence 41, Appl 5219991
6	31	30.4	15	2	US-08-414-417B-41
7	31	30.4	15	2	Sequence 41, Appl 5219991
8	31	30.4	15	2	US-08-468-545B-41
9	30	29.4	17	3	US-08-466-680B-41
10	29	28.4	17	2	US-08-622-720A-23
11	28	27.5	12	2	US-08-943-363-112
12	27	26.5	8	2	US-08-666-473-114
13	27	26.5	11	1	US-08-669-284B-26
14	27	26.5	11	1	Sequence 26, Appl 5219991
15	27	26.5	11	1	US-08-173-487-15
16	27	26.5	11	1	Sequence 15, Appl 5219991
17	27	26.5	11	1	US-08-286-889-15
18	27	26.5	11	1	Sequence 15, Appl 5219991
19	27	26.5	11	1	US-08-485-618-15
20	27	26.5	11	1	Sequence 15, Appl 5219991
21	27	26.5	11	1	US-08-362-652-15
22	27	26.5	11	1	Sequence 15, Appl 5219991
23	27	26.5	11	2	US-08-605-672-15
24	27	26.5	11	2	Sequence 15, Appl 5219991
25	27	26.5	11	2	US-08-482-293A-15
26	27	26.5	11	2	Sequence 15, Appl 5219991
27	27	26.5	11	2	US-08-943-363-15
28	27	26.5	11	2	Sequence 15, Appl 5219991
29	27	26.5	11	2	US-08-474-696A-1
30	27	26.5	11	2	Sequence 15, Appl 5219991
31	27	26.5	11	2	US-08-474-696A-1
32	27	26.5	11	2	Sequence 15, Appl 5219991
33	27	26.5	11	2	US-08-474-696A-1
34	27	26.5	11	2	Sequence 15, Appl 5219991
35	27	26.5	11	2	US-08-474-696A-1
36	27	26.5	11	2	Sequence 15, Appl 5219991
37	27	26.5	11	2	US-08-474-696A-1
38	27	26.5	11	2	Sequence 15, Appl 5219991
39	27	26.5	11	2	US-08-474-696A-1
40	27	26.5	11	2	Sequence 15, Appl 5219991
41	27	26.5	11	2	US-08-474-696A-1
42	27	26.5	11	2	Sequence 15, Appl 5219991
43	27	26.5	11	2	US-08-474-696A-1
44	27	26.5	11	2	Sequence 15, Appl 5219991
45	27	26.5	11	2	US-08-474-696A-1

29	26	25.5	11	1	US-08-466-647-106	Sequence 106, App
30	26	25.5	13	3	US-08-834-314-5	Sequence 5, Appl
31	26	25.5	14	3	US-09-120-365-82	Sequence 82, Appl
32	26	25.5	14	3	US-09-120-365-83	Sequence 83, Appl
33	26	25.5	14	3	US-09-120-365-84	Sequence 84, Appl
34	26	25.5	14	3	US-08-460-190-175	Sequence 175, App
35	26	25.5	16	2	US-08-488-379-175	Sequence 175, App
36	26	25.5	16	4	PCT-US93-07545-175	Sequence 175, App
37	25.5	25.0	20	1	US-08-218-025A-63	Sequence 63, Appl
38	25	24.5	5	3	US-08-570-761-3	Sequence 3, Appl
39	25	24.5	6	1	US-07-890-422B-14	Sequence 14, Appl
40	25	24.5	6	3	US-08-570-761-2	Sequence 2, Appl
41	25	24.5	7	1	US-08-462-880-32	Sequence 32, Appl
42	25	24.5	7	2	US-08-273-274-32	Sequence 32, Appl
43	25	24.5	7	2	US-08-475-041-32	Sequence 32, Appl
44	25	24.5	7	2	US-08-484-773-32	Sequence 32, Appl
45	25	24.5	9	2	US-08-934-222-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1

US-09-120-365-87

; Sequence 87, Application US/09120365

; Patent No. 6103514

; GENERAL INFORMATION:

; APPLICANT: Natori, Shunji

; TITLE OF INVENTION: NEW PROTEASE

; FILE REFERENCE: 32290-144749

; CURRENT APPLICATION NUMBER: US/09/120,365

; CURRENT FILING DATE: 1998-07-22

; EARLIER APPLICATION NUMBER: JP 9-333 474

; NUMBER OF SEQ ID NOS: 101

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 87

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Nicotiana

US-09-120-365-87

Query Match 35.3%; Score 36; DB 3; Length 14;

Best Local Similarity 66.7%; Pred. No. 1.3;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 EIEPEVVGFP 13

Db 3 EIEPEVVGFP 14

RESULT 2

5219991-12

; Patent No. 5219991

; APPLICANT: LEONARD, EDWARD;SKEEL, ALISON H.;YOSHIMURA.

; TITLE OF INVENTION: MACROPHAGE STIMULATING PROTEIN

; NUMBER OF SEQUENCES: 12

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/586,085

; FILING DATE: 21-SEP-1990

; SEQ ID NO:12:

; LENGTH: 19

5219991-12

Query Match 33.3%; Score 34; DB 5; Length 19;

Best Local Similarity 53.8%; Pred. No. 4.4;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 VVGFPQAQVTV 19

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Search completed: December 21, 2000, 08:35:38
Job time: 601 sec

RT "Proteus mirabilis flagella and MR/P fimbriae: isolation,
RT purification, N-terminal analysis, and serum antibody response
RL following experimental urinary tract infection."
SEQUENCE 20 AA; 1923 MW; 6B3ADDD464F4CD11 CRC64;

Query Match 22.5%; Score 23; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 3.3e+03;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 3 SGERAVMLGKV 14
DB 2 SGGDTITFTGKV 13

RESULT 12

ID 09TWL3 PRELIMINARY; PRT; 20 AA.
AC 09TWL3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE INITIATORIN (FRAGMENT).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Bombycoidea; Bombycidae; Bombyx.
RN [1]
RP SEQUENCE.
RA MEDLINE: 95218779.
RA Aigaki T., Kasuga H., Nagaoka S., Osana M.;
RT "Purification and partial amino acid sequence of Initiatorin, a
RT prostatic endopeptidase of the silkworm, Bombyx mori."
RL Insect Biochem. Mol. Biol. 24:969-975(1994).
DR INTERPRO: IPR001254.
DR PFM: PFO0089; trypsin; 1.
SEQUENCE 20 AA; 2205 MW; 8BE047E96CFF1BA CRC64;

Query Match 22.5%; Score 23; DB 5; Length 20;
Best Local Similarity 71.4%; Pred. No. 3.3e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 VSGRAV 8
DB 2 VCGRAV 8

RESULT 13

ID 028734 PRELIMINARY; PRT; 20 AA.
AC 028734;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE TROONIN T (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE: 83167564.
RA Putney S.D., Herlihy W.C., Schimmel P.R.;
RT "A new tropomyosin T and cDNA clones for 13 different muscle proteins,
RL Nature 302:718-721(1983).
DR EMBL: V00901; CAA24266.1; -.
FT NON_TER 1 1
FT NON_TER 20 20
SEQUENCE 20 AA; 2495 MW; 83572E605F56A884 CRC64;

Query Match 22.5%; Score 23; DB 6; Length 20;
Best Local Similarity 41.2%; Pred. No. 3.3e+03;
Matches 7; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

OY 4 GERAVMLGRVYGLN 20
DB 3 GER-----LKRQKIDITN 15

RESULT 14

ID 005403 PRELIMINARY; PRT; 8 AA.
AC 005403;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE DNA FOR ORF'S FROM CHROMOSOME XV (FRAGMENT).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-FY1679;
RX MEDLINE: 96021609.
RA Zumslein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RT "A 29,425 bp segment on the left arm of yeast chromosome XV contains
RT more than twice as many unknown as known open reading frames."
RL Yeast 11:975-986(1995).
DR EMBL: X83121; CAA58183.1; -.
FT NON_TER 8 8
FT NON_TER 8 8
SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 21.6%; Score 22; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 17 GLHN 20
DB 1 GHN 4

RESULT 15

ID P70007 PRELIMINARY; PRT; 14 AA.
AC P70007;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE HISTONE H4-1 (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE: 85160855.
RA Cardullo G., Razvi F., Ruberti I., Mohr I., Worcel A.;
RT "Chromatin-specific hypersensitive sites are assembled on a Xenopus
RT histone gene injected into Xenopus oocytes."
RL J. Mol. Biol. 181:333-349(1985).
DR EMBL: M23777; AAA49737.1; -.
FT NON_TER 1 1
FT NON_TER 14 14
SEQUENCE 14 AA; 1524 MW; 65A76B0A927B34B4 CRC64;

Query Match 21.6%; Score 22; DB 13; Length 14;
Best Local Similarity 66.7%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 12 GRVYKG 17
DB 6 GRTLYG 11

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RESULT 7
Q9TWT8      PRELIMINARY;      PRT;      20 AA.
AC O9TWT8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE GLUTATHIONE TRANSFERASE ISOZYME II (EC 2.5.1.18) (FRAGMENT).
OS Penaeus japonicus (Kuruma prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
RN [1]
RP SEQUENCE.
RX MEDLINE; 93278989.
RA Lin K.S., Chuang N.N.;
RT "Anionic glutathione S-transferases in shrimp eyes."
RL Comp. Biochem. Physiol. B, Comp. Biochem. 105:151-156(1993).
SQ SEQUENCE 20 AA; 2254 MW; 5D6A7ABC09AD38 CRC64;

Query Match      23.5%; Score 24; DB 5; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ERAVML 10
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Db 13 ERSVWL 18

RESULT 8
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AC Q25355;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE VITELLOGENIN A (FRAGMENT).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Phryganea; Megaloptera; Orthopteroidea; Orthoptera; Caellifera;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88003971.
RA Locke J., White B.N., Wyatt G.R.;
RT "Cloning and 5' end nucleotide sequences of two juvenile hormone-
inducible vitellogenin genes of the African migratory locust.";
RL DNA 6:331-342(1987).
DR EMBL; M17333; AAA29284.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1128 MW; D1B31177272042CD CRC64;

Query Match      22.5%; Score 23; DB 5; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 AVMLG 12
   ||:|
Db 3 AVILG 8

RESULT 9
Q24445      PRELIMINARY;      PRT;      17 AA.
AC Q24445;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE THIS ORF RESIDES IN THE 5' UTR OF CPHY2.
OS Ceratodon purpureus (Moss).
OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;

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OC Dicronidae; Dicronales; Ditrichaceae; Ceratodon.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WT3;
RA Hughes J.E., Lamparter T., Miltmann F.;
RL Plant Physiol. 112:446-446(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-WT3;
RA Pasentis K., Paulo N., Dittich P., Algarra P., Thuenmler F.;
RL Submitted (Oct-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL; U72993; AAB19059.1; -.
SQ SEQUENCE 17 AA; 1949 MW; 072DF72059DF1C7C CRC64;

Query Match      22.5%; Score 23; DB 10; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 SGERAVMLG 12
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Db 6 STSRSLMTVG 15

RESULT 10
Q53545      PRELIMINARY;      PRT;      19 AA.
AC Q53545;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE VIRE (FRAGMENT).
GN VIRE.
OS Shigella sonnei.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95394812.
RA Nakayama S., Matnabe H.;
RT "Involvement of cpkA, a sensor of a two-component regulatory system,
in the pH-dependent regulation of expression of Shigella sonnei vire
gene.";
RL J. Bacteriol. 177:5062-5069(1995).
DR EMBL; S79443; AAB35192.1; -.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2344 MW; 52A53BDABEFCF4 CRC64;

Query Match      22.5%; Score 23; DB 2; Length 19;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 14 VKRYGLHN 20
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Db 12 IKVRLHN 18

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Q9R5T4      PRELIMINARY;      PRT;      20 AA.
AC Q9R5T4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MRA-MANNOSE-RESISTANT/PROTEUSLIKE (MR/P) FIMBRIAL SUBUNIT.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
RN [1]
RP SEQUENCE.
RX MEDLINE; 91372967.
RA Bahmani F.K., Johnson D.E., Robbins D., Mobley H.L.;

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RX MEDLINE: 95232503.
 RA Smith A.B., Esko J.D., Hajduk S.L.:
 RT "Killing of trypanosomes by the human haptoglobin-related protein."
 RL Science 266:284-286(1995).
 SQ SEQUENCE 19 AA; 2072 MW; 5BE2440A3DB3ABD6 CRC64;

Query Match 24.5%; Score 25; DB 5; Length 19;
 Best Local Similarity 26.3%; Pred. No. 1.5e+03;
 Matches 5; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 1 DVSGERAVMLGRVYGLH 19
 DB 1 DLGAVISLLXGROLFALY 19

RESULT 3
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 AC 015892;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
 DE (CLONE XP384A) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Cooblaugh M.I., Chinnault C.A., Baldwin A., Lindsay E.A., Zhao Z.Y.,
 RA Caskey C.T.H.;
 RL Hum. Mol. Genet. 0:0-0(0).
 DR EMBL: U32071; AAA73882.1; -.
 FT NON_TER 1 1
 FT SEQUENCE 9 AA; 971 MW; 49B22732CDC40B17 CRC64;

Query Match 23.5%; Score 24; DB 4; Length 9;
 Best Local Similarity 83.3%; Pred. No. 3e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 ERAVML 10
 DB 3 ERAVIL 8

RESULT 4
 ID 097025 PRELIMINARY; PRT; 17 AA.
 AC 097025;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE GLYERLADENYDE 3-PHOSPHATE DEHYDROGENASE (FRAGMENT).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 96273610.
 RA Nicolas M.G., Fujiki K., Murayama K., Suzuki M.T., Mineki R.,
 RA Hayakawa M., Yoshikawa Y., Cho F., Kanai A.:
 RT "Studies on the mechanism of early onset macular degeneration in
 cynomolgus (Macaca fascicularis) monkeys. I. Abnormal concentrations
 of two proteins in the retina."
 RL Exp. Eye Res. 62:211-219(1996).
 SQ SEQUENCE 17 AA; 1671 MW; 52CCD0D1A9B3B3DAF CRC64;

Query Match 23.5%; Score 24; DB 6; Length 17;
 Best Local Similarity 50.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 12 GRVYVGLH 19
 DB 1 GRVYGVN 8

RESULT 5
 ID 057012 PRELIMINARY; PRT; 19 AA.
 AC 057012;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE LEADER PEPTIDE.
 GN BRMA.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86135972.
 RA Murphy E., Huwyler L., De Freire Bastos M.D.C.;
 RT "Transposon Tn554: complete nucleotide sequence and isolation of
 transposition-defective and antibiotic-sensitive mutants."
 RL EMBO J. 4:3357-3365(1985).
 DR EMBL: X03216; CAA26965.1; -.
 SQ SEQUENCE 19 AA; 2257 MW; 19F81AD99E4F2F9B CRC64;

Query Match 23.5%; Score 24; DB 2; Length 19;
 Best Local Similarity 23.1%; Pred. No. 2.2e+03;
 Matches 3; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 4 GERAVMLGRVY 16
 DB 2 GTFSTFVINKVRY 14

RESULT 6
 ID 09S8G6 PRELIMINARY; PRT; 19 AA.
 AC 09S8G6;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE TYPE 2 LECTIN (FRAGMENT).
 OS Colocasia esculenta (Elephant's ear) (Taro).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
 OC Magnoliophyta; Liliopsida; Araceae; Colocasia.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 95288362.
 RA Van Damme E.J., Goossens K., Smeets K., van Leuven F., Verhaert P.,
 RA Peumans W.J.:
 RT "The major tuber storage protein of araceae species is a lectin.
 Characterization and molecular cloning of the lectin from Arum
 maculatum L."
 RL Plant Physiol. 107:1147-1158(1995).
 SQ SEQUENCE 19 AA; 2066 MW; F9C18865CA58608A CRC64;

Query Match 23.5%; Score 24; DB 10; Length 19;
 Best Local Similarity 40.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 8 VMLGRVYK 17
 DB 8 LTFSGVYXG 17

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:35:37 ; Search time 157.2 Seconds
(without alignments)
11.880 Million cell updates/sec

Title: US-08-934-367-7

Perfect score: 102
Sequence: 1 DVSGERAVMLGRVKYGLHN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPTRMBL_14:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	24.5	19	2	031045
2	25	24.5	19	5	09TWM7
3	24	23.5	9	4	015892
4	24	23.5	17	6	09T025
5	24	23.5	19	2	057012
6	24	23.5	19	10	09S8G6
7	24	23.5	10	5	09TWT8
8	23	22.5	17	5	025355
9	23	22.5	17	10	024445
10	23	22.5	19	2	053545
11	23	22.5	20	2	09R574
12	23	22.5	20	5	09TWM3
13	23	22.5	20	6	028734
14	22	21.6	8	3	005403
15	22	21.6	14	13	P70007
16	22	21.6	15	2	09R4P5
17	22	21.6	15	6	09T0Q5
18	22	21.6	19	2	09R4X3
19	22	21.6	20	6	09TRQ4

20	22	21.6	20	10	09S739	09S739 arabidopsis
21	21	20.6	8	2	09R4M3	09R4M3 enterococcu
22	21	20.6	14	2	060199	060199 escherichia
23	21	20.6	14	12	085718	085718 reovirus sp
24	21	20.6	15	3	09URC5	09URC5 saccharomyc
25	21	20.6	15	6	09TRR9	09TRR9 oryctolagus
26	21	20.6	15	12	079359	079359 human immun
27	21	20.6	15	12	097098	097098 human immun
28	21	20.6	17	4	09UD18	09UD18 homo sapien
29	21	20.6	17	10	09S8U7	09S8U7 solanum tub
30	21	20.6	17	11	088868	088868 mus muscula
31	21	20.6	17	11	09QX07	09QX07 mus muscula
32	21	20.6	19	2	09R2E7	09R2E7 escherichia
33	21	20.6	19	4	09UC73	09UC73 homo sapien
34	21	20.6	19	8	036277	036277 zea mays (m
35	21	20.6	19	11	09QXP9	09QXP9 mus musculi
36	21	20.6	19	12	084863	084863 unidentified
37	21	20.6	19	12	085671	085671 reovirus sp
38	21	20.6	20	2	034197	034197 rickettsia
39	21	20.6	20	2	09R9A5	09R9A5 nitrososplr
40	21	20.6	20	2	09R987	09R987 nitrososplr
41	21	20.6	20	12	085670	085670 reovirus sp
42	21	20.6	20	13	09RPR2	09RPR2 gallus gall
43	20	19.6	13	2	034770	034770 borrelia at
44	20	19.6	14	2	045876	045876 clostridium
45	20	19.6	15	10	P93515	P93515 arabidopsis

ALIGNMENTS

RESULT 1	031045	PRELIMINARY:	PRT:	19 AA.
ID	031045			
AC	031045			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DR	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-AUG-1998 (TREMBLrel. 07, Last annotation update)			
DE	LEUA LEADER PEPTIDE.			
GN	LEUA.			
OS	Streptomyces coelicolor.			
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;			
OC	Actinomycetales; Streptomyocinae; Streptomyocetaceae; Streptomyces.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-D132;			
RA	Potter C.A., Baumberg S.;			
RL	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF026444; AAB82585.1;			
SO	SEQUENCE 19 AA; 2080 MW; 1A591DC299760D4 CRC64;			

Query Match	24.5%	Score 25;	DB 2;	Length 19;
Best Local Similarity	44.4%	Pred. No. 1.3e+03;		
Matches 4;	Conservative	4;	Mismatches 1;	Indels 0;
Gaps	0;			

QY	10	LIIGRVKYL 18		
DB	1	MICIMRFL 9		

RESULT 2	09TWM7	PRELIMINARY:	PRT:	19 AA.
ID	09TWM7			
AC	09TWM7			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)			
DE	HAPTOGLOBIN-RELATED PROTEIN ALPHA SUBUNIT (FRAGMENT).			
OS	Trypanosoma brucei.			
OC	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.			
RN	[1]			
RP	SEQUENCE.			


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RP SEQUENCE FROM N.A.
RA STRAIN-ATCC 4359;
RC Wilson S.D., Wang M., Filipula D.;
RL Submitted (Feb-1994) to the EMBL/GenBank/DBJ databases
CC -1- FUNCTION: CATALYZES AN ELECTRONEUTRAL EXCHANGE BETWEEN ARGININE
CC AND ORNITHINE TO ALLOW HIGH-EFFICIENCY ENERGY CONVERSION IN THE
CC ARGININE DEIMINASE PATHWAY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
CC PERMASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U07185; AAA16963.1; -
KW Transport: Amino-acid transport; Transmembrane; Inner membrane.
FT NON_TER 1 1
SQ SEQUENCE 16 AA: 1644 MW: 90848A7C8F9A9705 CRC64;

Query Match 19.6%; Score 20; DB 1; Length 16;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 16 YGLHN 20
   |||:
Db 7 YGLVD 11

RESULT 14
PGK_VIBCH STANDARD: PRT: 16 AA.
ID PGK_VIBCH
AC P6154;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PHOSPHOGLYCERATE KINASE (EC 2.7.2.3) (FRAGMENT).
KW PGK.
OS Vibrrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OGAWA 395;
RX MEDLINE: 97136637.
RA Carroll P.A., Zhao G., Boyko S.A., Winkler M.E., Calderwood S.B.;
RT "Identification, sequencing, and enzymatic activity of the
RT erythrose-4-phosphate dehydrogenase gene of Vibrio cholerae.";
RL J. Bacteriol. 179:293-296(1997).
CC -1- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE = ADP +
CC 3-PHOSPHO-D-GLYCEROYL PHOSPHATE.
CC -1- PATHWAY: SECOND STEP IN THE SECOND PHASE OF GLYCOLYSIS.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U72152; AAC44768.1; -
DR INTERPRO: IPR001576; -
DR PROSITE: PS0011; GLYCERATE_KINASE; PARTIAL.
KW Transferase; Kinase; Glycolysis.

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FT NON_TER 16 16
SQ SEQUENCE 16 AA: 1789 MW: 6BEA715980B8E227 CRC64;

Query Match 19.6%; Score 20; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSGR 6
   |::|
Db 10 DIAGR 15

RESULT 15
COXO_ONCMY STANDARD: PRT: 20 AA.
ID COXO_ONCMY
AC P80335;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE VIII-LIVER/HEART (EC 1.9.3.1)
DE (FRAGMENT).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
RN [1]
RP SEQUENCE.
RC TISSUE=HEART, AND LIVER;
RX MEDLINE: 94237150.
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
CC 4 FERRICYTOCHROME C.
CC PIR: S43635; S43635.
DR Oxidoreductase; Mitochondrion.
KW NON_TER 20 20
FT SEQUENCE 20 AA: 2048 MW: 4977B9DE80B62C58 CRC64;

Query Match 19.6%; Score 20; DB 1; Length 20;
Best Local Similarity 42.9%; Pred. No. 2.8e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 GERAVML 10
   |||:
Db 13 GERATAM 19

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Search completed: December 21, 2000, 08:32:57
 Job time: 440 sec

CC -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -1- TISSUE SPECIFICITY: MIDGUT.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
CC Tachykinin; Neuropeptide; Amidation.
FW MOD.RES 19 19 AMIDATION.
SQ SEQUENCE 19 AA; 1930 MW; 99B5471A011625E5 CRC64;

Query Match 20.6%; Score 21; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 SCERA 7
DB 1 NGERA 5

RESULT 10
UP25.UPEIN STANDARD; PRT; 19 AA.
AC P82031;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE UPERIN 2.5.
OS Uperoleia inundata (Ploodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Uperoleia.
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RA TISSUE-SKIN SECRETION.
RA Bradford A.M., Rattery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
Adams G.W., Severini C.;
RT "Novel uperin peptides from the dorsal glands of the Australian
RT floodplain toadlet Uperoleia inundata.";
RL Aust. J. Chem. 49:475-484(1996).
CC -1- FUNCTION: SHOWS A MEDIUM ANTIBACTERIAL ACTIVITY AGAINST M. LUTUEUS.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=1940; METHOD=FMAB.
KW Amphibian skin; Antidiotic.
SQ SEQUENCE 19 AA; 1941 MW; 5E94C6C757B463D9 CRC64;

Query Match 20.6%; Score 21; DB 1; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 10 LIGRVR 15
DB 9 VLKIK 14

RESULT 11
COXO.THUOB STANDARD; PRT; 20 AA.
AC P80983;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE VII-1 (EC 1.9.3.1) (FRAGMENT);
OS Thunus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
RN [1]
RP SEQUENCE.
RA TISSUE=HEART, AND LIVER;
RX MEDLINE: 97454291.
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,

RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
CC 4 FERRICYTOCHROME C.
CC Oxidoreductase; Mitochondrion.
KW NON_TER 20
SQ SEQUENCE 20 AA; 1993 MW; 5BFEA5080A862C58 CRC64;

Query Match 20.6%; Score 21; DB 1; Length 20;
Best Local Similarity 37.5%; Pred. No. 1.9e+03;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 3 SCERAVWL 10
DB 12 AGEQAIAM 19

RESULT 12
AL16.CARMA STANDARD; PRT; 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE CARCINUS SPARTIN 16.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunidae; Portunidae; Carcinus.
RN [1]
RP SEQUENCE.
RA TISSUE=CEBRAL GANGLION, AND THORACIC GANGLION;
RX MEDLINE: 96121193.
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
CC Neuropeptide; Amidation; Multigene family.
FW MOD.RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match 19.6%; Score 20; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 8.8e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 12 GRVYGL 18
DB 2 GPYSTGL 8

RESULT 13
ARCD.PSEPU STANDARD; PRT; 16 AA.
AC P41147;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE ARGININE/ORNITHINE ANTIPORTER (FRAGMENT).
GN ARCD.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
RN [1]

1.

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TEMPORIN F.
 OS Rana temporaria (European common frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=SKIN;
 RX MEDLINE: 97175050.
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Bartra D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
 CC GRAM-POSITIVE BACTERIA.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAGURIN/RUGOSIN
 CC FAMILY.
 CC Amphibian skin; Antibiotic; Amidation; Multigene family.
 KW MOD RES 14 14 AMIDATION.
 FT SEQUENCE 14 AA: 1441 MW: 4D1653612B9DECC3 CRC64;
 SQ

Query Match 21.6%; Score 22; DB 1; Length 14;
 Best Local Similarity 44.4%; Pred. No. 9e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 4; Conservative 3;

OY 10 LIGRWYGL 18
 DB 4 LIGRWYGL 12

RESULT 7
 DSIP_RABIT STANDARD; PRT; 9 AA.
 ID DSIP_RABIT
 AC P01158;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE DELTA SLEEP-INDUCING PEPTIDE (DSIP).
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 77185324.
 RA Monnier M., Dudler L., Gachter R., Maier P.F., Tobler H.J.,
 RA Schoenenberger G.A.;
 RT "The delta sleep inducing peptide (DSIP). Comparative properties of
 RT the original and synthetic nonapeptide.";
 RL Experientia 33:548-552(1977).
 RN [2]
 RP SEQUENCE AND SYNTHESIS.
 RX MEDLINE: 79054421.
 RA Schoenenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.;
 RT "The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid
 RT analysis, sequence, synthesis and activity of the nonapeptide.";
 RL Pflügers Arch. 376:119-129(1978).
 CC -1- FUNCTION: WHEN INFUSED INTO THE MESODIENCEPHALIC VENTRICLE OF
 CC RECIPIENT RABBITS INDUCES SPINDLE AND DELTA EEG ACTIVITY AND
 CC REDUCED MOTOR ACTIVITIES.
 CC -1- MISCELLANEOUS: THIS PEPTIDE WAS OBTAINED FROM DIALYSATES OF
 CC OCCIPITAL VENOUS SINUS BLOOD FROM RABBITS KEPT ASLEEP BY ELECTRIC
 CC STIMULATION OF THE THALAMUS.
 RX PIR: A01422; ODRB.
 DR SEQUENCE 9 AA: 849 MW: DDD365BDDAA8787D CRC64;
 SQ

Query Match 20.6%; Score 21; DB 1; Length 9;
 Best Local Similarity 80.0%; Pred. No. 8.8e+04;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DVSGE 5
 DB 5 DASGE 9

RESULT 8
 PHLC-STAIN STANDARD; PRT; 19 AA.
 ID PHLC-STAIN
 AC P80924;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE SPHINGOMYELINASE C (EC 3.1.4.12) (BETA-TOXIN) (BETA-HEMOLYSIN)
 DE (NEUTRAL SPHINGOMYELINASE) (FRAGMENT).
 OS Staphylococcus intermedius.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/staphylococcus group; staphylococcus.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=94-072594;
 RX MEDLINE: 97072006.
 RA Dziwanowska K., Edwards V.M., Deringer J.R., Bohach G.A.,
 RA Guerra D.J.;
 RT "Comparison of the beta-toxins from Staphylococcus aureus and
 RT Staphylococcus intermedius.";
 RL Arch Biochem Biophys. 335:102-108(1996).
 CC -1- FUNCTION: REQUIRED. THE PH OPTIMUM IS 6.0-7.5. IT HAS A HIGH
 CC LYSIS (HEMOLYSIS).
 CC SPECIFICITY FOR SPHINGOMYELIN, HYDROLYZES LYSOPHOSPHATIDYLCHOLINE
 CC AT A MUCH LOWER RATE, BUT HAS NO ACTIVITY TOWARDS
 CC PHOSPHATIDYLCHOLINE, PHOSPHATIDYLETHANOLAMINE, OR
 CC PHOSPHATIDYLSERINE.
 CC -1- CATALYTIC ACTIVITY: SPHINGOMYELIN + H(2)O = N-ACYLSPHINGOSINE +
 CC CHOLINE PHOSPHATE.
 CC -1- COFACTOR: MAGNESIUM.
 CC -1- SUBUNIT: MONOMER.
 KW Hemolysis; Hydrolase; Toxin; Magnesium.
 FT NON TER 19 19
 SQ SEQUENCE 19 AA: 2089 MW: A50753FCF500F80E CRC64;

Query Match 20.6%; Score 21; DB 1; Length 19;
 Best Local Similarity 38.9%; Pred. No. 1.8e+03;
 Matches 7; Conservative 0; Mismatches 7; Indels 4; Gaps 1;

OY 3 SGERAVMLGRVYGLN 20
 DB 2 SGENAEL---KLATHN 15

RESULT 9
 TRP3_LEUMA STANDARD; PRT; 19 AA.
 ID TRP3_LEUMA
 AC P81735;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TACHYKININ-RELATED PEPTIDE 3 (LEMRP 3).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberoidea; Blaberidae; Leucophaea.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=MIDGUT;
 RX MEDLINE: 97053012.
 RA Muren J.E., Neessel D.R.;
 RT "Isolation of five tachykinin-related peptides from the midgut of
 RT the cockroach Leucophaea maderae: existence of N-terminally extended
 RT isoforms.";
 RL Regul. Pept. 65:185-196(1996).

"Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5.";
 RT Electrophoresis 19:802-806(1998).
 CC -1- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE = ADP + 3-PHOSHO-D-GLYCEROYL PHOSPHATE.
 CC -1- PATHWAY: SECOND STEP IN THE SECOND PHASE OF GLYCOLYSIS.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS: 5.6. ITS MW IS: 56.2 KDA.
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
 DR INTERPRO: IPR001576; -
 DR PROSITE: PS00111; PGLYCERATE_KINASE; PARTIAL.
 KW transferase; kinase; glycolysis.
 FT NON_TER 20
 SQ SEQUENCE 20 AA: 2355 MW: 749931E595C85529 CRC64;

Query Match 23.5%; Score 24; DB 1; Length 20;
 Best Local Similarity 44.4%; Pred. No. 66+02;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DVSGERAVM 9
 DB 11 DVKGRVLY 19

RESULT 3
 TAL3_PICJA STANDARD; PRT; 9 AA.
 AC P17441;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE TRANSALDOLASE III (EC 2.2.1.2) (FRAGMENT).
 OS Pichia jadinii (yeast) (Candida utilis).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 75145197.
 RA Tsolis O., Sun S.C.;
 RT "Isolation of a peptide containing a histidinyl-cysteiny sequence from the active center of transaldolase.";
 RL Arch. Biochem. Biophys. 167:525-533(1975).
 CC -1- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
 CC -1- CATALYTIC ACTIVITY: SEDOHEPTULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE 3-PHOSPHATE = D-ERYTHROSE 4-PHOSPHATE + D-FRUCTOSE 6-PHOSPHATE.
 CC -1- PATHWAY: NONOXIDATIVE PART OF THE PENTOSE-PHOSPHATE PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY.
 DR INTERPRO: IPR001585; -
 DR PIR: A11497; A11497.
 DR PROSITE: PS00958; TRANSALDOLASE_2; PARTIAL.
 DR PROSITE: PS01054; TRANSALDOLASE_1; PARTIAL.
 KW transferase; pentose shunt.
 FT NON_TER 1
 FT NON_TER 9
 SQ SEQUENCE 9 AA: 1033 MW: 325A31A44EB1E058 CRC64;

Query Match 22.5%; Score 23; DB 1; Length 9;
 Best Local Similarity 75.0%; Pred. No. 8.8e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 YGILH 19
 DB 1 YGILH 4

RESULT 4
 CRBL_VESOR STANDARD; PRT; 14 AA.
 ID CRBL_VESOR

AC P17236;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-AUG-1990 (Rel. 15, Last annotation update)
 DE HISTAMINE RELEASING PEPTIDE II (HR-II).
 OS Vespa orientalis (Oriental hornet).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=VENOM;
 RA Miroshnikov A.I., Snehkova L.G., Nazimov I.V., Reshetova O.I., Roznov B.V., Gushchin I.S.;
 RT "Structure and properties of histamine releasing peptides from the venom of Vespa orientalis hornet.";
 RL Bioorg. Khim. 7:1467-1477(1981).
 CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS OF NEUTROPHILS.
 DR PIR: JN0390; JN0390.
 DR MAST cell degranulation; Chemotaxis; Venom; Amidation.
 FT MOD_RES 14
 FT MOD_RES 14
 SQ SEQUENCE 14 AA: 1524 MW: 22015B4A6CEDFD38 CRC64;

Query Match 22.5%; Score 23; DB 1; Length 14;
 Best Local Similarity 40.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 9 MLGRVYKGL 18
 DB 4 ILGKLVKGL 13

RESULT 5
 CRBL_VESOR STANDARD; PRT; 13 AA.
 ID CRBL_VESOR
 AC P17231;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE VESPID CHEMOTACTIC PEPTIDE T (VESPCT-T).
 OS Vespa tropica (Hornet).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=VENOM;
 RA yasuhara T., Nakajima T., Erspaeer V.;
 RL (in) Sakakibara S. (eds.);
 RL Peptide chemistry 1982, pp.213-218. Protein Research Foundation, Osaka (1983).
 CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS OF NEUTROPHILS.
 CC MAST cell degranulation; Chemotaxis; Venom; Amidation.
 KW MOD_RES 13
 KW MOD_RES 13
 SQ SEQUENCE 13 AA: 1354 MW: 220140365DFE5338 CRC64;

Query Match 21.6%; Score 22; DB 1; Length 13;
 Best Local Similarity 44.4%; Pred. No. 8.4e+02;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 10 LGRVYKGL 18
 DB 4 ILGKLVKGL 12

RESULT 6
 TEMP_RANNE STANDARD; PRT; 14 AA.
 ID TEMP_RANNE
 AC P56921;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:32:56 ; Search time 62.7 Seconds
(without alignments)
10.191 Million cell updates/sec

Title: US-08-934-367-7

Perfect score: 102

Sequence: 1 DVSGERAVMLLGRVKYGLHN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	24.5	14	1	TEMA_RANTE
2	24	23.5	20	1	PGK_CLOPA
3	23	22.5	9	1	TAL3_PICJA
4	23	22.5	14	1	CRBL_VESOR
5	22	21.6	13	1	TEMF_RANTE
6	22	21.6	14	1	TEMF_RANTE
7	21	20.6	9	1	DSIP_RABIT
8	21	20.6	19	1	PHIC_STAIN
9	21	20.6	19	1	TRP3_LEUMA
10	21	20.6	19	1	UP25_UPEIN
11	21	20.6	20	1	COXO_THIOB
12	20	19.6	8	1	AL16_CARMA
13	20	19.6	16	1	ARCD_PSEPU
14	20	19.6	16	1	PGK_VIBCH
15	20	19.6	20	1	COXO_ONCMY
16	20	19.6	20	1	FIBR_PACLE
17	19.5	19.1	20	1	TRY8_ECOLI
18	19	18.6	8	1	AL17_CARMA
19	19	18.6	13	1	CRBL_VESMA
20	19	18.6	13	1	IDHC_PIG
21	19	18.6	14	1	DCMA_PSECF
22	19	18.6	14	1	TEMC_RANTE
23	19	18.6	14	1	UC18_MAIZE
24	19	18.6	15	1	LPL_THETH
25	19	18.6	15	1	URE1_MORMO
26	19	18.6	17	1	BOLA_MEGPE
27	19	18.6	18	1	LUXB_KRYAS
28	19	18.6	19	1	FIBA_BUBAR
29	19	18.6	20	1	KORC_METTM
30	19	18.6	20	1	LEC1_ARTIN
31	19	18.6	20	1	MDR_KIBAR
32	19	18.6	20	1	MDR_MTCGL
33	18	17.6	9	1	AL11_CARMA

34	18	17.6	9	1	TAL1_PICJA	P17440 pichia jadi
35	18	17.6	15	1	FIBA_SYNCA	P14463 syncerus ca
36	18	17.6	16	1	CPAB_BOVIN	P81187 bos taurus
37	18	17.6	17	1	NU4M_TRIRU	O36834 trichophyto
38	18	17.6	19	1	RS19_SPICI	O31159 spiriplasma
39	18	17.6	20	1	CUDE_VERCH	P80406 verticillu
40	18	17.6	20	1	SAMP_PLEPL	P20677 pleurosecte
41	17	16.7	10	1	GONI_ALIMI	P37041 alligator m
42	17	16.7	10	1	RL16_ACHLA	P29221 acholeplasm
43	17	16.7	10	1	TKNB_SCYCA	P06608 scylliorhinu
44	17	16.7	10	1	TKNB_RANCA	P22689 rana catesb
45	17	16.7	10	1	TKS1_AEDAE	P42634 aedes aegypt

ALIGNMENTS

RESULT 1

TEMA_RANTE STANDARD; PRT; 14 AA.

ID TEMA_RANTE

AC P56917;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE TEMPORIN A.

OS Rana temporaria (European common frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

RN [1]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=SKIN;

RX MEDLINE: 97175050.

RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,

RA Barra D.;

RT "temporins, antimicrobial peptides from the European red frog Rana

temporaria.";

RL Eur. J. Biochem. 242:788-792(1996).

CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE

BACTERIA.

CC -1- SUBCELLULAR LOCATION: SECRETED.

CC -1- SIMILARITY: BELONGS TO THE BREVITININ/ESCULENTIN/GAEGURIN/RUGOSIN

FAMILY.

CC Amphibian skin; Antibiotic; Amidation; Multigene family.

KW MOD_RES 14

FT MOD_RES 14

SO SEQUENCE 14 AA; 1469 MW; 601653612B9DECD4 CRC64;

Query Match

Best Local Similarity 24.5%; Score 25; DB 1; Length 14;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 10 ILGRVYGL 18

DB 4 LIGRLVSL 12

RESULT 2

PGK_CLOPA

AC P81346;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE PUTATIVE PHOSPHOGLYCERATE KINASE (EC 2.7.2.3) (CP 11) (FRAGMENT).

GN PGK.

OS Clostridium pasteurianum.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;

CC Clostridium.

RN [1]

RP SEQUENCE.

KC STRAIN=M5;

MD MEDLINE: 96291870.

RX Flenegrud R., Skjeldal L.;

Query Match 22.5%; Score 23; DB 2; Length 17;
 Best Local Similarity 57.1%; Pred. No. 1.7e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 11 LGRVXYG 17
 |||:|
 pb 11 LGRVYFG 17

RESULT 14

S58129
 hypothetical protein - moss (Ceratodon purpureus)
 C:Species: Ceratodon purpureus
 C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 31-Oct-1997
 C:Accession: S58129
 R:Hughes, J.; Miltmann, F.
 A:Description: The moss Ceratodon purpureus contains and expresses a second, conventional
 A:Reference number: S58129
 A:Accession: S58129
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-17 <HUG>
 A:Cross-references: GB:U56698; EMBL:X89725; NID:g1314836; PID:g1322246

Query Match 22.5%; Score 23; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 SCERAVMLLG 12
 |::|::|
 Db 6 STSRSLMIYV 15

RESULT 15

B43594
 fimbrial protein mrpa - Proteus mirabilis (fragment)
 C:Species: Proteus mirabilis
 C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
 C:Accession: B43594
 R:Bahrani, F.K.; Johnson, D.E.; Robbins, D.; Mobley, H.L.T.
 Infect. Immun. 59, 3574-3580, 1991
 A:Title: Proteus mirabilis flagella and MR/P fimbriae: isolation, purification, N-termi
 A:Reference number: A43594; MUID:91372967
 A:Accession: B43594
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <BAH>

Query Match 22.5%; Score 23; DB 2; Length 20;
 Best Local Similarity 33.3%; Pred. No. 2e+03;
 Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 3 SCERAVMLLGRV 14
 ||:|:|
 Db 2 SGDGITFTGKV 13

Search completed: December 21, 2000, 08:30:06
 Job time: 270 sec

C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match 23.5%; Score 24; DB 2; Length 20;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 VSGERAV 8
1:1111
Db 2 VNGENAV 8

RESULT 9

S65399
Immunodeficiency virus type 1, HIV-1 gp120 - human (fragments)
C:Species: Homo sapiens (man)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S65399
R:Nlwa, Y.; Yano, M.; Futaki, S.; Okumura, Y.; Kido, H.
Eur. J. Biochem. 237, 64-70, 1996
A:Title: T-cell membrane-associated serine protease, tryptase TL(2), binds human immunod
man immunodeficiency virus 1 inhibit cleavage of gp120.
A:Reference number: S65399; MUID:96203909
A:Accession: S65399
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10;11-20 <NIM>
C:Superfamily: type E retrovirus env polyprotein

Query Match 23.5%; Score 24; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 6 RAVMLGRV 14
1:1:111
Db 5 RAVVTIGRI 13

RESULT 10

A11497
transglutaminase (EC 2.2.1.2) III - yeast (Pichia jadinii) (fragment)
C:Species: Pichia jadinii, Candida utilis
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 30-Sep-1993
C:Accession: A11497
R:Tsolas, O.; Sun, S.C.
Arch. Biochem. Biophys. 167, 525-533, 1975
A:Title: Isolation of a peptide containing a histidyl-cysteiny sequence from the acti
A:Reference number: A11497; MUID:75145197
A:Accession: A11497
A:Molecule type: protein
A:Residues: 1-9 <TISO>
C:Keywords: transferase

Query Match 22.5%; Score 23; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 16 YGLH 19
1:1:1
Db 1 YGTH 4

RESULT 11

S26557
T-cell receptor beta chain (clone Cw3/HLA2A3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C:Accession: S26557
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wic
J. Exp. Med. 176, 439-447, 1992

A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recep
A:Reference number: S26512; MUID:92364546

A:Accession: S26557
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: EMBL:X68007
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/HLA2A3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 22.5%; Score 23; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 12 GRVXY 16
1:1:1
Db 6 GRVXY 10

RESULT 12

JN0390
histamine-releasing peptide II - oriental hornet
N:Alternate names: venom protein HR-2
C:Species: Vespa orientalis (oriental hornet)
C>Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 23-Aug-1997
C:Accession: JN0390; S10919
R:Miroshnikov, A.I.; Snezhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozinov, B.V.;
Biorog. Khim. 7, 1467-1477, 1981
A:Title: Structure and properties of histamine releasing peptides from the venom of V
A:Reference number: JN0389
A:Accession: JN0390
A:Molecule type: protein
A:Residues: 1-14 <MIR>
R:Tutubbaev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.
Biochemistry (N.Y.) 53, 183-190, 1988
A:Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis.
A:Reference number: S06445
A:Accession: S10919
A:Molecule type: protein
A:Residues: 1-14 <TRU>
C:Superfamily: crabrolin
C:Keywords: amidated carboxyl end; venom
F:14/Modified site: amidated carboxyl end (leu) #status experimental

Query Match 22.5%; Score 23; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 9 MLGRVYKYL 18
::1:1:1
Db 4 LILGKLVKGL 13

RESULT 13

PH1754
T cell receptor alpha chain V region (clone IV alpha 24-1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 17-Mar-1999
C:Accession: PH1754
R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balik, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral bio
A:Reference number: PH1754; MUID:93301585
A:Accession: PH1754
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-17 <POR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology

RESULT 3
B56899
serum heterodimer, 24k chain - sandbar shark (fragment)
C:Species: *Carcharias plumbeus* (sandbar shark)
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 20-Jun-2000
C:Accession: B56899
R:Vazquez-Moreno, L.; Porath, J.; Schluter, S.F.; Marchalonis, J.J.; Comp. Biochem. Physiol. B 103, 563-568, 1992
A:Title: Purification of a novel heterodimer from shark (*Carcharias plumbeus*) serum by A:Reference number: A56899; MUID:93092392
A:Accession: B56899
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <VAZ>
C:Keywords: glycoprotein; plasma

Query Match 23.5%; Score 24; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 VSGERAV 8
1 1 1 1 1
DB 2 VSGERAV 8

RESULT 4
S74147
glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - pig (fragment)
C:Species: *Sus scrofa domestica* (domestic pig)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C:Accession: S74147
R:Fukuda, A.; Osawa, T.; Hltonl, K.; Uchida, K.
Arch. Biochem. Biophys. 333, 419-426, 1996
A:Title: 4-Hydroxy-2-nonenal cytotoxicity in renal proximal tubular cells: protein modification
A:Reference number: S74147; MUID:96404942
A:Accession: S74147
A:Molecule type: protein
A:Residues: 1-10 <FUK>
A:Experimental source: LLC-PK1 cells (renal tubular epithelial cells)
C:Keywords: NAD; oxidoreductase

Query Match 23.5%; Score 24; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 12 GKVKYGLH 19
1 1 1 1 1 1 1 1 1 1 1 1 1
DB 1 GKVKYGLH 19

RESULT 5
P00025
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) - rice (strain Nihonbare) (fragment)
C:Species: *Oryza sativa* (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C:Accession: P00025
R:Tauglia, A.
submitted to JRPID, April 1993
A:Reference number: P00025
A:Accession: P00025
A:Molecule type: protein
A:Residues: 1-15 <TSU>
A:Experimental source: root
C:Keywords: oxidoreductase

Query Match 23.5%; Score 24; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 VSGERAV 8
1 1 1 1 1
DB 5 ISDERAV 11

RESULT 6
PH0779
T-cell receptor alpha chain (B83) - mouse (fragment)
C:Species: *Mus musculus* (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0779
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex allele exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:9207846
A:Accession: PH0779
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: EMBL:X60877
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 23.5%; Score 24; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 11 LGRVKYK 17
1 1 1 1 1
DB 9 LGRVHFC 15

RESULT 7
PH1455
T-cell receptor alpha chain (clone A24/PEF4) - mouse (fragment)
C:Species: *Mus musculus* (house mouse)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1455
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatibility complex superfamily: immunoglobulin homology
A:Reference number: PH1430; MUID:93171821
A:Accession: PH1455
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 23.5%; Score 24; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 11 LGRVKYK 17
1 1 1 1 1
DB 9 LGRVHFC 15

RESULT 8
B61333
chymotrypsin (EC 3.4.21.1) - edible frog (fragment)
C:Species: *Rana esculenta* (edible frog)
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C:Accession: B61333
R:Piles, W.; Zwilling, R.; Woodbury, R.G.; Neurath, H.
FEBS Lett. 109, 45-49, 1980
A:Title: Amino-terminal amino acid sequences and the evolution of frog (*Rana esculenta*)
A:Reference number: B61333; MUID:80113255
A:Accession: B61333
A:Molecule type: protein
A:Residues: 1-20 <PIE>

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:30:05 ; Search time 112.59 Seconds
(without alignments)
11.273 Million cell updates/sec

Title: US-08-934-367-7

Perfect score: 102

Sequence: 1 DVSGERAVMLGRVKYGLHN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 segs, 63460219 residues

Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	24.5	20	2	PH1338
2	24.5	24.0	15	2	PH0775
3	24	23.5	10	2	B56899
4	24	23.5	10	2	S74147
5	24	23.5	15	2	PU0025
6	24	23.5	15	2	PH0779
7	24	23.5	15	2	PH1455
8	24	23.5	20	2	B61333
9	24	23.5	20	2	S65399
10	23	22.5	9	2	A11497
11	23	22.5	12	2	S26557
12	23	22.5	14	2	JN0390
13	23	22.5	17	2	PH1754
14	23	22.5	17	2	S58129
15	23	22.5	20	2	B43594
16	22.5	22.1	15	2	PA0106
17	22	21.6	14	2	I51432
18	22	21.6	15	2	A27504
19	22	21.6	18	2	I52623
20	22	21.6	20	2	S32502
21	22	21.6	20	2	S10876
22	21	20.6	9	2	QDR8
23	21	20.6	12	2	S65629
24	21	20.6	15	2	A49887
25	21	20.6	16	2	S02455
26	21	20.6	16	2	S65709
27	21	20.6	16	2	PH1475
28	21	20.6	17	2	PH1802
29	21	20.6	17	2	S78421

ALIGNMENTS

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30      21      20.6      18      2      A39997      group III allergen
31      21      20.6      19      2      E49048      T-cell receptor be
32      21      20.6      20      2      S77991      cytochrome-c oxida
33      21      20.6      20      2      PH1358      Ig heavy chain DJ
34      21      20.6      20      2      S78419      ribosomal protein
35      20      19.6      12      2      A61332      Na+/K+-exchanging
36      20      19.6      12      2      PH1635      Ig H chain V-D-J r
37      20      19.6      13      2      PS0277      glyceraldehyde-3-P
38      20      19.6      13      2      PS0325      tetrahydropteridin
39      20      19.6      14      2      S58866      botulinum neurotox
40      20      19.6      15      2      A30330      neuropeptide pep -
41      20      19.6      16      2      S36876      aquacabalamine redu
42      20      19.6      18      2      S54272      CTC 75 protein - h
43      20      19.6      18      2      G42753      interferon alpha (
44      20      19.6      19      2      A39504      octamer-binding pr
45      20      19.6      20      2      F42762      multicatalytic end

```

```

RESULT 1
PH1338
Ig heavy chain DJ region (clone C372-115) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1338
R:Masserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor ly
A:Reference number: PH1302; MUID:93094761
A:Accession: PH1338
A:Molecule type: DNA
A:Residues: 1-20 <CAS>
C:Keywords: heterotetramer; immunoglobulin

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Query Match 24.5%, Score 25; DB 2; Length 20;
Best Local Similarity 30.0%; Pred. No. ge+02;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 8 VMLGRVRYG 17
DB 4 ILRLGLRLG 13

```

RESULT 2
PH0775
T-cell receptor alpha chain (B28) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0775
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility comple
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078646
A:Accession: PH0775
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: EMBL:X60871
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

```

Query Match 24.0%; Score 24.5; DB 2; Length 15;
Best Local Similarity 43.8%; Pred. No. 8.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

OY 2 VSGERAVMLGRVRYG 17
DB 3 LSGGSA--LGRHLFG 15

Query Match 28.4%; Score 29; DB 2; Length 16;
 Best Local Similarity 62.5%; Pred. No. 53;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 12 GRVRYGLH 19
 |||||
 Db 8 GRIKYTLN 15

RESULT 15

US-08-488-379-76
 ; Sequence 76, Application US/08488379
 ; Patent No. 5880103
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Urban
 ; APPLICANT: Roman M. Chicz
 ; APPLICANT: Dario A. A. Vignali
 ; APPLICANT: Mary L. Hedley
 ; APPLICANT: Lawrence J. Stern
 ; APPLICANT: Jack L. Strominger
 ; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
 ; NUMBER OF SEQUENCES: 274
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/488,379
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/077,255
 ; FILING DATE: June 15, 1993
 ; APPLICATION NUMBER: 07/925,460
 ; FILING DATE: August 11, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 00246/168001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 76:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-488-379-76

Query Match 28.4%; Score 29; DB 2; Length 16;
 Best Local Similarity 62.5%; Pred. No. 53;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 12 GRVRYGLH 19
 |||||
 Db 8 GRIKYTLN 15

Search completed: December 21, 2000, 08:31:47
 Job time: 370 sec

MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-488-379-77

Query Match 28.4% Score 29; DB 2; Length 15;
Best Local Similarity 62.5% Pred. No. 49;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 GRVKGGLH 19
11:1111:
DB 8 GRIKYTLN 15

RESULT 13
PCT-US93-07545-77
Sequence 77, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darlo A. A. Vignall
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-77

Query Match 28.4% Score 29; DB 4; Length 15;
Best Local Similarity 62.5% Pred. No. 49;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 GRVKGGLH 19
11:1111:
DB 8 GRIKYTLN 15

RESULT 14
US-08-480-190-76
Sequence 76, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darlo A. A. Vignall
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-76

; MOLECULE TYPE: peptide
US-08-164-618-20

Query Match 28.4%; Score 29; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 VKYGLHN 20
| | | | |
Db 8 VHYGTHN 14

RESULT 10
US-08-159-340A-17
; Sequence 17, Application US/08159340A
; Patent No. 5565352
; GENERAL INFORMATION:
; APPLICANT: Hochstrasser, Mark
; TITLE OF INVENTION: DEUBIQUITINATING ENZYME: COMPOSITIONS
; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,340A
; FILING DATE: 24-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:112/HYL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-340A-17

Query Match 28.4%; Score 29; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 VKYGLHN 20
| | | | |
Db 8 VHYGTHN 14

RESULT 11
US-08-480-190-77
; Sequence 77, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali

; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEEX: 200154
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-480-190-77

Query Match 28.4%; Score 29; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 49;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 GRVXYGLH 19
| | | | |
Db 8 GRIKYYTLN 15

RESULT 12
US-08-488-379-77
; Sequence 77, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:

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1 ADDRESS: Fish & Richardson
2 STREET: 225 Franklin Street
3 CITY: Boston
4 STATE: Massachusetts
5 COUNTRY: U.S.A.
6 ZIP: 02110-2804
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
10 COMPUTER: IBM PS/2 Model 502 or 55SX
11 OPERATING SYSTEM: MS-DOS (Version 5.0)
12 SOFTWARE: Wordperfect (Version 5.1)
13
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/488,379
16 FILING DATE:
17 CLASSIFICATION: 514
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: 08/077,255
20 FILING DATE: June 15, 1993
21 APPLICATION NUMBER: 07/925,460
22 FILING DATE: August 11, 1992
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Clark, Paul T.
25 REGISTRATION NUMBER: 30,162
26 REFERENCE/DOCKET NUMBER: 00246/168001
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (617) 542-5070
29 TELEFAX: (617) 542-8906
30
31 INFORMATION FOR SEQ ID NO: 53:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 20
34 TYPE: amino acid
35 STRANDEDNESS:
36 TOPOLOGY: linear
37
38 US-08-488-379-53
39
40 Query Match 29.4%; Score 30; DB 2; Length 20;
41 Best Local Similarity 61.5%; Pred. NO. 45;
42 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
43
44 Db 1 DVSGERAVMLGR 13
45 1 DVGERRAVTELGR 13
46
47 RESULT 8
48 PCT-US93-07545-53
49 Sequence 53, Application PC/TUS9307545
50 GENERAL INFORMATION:
51 APPLICANT: Robert G. Urban
52 APPLICANT: Roman M. Chicz
53 APPLICANT: Darlo A. A. Vignall
54 APPLICANT: Mary L. Hedley
55 APPLICANT: Lawrence J. Stern
56 APPLICANT: Jack L. Strominger
57 TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
58 NUMBER OF SEQUENCES: 273
59 CORRESPONDENCE ADDRESS:
60 ADDRESSEE: Fish & Richardson
61 STREET: 225 Franklin Street
62 CITY: Boston
63 STATE: Massachusetts
64 COUNTRY: U.S.A.
65 ZIP: 02110-2804
66
67 COMPUTER READABLE FORM:
68 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
69 COMPUTER: IBM PS/2 Model 502 or 55SX
70 OPERATING SYSTEM: MS-DOS (Version 5.1)
71 SOFTWARE: Wordperfect (Version 5.1)
72 CURRENT APPLICATION DATA:
73 APPLICATION NUMBER: PCT/US93/07545
74 FILING DATE: 19930811

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SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-21
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Query Match 29.4%; Score 30; DB 4; Length 19;
Best Local Similarity 61.5%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 DVSGERAVMLLGR 13
    |||||
Db 1 DVGEYRAVTELGR 13
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RESULT 5
PCT-US96-09303-21
Sequence 21, Application PC/TUS9609303
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES OF PROSTATE
NUMBER OF INVENTION: SPECIFIC ANTIGEN
NUMBER OF SEQUENCES: 22
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09303
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,228
FILING DATE: 07-JUN-1995
INFORMATION FOR SEQ. ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US96-09303-21
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Query Match 29.4%; Score 30; DB 4; Length 19;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 6 RAVMLLGR 13
    |:|:|
Db 10 RSVLLGR 17
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RESULT 6

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US-08-480-190-53
Sequence 53, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-53
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Query Match 29.4%; Score 30; DB 2; Length 20;
Best Local Similarity 61.5%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 DVSGERAVMLLGR 13
    |||||
Db 1 DVGEYRAVTELGR 13
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```
RESULT 7
US-08-488-379-53
Sequence 53, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
```

Db 10 RSVILGR 17

RESULT 2

US-08-480-190-21

Sequence 21, Application US/08480190

Patent No. 5827516

GENERAL INFORMATION:

APPLICANT: Robert G. Urban

APPLICANT: Roman M. Chicz

APPLICANT: Dario A. A. Vignali

APPLICANT: Mary L. Hedley

APPLICANT: Lawrence J. Stern

APPLICANT: Jack L. Strominger

TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES

NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 555X

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,190

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/077,255

FILING DATE: June 15, 1993

APPLICATION NUMBER: 07/925,460

FILING DATE: August 11, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00246/168001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ. ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 19

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-480-190-21

Query Match 29.4%; Score 30; DB 2; Length 19;

Best Local Similarity 61.5%; Pred. No. 42;

Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DVSGEYRAVTELGR 13

Db 1 DVGEYRAVTELGR 13

RESULT 3

US-08-488-379-21

Sequence 21, Application US/08488379

Patent No. 5860103

GENERAL INFORMATION:

APPLICANT: Robert G. Urban

APPLICANT: Roman M. Chicz

APPLICANT: Dario A. A. Vignali

APPLICANT: Mary L. Hedley

APPLICANT: Lawrence J. Stern

RESULT 4

PCT-US93-07545-21

Sequence 21, Application PC/TUS9307545

GENERAL INFORMATION:

APPLICANT: Robert G. Urban

APPLICANT: Roman M. Chicz

APPLICANT: Dario A. A. Vignali

APPLICANT: Mary L. Hedley

APPLICANT: Lawrence J. Stern

APPLICANT: Jack L. Strominger

TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 555X

OPERATING SYSTEM: MS-DOS (Version 5.0)

US-08-488-379-21

Query Match 29.4%; Score 30; DB 2; Length 19;

Best Local Similarity 61.5%; Pred. No. 42;

Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DVSGEYRAVTELGR 13

Db 1 DVGEYRAVTELGR 13

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2000, 08:31:46 ; Search time 99.91 Seconds
(without alignments)
3.355 Million cell updates/sec

Title: US-08-934-367-7
Perfect score: 102
Sequence: 1 DVSGERAVMLGRVKYGLIN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 1676186 residues

Total number of hits satisfying chosen parameters: 87906

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA: *
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
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4: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	30	29.4	19	1	US-08-472-228A-21
2	30	29.4	19	2	US-08-480-190-21
3	30	29.4	19	2	US-08-488-379-21
4	30	29.4	19	4	PCT-US93-07545-21
5	30	29.4	19	4	PCT-US96-09303-21
6	30	29.4	20	2	US-08-480-190-53
7	30	29.4	20	2	US-08-488-379-53
8	30	29.4	20	4	PCT-US93-07545-53
9	29	28.4	12	1	US-08-164-618-20
10	29	28.4	14	1	US-08-159-340A-17
11	29	28.4	15	2	US-08-480-190-77
12	29	28.4	15	2	US-08-488-379-77
13	29	28.4	15	4	PCT-US93-07545-77
14	29	28.4	16	2	US-08-480-190-76
15	29	28.4	16	2	US-08-488-379-76
16	29	28.4	16	4	PCT-US93-07545-76
17	29	28.4	18	2	US-08-480-190-192
18	29	28.4	18	2	US-08-488-379-192
19	29	28.4	18	4	PCT-US93-07545-192
20	29	28.4	19	2	US-08-480-190-74
21	29	28.4	19	2	US-08-480-190-75
22	29	28.4	19	2	US-08-488-379-74
23	29	28.4	19	2	US-08-488-379-75
24	29	28.4	19	4	PCT-US93-07545-74
25	29	28.4	19	4	PCT-US93-07545-75
26	29	28.4	20	2	US-08-480-190-191
27	29	28.4	20	2	US-08-749-852-55
28	29	28.4	20	2	US-08-488-379-191

29	29	28.4	20	4	PCT-US93-07545-191	Sequence 191, App
30	28	27.5	15	1	US-08-625-691-1	Sequence 1, Appl
31	28	27.5	17	2	US-08-480-190-193	Sequence 193, App
32	28	27.5	17	2	US-08-488-379-193	Sequence 193, App
33	28	27.5	17	4	PCT-US93-07545-193	Sequence 193, App
34	27	26.5	13	4	PCT-US93-06751-102	Sequence 102, App
35	27	26.5	19	3	US-08-792-832A-60	Sequence 60, Appl
36	26	25.5	16	2	US-08-934-222-60	Sequence 60, Appl
37	26	25.5	16	2	US-08-933-402-60	Sequence 60, Appl
38	26	25.5	16	2	US-09-207-621-60	Sequence 60, Appl
39	26	25.5	16	2	US-08-532-818-60	Sequence 60, Appl
40	26	25.5	16	3	US-09-231-797-60	Sequence 60, Appl
41	26	25.5	16	3	US-08-934-224-60	Sequence 60, Appl
42	26	25.5	16	3	US-08-933-843-60	Sequence 60, Appl
43	26	25.5	19	3	US-08-792-832A-34	Sequence 34, Appl
44	25.5	25.0	20	1	US-08-218-025A-8	Sequence 8, Appl
45	25	24.5	17	1	US-07-894-212A-3	Sequence 3, Appl

ALIGNMENTS

```

RESULT 1
US-08-472-228A-21
; Sequence 21, Application US/08472228A
; Patent No. 5807978
; GENERAL INFORMATION:
; APPLICANT: Kokolus, William J.
; APPLICANT: Fritsche, Herbert A.
; APPLICANT: Johnston, Dennis A.
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES OF PROSTATE
; NUMBER OF INVENTION: SPECIFIC ANTIGEN
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08472,228A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSC:388
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-472-228A-21

Query Match 29.4%; Score 30; DB 1; Length 19;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
I:|:|||||
QY 6 RAYMLGR 13

```



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RESULT 7
Q9TR9 PRELIMINARY; PRT; 17 AA.
AC Q9TR9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CYTOCHROME-C REDUCTASE 55 KDA SUBUNIT (EC 1.10.2.2) (FRAGMENT).
OS Solanum tuberosum (Potato).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
OC Solanaceae; Solanum.
RN [1]
RP SEQUENCE.
RA Braun H.P., Kruff V., Schmitz U.K.;
RL Planta 193:99-106(1994).
SQ SEQUENCE 17 AA; 1758 MW; F95F7BF7940F5F21 CRC64;

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Query Match 23.9%; Score 26; DB 8; Length 17;
Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 LLLHLOG 7
|:|:|
Db 4 LMLHIDG 10

```

```

RESULT 8
Q9UCG3 PRELIMINARY; PRT; 19 AA.
ID Q9UCG3;
AC Q9UCG3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE ALPHA 2-PLASMIN INHIBITOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE.
RA MEDLINE; 93249387.
RA Bangert K., Johnsen A.H., Christensen U., Thorsen S.;
RT "Different N-terminal forms of alpha 2-plasmin inhibitor in human
RT plasma."
RL Biochem. J. 291:623-625(1993).
SQ SEQUENCE 19 AA; 2065 MW; 41352BF04D1EEA9 CRC64;

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Query Match 23.4%; Score 25.5; DB 4; Length 19;
Best Local Similarity 63.6%; Pred. No. 1.6e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

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QY 2 LMLHLOG 12
|:|:|
Db 10 LKL-GMOEPG 19

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RESULT 9
Q16045 PRELIMINARY; PRT; 14 AA.
ID Q16045;
AC Q16045;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE D3 DOPAMINE RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.

```

```

RX MEDLINE; 93326145.
RA Nagai Y., Ueno S., Saeki Y., Soga F., Yanagihara T.;
RT "Expression of the D3 dopamine receptor gene and a novel variant
RT transcript generated by alternative splicing in human peripheral blood
RT lymphocytes."
RL Biochem. Biophys. Res. Commun. 194:368-374(1993).
DR EMBL; S63845; CAB32270.1; -.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1586 MW; EA310BFE94CF1B1 CRC64;

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Query Match 22.9%; Score 25; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 LLLHLOG 6
|:|:|
Db 9 LMLHLOG 13

```

```

RESULT 10
Q9RSF6 PRELIMINARY; PRT; 18 AA.
ID Q9RSF6;
AC Q9RSF6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE UREASE SMALL SUBUNIT (FRAGMENT).
OS Helicobacter mustelae.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE.
RX MEDLINE; 93084378.
RA Turbett G.R., Hoj P.B., Horne R., Mee B.J.;
RT "Purification and characterization of the urease enzymes of
RT Helicobacter species from humans and animals."
RL Infect. Immun. 60:5259-5266(1992).
SQ SEQUENCE 18 AA; 2060 MW; 29C8E0AB7E21805 CRC64;

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Query Match 22.9%; Score 25; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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```

QY 1 LLLHLOG 8
|:|:|
Db 9 LMLHYAGE 16

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```

RESULT 11
Q9UC87 PRELIMINARY; PRT; 18 AA.
ID Q9UC87;
AC Q9UC87;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 31 KDA EXTRACELLULAR MATRIX-ASSOCIATED SERINE PROTEINASE INHIBITOR
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 95177668.
RA Rao C.N., Liu Y.Y., Peavey C.L., Woodley D.T.;
RT "Novel extracellular matrix-associated serine proteinase inhibitors
RT from human skin fibroblasts."
RL Arch. Biochem. Biophys. 317:311-314(1995).
SQ SEQUENCE 18 AA; 1968 MW; BA65E727DB150CD6 CRC64;

```

RN [1]
RP SEQUENCE:
RX MEDLINE: 95337087.
RA Thulin C.D., Walsh K.A.;
RT Identification of the amino terminus of human filaggrin using
RT differential LC/MS techniques: implications for profilaggrin
RT processing.";
RL Biochemistry 34:8687-8692(1995).
SQ SEQUENCE 20 AA; 2199 MW; 0FD0856B199AB332 CRC64;

Query Match 26.6%; Score 29; DB 4; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 4 HUGEREPCW 13
DB 5 HEQSESHGW 14

RESULT 3
O9PRJ4 PRELIMINARY; PRT; 9 AA.
AC O9PRJ4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE BRADYKININ.
OS Lepistosteus osseus (long-nosed gar), and Amia calva (bowfin).
OC Eukaryota; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Semionotiformes; Lepistosteidae;
RN [1]
RP SEQUENCE:
RX MEDLINE: 95380361.
RA Conlon J.M., Platack B., Maria L.E., Youson J.H., Olson K.R.;
RT "Isolation and biological activity of [Trp5]bradykinin from the plasma
RT of the phylogenetically ancient fish, the bowfin and the longnosed
RT gar.";
RL Peptides 16:485-489(1995).
SQ SEQUENCE 9 AA; 1099 MW; 3393D775A3786777 CRC64;

Query Match 25.7%; Score 28; DB 13; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 REKGV 13
DB 1 RPPGW 5

RESULT 4
O18502 PRELIMINARY; PRT; 14 AA.
AC O18502;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE LYSOPHOSPHOLIPASE HOMOLOG (FRAGMENT).
GN SMPPLH
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeididae;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-EGYPTIAN:
RA Hamdan F.F., Ribeiro P.;
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF006679; AAC62255.1; -;
FT NON_TER 14
SQ SEQUENCE 14 AA; 1541 MW; 48B847C2E5D89177 CRC64;

Query Match 25.7%; Score 28; DB 5; Length 14;
Best Local Similarity 38.5%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 LLLHLOGERPCW 13
DB 2 IFLHGLDGTGHW 14

RESULT 5
O9R4W5 PRELIMINARY; PRT; 20 AA.
AC O9R4W5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 30 KDA MAJOR HEAT SHOCK PROTEIN (FRAGMENT).
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE:
RX MEDLINE: 95020803.
RA Yokota K., Hirai Y., Haque M., Hayashi S., Isogai H., Sugiyama T.,
RA Nagamachi E., Tsukada Y., Fujii N., Oguma K.;
RT "Heat shock protein produced by Helicobacter pylori.";
RL Microbiol. Immunol. 38:403-405(1994).
DR INTERPRO: IPR002026; -;
DR PFAM: PF00547; urease_gamma; 1.
SQ SEQUENCE 20 AA; 2302 MW; 29C9DFBFD6D21805 CRC64;

Query Match 24.8%; Score 27; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LLLHLOGE 8
DB 11 LMLHVLAGE 18

RESULT 6
O9X3I3 PRELIMINARY; PRT; 17 AA.
AC O9X3I3;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE CYTOCHROME B (FRAGMENT).
GN PETB.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL: AF070176; MMD20791.1; -;
FT NON_TER 1
SQ SEQUENCE 17 AA; 1953 MW; 630843039AD51B4 CRC64;

Query Match 23.9%; Score 26; DB 2; Length 17;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 LLLHLOGERPCW 12
DB 1 LMLHVLXDRKOG 12

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:35:36 ; Search time 157.2 Seconds

(without alignments)
11.880 Million cell updates/sec

Title: US-08-934-367-6

Perfect score: 109

Sequence: 1 LLLHLQGEREPGMLKQLFTN 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

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2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_mammal:*
9: sp_organelle:*
10: sp_phase:*
11: sp_plant:*
12: sp_protist:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	26.6	10	13	Q9PRZ1 oncorhynchu
2	29	26.6	20	4	Q9UC71 homo sapien
3	28	25.7	9	13	Q9PRJ4 lepisosteus
4	28	25.7	14	5	Q18502 schistosoma
5	27	24.8	20	2	Q9R4W5 helicobacte
6	26	23.9	17	2	Q9X313 prochloroco
7	26	23.9	17	8	Q9T2R9 solanum tub
8	25.5	23.4	19	4	Q9UCG3 homo sapien
9	25	22.9	18	4	Q9R5F6 helicobacte
10	25	22.9	18	4	Q9UC87 homo sapien
11	25	22.9	19	2	Q44850 borrelia bu
12	25	22.9	19	4	Q9UCJ18 homo sapien
13	25	22.9	19	8	Q9YJW2 dolopsidea
14	24	22.0	11	7	Q77893 oreochromis
15	24	22.0	12	12	Q12068 caprine art
16	24	22.0	12	12	Q12074 caprine art
17	24	22.0	12	12	Q12076 caprine art
18	24	22.0	12	12	Q12076 caprine art
19	24	22.0	12	12	Q12078 caprine art

20	24	22.0	12	12	Q12080 caprine art
21	24	22.0	12	12	Q12082 caprine art
22	24	22.0	12	12	Q12084 caprine art
23	24	22.0	12	12	Q12086 caprine art
24	24	22.0	12	12	Q12090 caprine art
25	24	22.0	12	12	Q12092 caprine art
26	24	22.0	12	12	Q12094 caprine art
27	24	22.0	12	12	Q12106 caprine art
28	24	22.0	12	12	Q12108 caprine art
29	24	22.0	12	12	Q12110 caprine art
30	24	22.0	12	12	Q12112 caprine art
31	24	22.0	12	12	Q12114 caprine art
32	24	22.0	12	12	Q12116 caprine art
33	24	22.0	12	12	Q12118 caprine art
34	24	22.0	15	2	Q46963 escherichia
35	24	22.0	15	2	Q9R4U7 acinetobact
36	24	22.0	16	4	Q9UCX9 homo sapien
37	24	22.0	16	4	Q9UCH1 homo sapien
38	24	22.0	19	2	Q47079 escherichia
39	24	22.0	19	10	Q9S8W5 avena sativa
40	24	22.0	20	10	Q9S930 glycine max
41	23	21.1	11	5	Q9V7K6 drosophila
42	23	21.1	13	4	Q9Y674 homo sapien
43	23	21.1	18	13	Q9PRM7 xenopus. ac
44	23	21.1	19	10	Q40183 lemna gibba
45	22.5	20.6	20	2	Q9R4A6 g9r4a6 hydrogenoba

ALIGNMENTS

RESULT 1
Q9PRZ1 PRELIMINARY; PRT; 10 AA.

ID Q9PRZ1
AC Q9PRZ1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE LYSYL-BRADYKININ-VASOACTIVE PEPTIDE KALIDIN HOMOLOG.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proleacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
RN [1]
RP
RX MEDLINE: 94039817.
RA Conlon J.M., Olson K.R.:
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
trout plasma."
RL FEBS Lett. 334:75-78(1993).
SQ SEQUENCE 10 AA: 1193 MW: 33C59075A3786777 CRC64;

Query Match 26.6%; Score 29; DB 13; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 EREPGW 13
: |||
Db 1 KRPGW 6

RESULT 2
Q9UC71 PRELIMINARY; PRT; 20 AA.
ID Q9UC71:
AC Q9UC71:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE FLAGGRIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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Search completed: December 21, 2000, 08:32:56
Job time: 439 sec

RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
 RA Naboriak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
 RT "distinct sequence of gonadotropin-releasing hormone (GnRH) in
 RT dogfish brain provides insight into GnRH evolution.",
 RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).
 CC -1- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.
 CC -1- SIMILARITY: BELONGS TO THE GnRH FAMILY.
 DR INTERPRO: IPR002012;
 DR PFM: PF00446; GNRH: 1.
 DR PROSITE: PS00473; GNRH: 1.
 KM Hormone; Amidation; Hypothalamus.
 FT MOD_RES 1
 FT MOD_RES 1
 FT MOD_RES 1
 SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;

Query Match 19.3%; Score 21; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 GWL 14
 Db 6 GWL 8

RESULT 13
 020G_COMTE STANDARD; PRT; 10 AA.
 ID P80466;
 AC 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE QUINOLINE 2-OXIDOREDUCTASE, GAMMA CHAIN (EC 1.-.-.-) (FRAGMENT).
 OS Comamonas testosteroni (Pseudomonas testosteroni).
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-63;
 RX MEDLINE: 96035889.
 RA Schach S., Tshisuka B., Fetzner S., Lingens F.;
 RT "Quinolone 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
 RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
 RT quinoline and 3-methylquinoline degradation.",
 RL Eur. J. Biochem. 232:536-544(1995).
 CC -1- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-
 CC 1,2-DIHYDROQUINOLINE.
 CC -1- COFACTOR: FAD AND MOLYBDENUM.
 CC -1- PATHWAY: FIRST STEP IN THE DEGRADATION OF QUINOLINE AND
 CC (3-METHYL-)-QUINOLINE.
 CC -1- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
 CC TWO GAMMA CHAINS (PROBABLE).
 CC Oxidoreductase; Flavoprotein; FAD; Molybdenum.
 KM NON_TER 10
 KM NON_TER 10
 SQ SEQUENCE 10 AA; 1153 MW; C84BCE64433BDC6 CRC64;

Query Match 19.3%; Score 21; DB 1; Length 10;
 Best Local Similarity 42.9%; Pred. No. 9.8e+02;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 LOGREP 11
 Db 2 IQAEKNP 8

RESULT 14
 CXET_COMTE STANDARD; PRT; 13 AA.
 ID P81755;
 AC 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE EPSILON-CONOTOXIN TXIX.

OS Conus textile (cloth-of-gold cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 RN [1]
 RP SEQUENCE, CARBOHYDRATE-LINKAGE SITE THR-10, AND STRUCTURE BY NMR.
 RC TISSUE-VENOM;
 RX MEDLINE: 99254114.
 RA Rigby A.C., Lucas-Meunier E., Kalume D.E., Czerwlec E., Hambe B.,
 RA Dahlqvist I., Fossier P., Baux G., Roepstorff P., Balleja J.D.,
 RA Furler B.C., Furler B., Stenflo J.P.;
 RT "A conotoxin from Conus textile with unusual posttranslational
 RT modifications reduces presynaptic Ca2+ influx".
 RL Proc. Natl. Acad. Sci. U.S.A. 96:5758-5763(1999).
 CC -1- FUNCTION: CONOTOXIN WHICH ACTS AT PRESYNAPTIC MEMBRANES, BLOCKING
 CC THE CALCIUM CHANNELS.
 CC -1- PTM: O-GLYCAN CONSISTS OF THE DISACCHARIDE GAL-GALINAC.
 DR PDB: 1WCT; 08-JUN-99.
 DR Presynaptic neurotoxin; Calcium channel inhibitor; Venom; Vitamin K;
 KW Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Bromination;
 KW 3D-structure.
 FT DISULFD 2 8
 FT DISULFD 3 9
 FT MOD_RES 1 1
 FT MOD_RES 4 4
 FT MOD_RES 7 7
 FT MOD_RES 13 13
 FT CARBOHYD 10 10
 FT SEQUENCE 13 AA; 1388 MW; 386C9E1C74AFA378 CRC64;

Query Match 19.3%; Score 21; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 EPGW 13
 Db 4 EDDGW 7

RESULT 15
 FARB_ASCSU STANDARD; PRT; 13 AA.
 ID FARB_ASCSU
 AC P43173;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRFAMIDE-LIKE NEUROPEPTIDE AF11.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
 CC Ascarididae; Ascaris.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 95380362.
 RA Cowden C., Stretton A.O.W.;
 RT "Eligible novel FMRFamide-like neuropeptides isolated from the nematode
 RT Ascaris suum".
 RL Peptides 16:491-500(1995).
 CC -1- SIMILARITY: BELONGS TO THE FARF (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 KM MOD_RES 13
 KM MOD_RES 13
 SQ SEQUENCE 13 AA; 1495 MW; 9CAEC650D686B05 CRC64;

Query Match 19.3%; Score 21; DB 1; Length 13;
 Best Local Similarity 44.4%; Pred. No. 1.3e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 GERPEGWK 15
 Db 4 GISEPNFLR 12

CC -1- FUNCTION: SMOOTH MUSCLE CONTRACTION.
 KM Bradykinin; Vasodilator.
 FT MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA; 1573 MW; 2673CB3DB3ECC867 CRC64;

Query Match 20.2%; Score 22; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 9e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 QGEREPGW 13
 1 1 1 1 1 1
 DB 1 QZKRPGF 8

RESULT 9
 HPAL_RANES STANDARD; PRT; 13 AA.
 AC P32415;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE HEMOLYTIC PROTEIN A1 (FRAGMENT).
 OS Rana esculenta (Edible frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 [1]
 RP SEQUENCE.
 RC TISSUE-SKIN SECRETION;
 RX MEDLINE; 90198965.

RA Simmaco M., de Blase D., Severini C., Alta M., Erspamer G.F.,
 Barra D., Bossa F.;
 RT "Purification and characterization of bioactive peptides from skin
 extracts of Rana esculenta."
 RL Biochim. Biophys. Acta 1033:318-323(1990).
 CC -1- FUNCTION: SHOWS HEMOLYTIC ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- TISSUE SPECIFICITY: SKIN.
 DR PIR: S09018; S09018.
 KW Amphibian skin; Amidation; Hemolysis.
 FT MOD.RES 13 13 AMIDATION.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1390 MW; C6BA768B9DFE587D CRC64;

Query Match 20.2%; Score 22; DB 1; Length 13;
 Best Local Similarity 71.4%; Pred. No. 9e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 12 GWLKOLF 18
 1 1 1 1 1 1
 DB 7 GILSOLF 13

RESULT 10
 NEUT_CHICK STANDARD; PRT; 13 AA.
 AC P13724;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE NEUTROTENSIN (NT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 88063566.
 RA Iwabuchi H., Komori S., Ohashi H., Kimura S.;
 RT "The amino acid sequence of a smooth muscle-contracting peptide from
 chicken rectum. Identity to chicken neotensin.";
 RL Jpn. J. Pharmacol. 44:455-459(1987).

CC -1- FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE.
 DR PIR: A28505; A28505.
 KM Vasodilator.
 FT MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA; 1608 MW; 4C949E71AC410DD3 CRC64;

Query Match 20.2%; Score 22; DB 1; Length 13;
 Best Local Similarity 44.4%; Pred. No. 9e+02;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 LHLQGEREP 11
 1 1 1 1 1 1
 DB 2 LHVNKARP 10

RESULT 11
 GON3_ONCKE STANDARD; PRT; 10 AA.
 AC P20367;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GONADOLIBERIN III (GONADOTROPIN-RELEASING HORMONE III) (GNRH-III) (LH-
 RH III) (LULIBERIN III).
 OS Oncorhynchus keta (Chum salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 83195140.

RA Sherwood N., Elden L., Brownstein M., Spiess J., Rivier J., Vale W.;
 RT "Characterization of a teleost gonadotropin-releasing hormone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
 CC -1- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND
 CC -1- FOLLICLE-STIMULATING HORMONES.
 CC -1- SIMILARITY: BELONGS TO THE GNRH FAMILY.
 DR PIR: A21114; A21114.
 DR INTERPRO: IPR002012;
 DR PFAM: PF00446; GNRH; 1.
 DR PROSITE: PS00473; GNRH; 1.
 KW Hormone; Amidation; Hypothalamus.
 FT MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD.RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;

Query Match 19.3%; Score 21; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 GWL 14
 1 1 1 1 1 1
 DB 6 GWL 8

RESULT 12
 GONL_SQUAC STANDARD; PRT; 10 AA.
 AC P27429;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GONADOLIBERIN (GONADOTROPIN-RELEASING HORMONE) (GNRH) (LH-RH)
 DE (LULIBERIN).
 OS Squallus acanthias (Spiny dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalae; Squaloidae; Squalidae; Squallus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-BRAIN;
 RX MEDLINE; 92335300.

DE (DCC II).
 OS Tabanus atratus (Horse fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
 OC Tabanidae; Tabanus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-CORPORA CARDIACA;
 RX MEDLINE: 90046758.
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH OF INSECTS).
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: B33995; B33995.
 DR INTERPRO: IPR002047; -.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;

Query Match 22.0%; Score 24; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PGW 13
 Db 6 PGW 8

RESULT 6
 AROO_AMEYE STANDARD; PRT; 20 AA.
 ID AROO_AMEYE
 AC P46380;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 32, Last annotation update)
 DE 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10) (3-DEHYDROQUINASE)
 DE (TYPE II DHOASE) (FRAGMENT).
 GN AROO.
 OS Amycolatopsis methanolica.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Pseudonocardiales; Pseudonocardiaceae;
 OC Amycolatopsis.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIB 11946;
 RX MEDLINE: 93123995.
 RA Eversink G.J.W., Hessels G.I., Vrijbloed J.W., Cogging J.R.,
 RA Dijkhuizen L.;
 RT "Purification and characterization of a dual function
 RT 3-dehydroquinate dehydratase from Amycolatopsis methanolica.";
 RL J. Gen. Microbiol. 138:2449-2457(1992).
 CC -1- FUNCTION: CATALYZE A TRANS-DEHYDRATION VIA AN ENOLATE
 CC INTERMEDIATE. IS INVOLVED IN BOTH THE CATABOLISM OF QUINATE AND
 CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS. HAS A TEMPERATURE
 CC OPTIMAL OF 76 DEGREES CELSIUS AND PH OPTIMAL OF 9.0. TYPE II
 CC ENZYMES ARE THERMOSTABLE.
 CC -1- CATALYTIC ACTIVITY: 3-DEHYDROQUINATE = 3-DEHYDROSHIKIMATE + H(2)O.
 CC -1- PATHWAY: THIRD STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
 CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
 CC -1- SUBUNIT: HOMODODECAMER.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-II 3-DEHYDROQUINASE FAMILY.
 DR INTERPRO: IPR001874; -.
 DR PROSITE: PS01029; DEHYDROQUINASE_II; PARTIAL.
 KW Quinate metabolism; Aromatic amino acid biosynthesis; Lyase.

FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2197 MW; C24AA183E5CFDE0A CRC64;

Query Match 22.0%; Score 24; DB 1; Length 20;
 Best Local Similarity 80.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GEREP 11
 Db 15 GKREP 19

RESULT 7
 LPKL_LOCM1 STANDARD; PRT; 16 AA.
 ID LPKL_LOCM1
 AC P20404;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE LOCUSTAPYROKININ 1 (LOW-PK-1).
 OS Locusta migratoria (migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;
 OC Acridomorpha; Acridoidea; Acrididae; Locusta.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-CORPORA CARDIACA;
 RX MEDLINE: 91224474.
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Isolation, primary structure, and synthesis of locustapyrokinin: a
 RT myotropic peptide of Locusta migratoria.";
 RL Gen. Comp. Endocrinol. 81:97-104(1991).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR PIR: A49761; A49761.
 DR INTERPRO: IPR001484; -.
 DR PROSITE: PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 16 16 AMIDATION.
 SQ SEQUENCE 16 AA; 1827 MW; A7178BBDCA0AFDD6 CRC64;

Query Match 21.1%; Score 23; DB 1; Length 16;
 Best Local Similarity 57.1%; Pred. No. 7.9e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 GWKOLF 18
 Db 6 GWPQOPF 12

RESULT 8
 BRK_PARID STANDARD; PRT; 13 AA.
 ID BRK_PARID
 AC P42717;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE WASPKININ.
 OS Parapolybia indica.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Vespoidae; Vespidae; Polistinae; Parapolybia.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=VENOM.
 RA Toki T., Yasuhara T., Nakajima T.;
 RT "Isolation and sequential analysis of peptides on the venom sac of
 RT Parapolybia indica.";
 RL Eisei Dobutsu 39:105-111(1988).

RA Jaffe H., Ralna A.K., Riley C.T., Fraser B.A., Nachman R.T.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.:
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hypertrehalosemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera)."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: A33995; A33995.
 DR INTERPRO: IPR002047; .
 DR PROSITE: PS00256; AKH: 1.
 KW Neuropeptide; Amidation; Flight.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 949 MW: 86786771A9D1A736 CRC64;

Query Match 22.0%; Score 24; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 PGM 13
 Db 6 PGM 8

RESULT 3
 ID RPCH_PANBO STANDARD; PRT; 8 AA.
 AC P08939;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE RED PIGMENT CONCENTRATING HORMONE (RPCH).
 OS Pandanus borealis (Northern red shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidae;
 OC Pandalidae; Pandalus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 75054965.
 RA Fernlund P.:
 RT "Structure of the red-pigment-concentrating hormone of the shrimp,
 RT Pandanus borealis.".
 RL Biochim. Biophys. Acta 371:304-311(1974).
 CC -1- FUNCTION: THIS HORMONE ADAPTS THE ANIMAL TO LIGHT BACKGROUNDS BY
 CC STIMULATING CONCENTRATION OF THE PIGMENT OF ITS RED BODY-
 CC CHROMATOPHORES.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: S07139; S07139.
 DR INTERPRO: IPR002047; .
 DR PROSITE: PS00256; AKH: 1.
 KW Pigment; Hormone; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 948 MW: 86786775B9C44736 CRC64;

Query Match 22.0%; Score 24; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 PGM 13
 Db 6 PGM 8

RESULT 4
 ID HTF_NAUCI STANDARD; PRT; 10 AA.
 HTF_NAUCI

AC P10939;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPERTREHALOSAEMIC HORMONE (HTH) (HYPERTREHALOSAEMIC NEUROPEPTIDE).
 OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach).
 OS Leucophaea maderae (Madelta cockroach),
 OS Blattella germanica (German cockroach), and
 OS Gromphadorfina portentosa (Cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberoidae; Blaberidae; Nauphoeta.
 RN [1]
 RP SEQUENCE.
 RC SPECIES=N.CINEREA; TISSUE=CORPORA CARDIACA;
 RX MEDLINE: 87100208.
 RA Gaede G., Rinehart K.L., Jr.:
 RT "Amino acid sequence of a hypertrehalosaemic neuropeptide from the
 RT corpus cardiaca of the cockroach, Nauphoeta cinerea.".
 RL Biochem. Biophys. Res. Commun. 141:774-781(1986).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=L.MADERAE, G.PORRENTOSA, AND B.GERMANICA;
 RX MEDLINE: 90253659.
 RA Gaede G., Rinehart K.L., Jr.:
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gromphadorfina portentosa, Blattella germanica and Blattella orientalis
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry.".
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=B.GERMANICA;
 RX MEDLINE: 91179584.
 RA Veenstra J.A., Camps F.:
 RT "Structure of the hypertrehalosemic neuropeptide of the German
 RT cockroach, Blattella germanica.".
 RL Neuropeptides 15:107-109(1990).
 CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: A26381; A26381.
 DR PIR: S08997; S08997.
 DR PIR: S08998; S08998.
 DR PIR: S09137; S09137.
 DR PIR: A60421; A60421.
 DR INTERPRO: IPR002047; .
 DR PROSITE: PS00256; AKH: 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA: 1092 MW: 056236786775B9C4 CRC64;

Query Match 22.0%; Score 24; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 PGM 13
 Db 6 PGM 8

RESULT 5
 ID HTF_TABAT STANDARD; PRT; 10 AA.
 AC P14596;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE HYPERTREHALOSAEMIC FACTOR (HTHF) (DIPTERAN CORPORA CARDIACA FACTOR II)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:32:55 ; Search time 62.7 Seconds
(Without alignments)
10.191 Million cell updates/sec

Title: US-08-934-367-6

Sequence: 1 LLLHLGGEREPGMLKOLFVN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues
Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	25.7	19	1	TRP3_LEUMA
2	24	22.0	8	1	AKH_TABAT
3	24	22.0	8	1	RPCH_PANBO
4	24	22.0	10	1	HTE_NAUCI
5	24	22.0	10	1	HTE_TABAT
6	24	22.0	20	1	ARCO_AMYME
7	23	21.1	16	1	LEPL_LOCHI
8	22	20.2	13	1	BRK_PARID
9	22	20.2	13	1	HPAL_RANES
10	22	20.2	10	1	NEUT_CHICK
11	21	19.3	10	1	GON3_ONCKE
12	21	19.3	10	1	GONT_SOUAC
13	21	19.3	10	1	Q2OG_COMTE
14	21	19.3	13	1	CHET_COMTE
15	21	19.3	13	1	FARB_ASCSU
16	21	19.3	15	1	VORA_METTM
17	21	19.3	17	1	CHH3_BOMMO
18	21	19.3	20	1	CHRC_SPIOL
19	20	18.3	12	1	PORD_METTM
20	20	18.3	15	1	TAL_TREBR
21	19.5	17.9	20	1	COG1_PARCM
22	19	17.4	7	1	UH11_RAT
23	19	17.4	8	1	CHRN_MACEU
24	19	17.4	10	1	CAER_LITXA
25	19	17.4	10	1	GON1_PETMA
26	19	17.4	12	1	RS19_ELTER
27	19	17.4	13	1	NEUT_RANTE
28	19	17.4	14	1	RS19_CLOPP
29	19	17.4	14	1	RS19_LOMBP
30	19	17.4	17	1	GAST_MACMO
31	19	17.4	17	1	LCK_RAT
32	19	17.4	18	1	NPA_BOVIN
33	19	17.4	19	1	FIBB_HORSE

34	19	17.4	19	1	PYRB_PSEFL	P56585 pseudomonas
35	18	16.5	8	1	AKH_LIBAU	P25418 libellula a
36	18	16.5	8	1	HTF1_PERAM	P04548 periplaneta
37	18	16.5	8	1	HTF2_PERAM	P04549 periplaneta
38	18	16.5	8	1	HTF_TENMO	P25419 tenebrio mo
39	18	16.5	8	1	UF06_MOUSE	P38644 mus musculus
40	18	16.5	10	1	HTF1_ROMMI	P11810 romalea mlt
41	18	16.5	10	1	HTF2_CARMO	P11385 carausius m
42	18	16.5	11	1	BRK_MEGFL	P12797 megascolia
43	18	16.5	11	1	TEMK_RANTE	P56922 rana tempor
44	18	16.5	11	1	TEMK_RANTE	P56923 rana tempor
45	18	16.5	13	1	TP13_PHYRO	P04096 phyllomedus

ALIGNMENTS

RESULT 1
TRP3_LEUMA STANDARD; PRT; 19 AA.

AC P81735;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TACHYKININ-RELATED PEPTIDE 3 (LEWTRP 3).
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
RN [1]
RP SEQUENCE.
RC TISSUE=MIDGUT;
RX MEDLINE; 97053012.
RA Muren J.E., Naessel D.R.;
RT "Isolation of five tachykinin-related peptides from the midgut of
RT the cockroach Leucophaea maderata: existence of N-terminally extended
RT isoforms.";
RL Regul. Pept. 65:185-196(1996).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -1- TISSUE SPECIFICITY: MIDGUT.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 19
SQ SEQUENCE 19 AA; 1930 MW; 99B5471A011625E5 CRC64;

Query Match 25.7%; Score 28; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GEREPE 12
||| ||
DB 2 GERAPG 7

RESULT 2
AKH_TABAT STANDARD; PRT; 8 AA.

AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH) (DIPTERAN CORPORA CARDIACA FACTOR 1)
DE (DCC 1).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
OC Tabanidae; Tabanus.
RN [1]
RP SEQUENCE.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE; 90046758.

=====

A:Accession: A58620
A:Molecule type: protein
A:Residues: 1-8 <JAN>
C:Superfamily: adipokinetie hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 22.0%; Score 24; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGW 13
111
DB 6 PCW 8

RESULT 14

A43405
6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2,6-bisphosphate 2-phosphatase (EC 3.1.1.11)
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Mar-2000
C:Accession: A43405
R:Ventura, F.; Rosa, J.L.; Ambrosio, S.; Pilakis, S.J.; Bartons, R.
J. Biol. Chem. 267, 17939-17943, 1992
A>Title: Bovine brain 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase. Evidence for
A:Reference number: A43405; MUID:92388154
A:Accession: A43405
A:Molecule type: protein
A:Residues: 1-10 <VEN>
C:Superfamily: 6-phosphofructo-2-kinase / fructose-2,6-bisphosphate 2-phosphatase; phospho-
C:Keywords: phosphoric monoester hydrolase; phosphotransferase

Query Match 22.0%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 HJGE 8
11:11
DB 5 HJKE 9

RESULT 15

A60421
hypertrehalosemic hormone - German cockroach
N:Alternate names: Bld-HrTH
C:Species: Blattea germanica (German cockroach)
C:Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 31-Oct-1997
C:Accession: A60421; S09137
R:Veenstra, J.A.; Camps, F.
Neuropeptides 15, 107-109, 1990
A>Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, Blattea
A:Reference number: A60421; MUID:91179584
A:Accession: A60421
A:Molecule type: protein
A:Residues: 1-10 <VEE>
R:Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A>Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora
entellae and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A:Reference number: S08995; MUID:90253659
A:Accession: S09137
A:Molecule type: protein
A:Residues: 1-10 <GAE>
C:Superfamily: adipokinetie hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 22.0%; Score 24; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 11 PGW 13
111
DB 6 PCW 8

Search completed: December 21, 2000, 08:30:05
Job time: 269 sec

C:Function:
A:Description: involved in turnover of connective tissues
C:Keywords: serine proteinase inhibitor

Query Match 22.0%; Score 25; DB 2; Length 18;
Best Local Similarity 46.2%; Pred. No. 8.5e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 8 EREGWIKOLEFTN 20
Db 3 EQEPFALXOFILN 15

RESULT 9
A34626
RPCII-related neuropeptide - ferruginous spindle
C:Species: fusinus ferrugineus (ferruginous spindle)
C>Date: 06-Jul-1990 #sequence-revision 06-Jul-1990 #text_change 31-Dec-1993
C:Accession: A34626
R:Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;
Biochem. Biophys. Res. Commun. 167, 273-279, 1990
A:Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A:Reference number: A34626; MUID:90179762
A:Accession: A34626
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <KUR>
C:Keywords: neuropeptide

Query Match 22.0%; Score 24; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 PGW 13
Db 2 PGW 4

RESULT 10
A61348
red pigment-concentrating hormone - northern shrimp
N:Alternate names: blanching hormone
C:Species: Pandalus borealis (northern shrimp)
C>Date: 02-Aug-1994 #sequence-revision 05-Aug-1994 #text_change 07-May-1999
C:Accession: A61348; S07139
R:Fernlund, P.; Jørgensen, L.
Science 177, 173-175, 1972
A:Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A:Reference number: A61348; MUID:72228738
A:Accession: A61348
A:Molecule type: protein
A:Residues: 1-8 <FERI>
R:Fernlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A:Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus borealis.
A:Reference number: S07139; MUID:75054965
A:Accession: S07139
A:Molecule type: protein
A:Residues: 'E', 2-8 <FER2>
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C:Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pig-
ment-containing cells.
C:Superfamily: adipoikine hormone
C:Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 22.0%; Score 24; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PGW 13
Db 6 PGW 8

RESULT 11
A33995
adipoikine hormone - black horse fly
C:Species: Tabanus atratus (black horse fly)
C>Date: 23-Mar-1990 #sequence-revision 23-Mar-1990 #text_change 31-Oct-1997
C:Accession: A33995
R:Jaftic, H.; Raine, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhan
Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A:Title: Primary structure of two neuropeptide hormones with adipoikine and hypotro-
pe
A:Reference number: A33995; MUID:90046758
A:Accession: A33995
A:Molecule type: protein
A:Residues: 1-8 <JAF>
C:Superfamily: adipoikine hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta-
mic
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 22.0%; Score 24; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PGW 13
Db 6 PGW 8

RESULT 12
S55310
adipoikine hormone - damselfly (Pseudagrion inconspicuum)
N:Alternate names: Psi-AKH
C:Species: Pseudagrion inconspicuum
C>Date: 19-Mar-1997 #sequence-revision 31-Oct-1997 #text_change 07-May-1999
C:Accession: S55310
R:Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A:Title: A novel adipoikine octapeptide found in the damselflies Pseudagrion in-
conspicuum
A:Reference number: S55310; MUID:94379987
A:Accession: S55310
A:Molecule type: protein
A:Residues: 1-8 <JAN>
C:Superfamily: adipoikine hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 22.0%; Score 24; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PGW 13
Db 6 PGW 8

RESULT 13
A58620
adipoikine hormone - damselfly (Ischnura senegalensis)
C:Species: Ischnura senegalensis
C>Date: 28-Oct-1997 #sequence-revision 31-Oct-1997 #text_change 07-May-1999
C:Accession: A58620
R:Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A:Title: A novel adipoikine octapeptide found in the damselflies Pseudagrion in-
conspicuum
A:Reference number: S55310; MUID:94379987

G02018
Proteasome chain LMP7 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 22-Jun-1999
C:Accession: G02018
R:Kim, T.
submitted to the EMBL Data Library, July 1995
A:Reference number: G09054
A:Accession: G02018
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
A:Residues: 1-18 <KIT>
A:Cross-references: EMBL:U32862; NID:g1045468; PIDN:AAA80234.1; PID:g1045469
C:Genetics:
A:Gene: LMP7
C:Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 26.6%; Score 29; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 9 REPOMUK 15
DB 4 KEDGWVK 10

RESULT 4
PH1788
T cell receptor alpha chain V region (clone 2PBL V alpha 24-4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1788
R:Porcelll, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585
A:Accession: PH1788
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <POR>

Query Match 24.8%; Score 27; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 HLOGERE 10
DB 1 HLCGERQ 7

RESULT 5
PH1802
T cell receptor alpha chain V region (clone 3PBL V alpha 24-8) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1802
R:Porcelll, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585
A:Accession: PH1802
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-17 <POR>

Query Match 22.9%; Score 25; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 HLOGER 9
DB 1 HLCGER 6

RESULT 6
PH1822
T cell receptor alpha chain V region (clone 5PBL V alpha 24-5) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1822
R:Porcelll, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blo

A:Reference number: PH1754; MUID:93301585
A:Accession: PH1822
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-17 <POR>

Query Match 22.9%; Score 25; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 HLOGER 9
DB 1 HLCGER 6

RESULT 7
F49215
urease (EC 3.5.1.5) small chain Urea - Helicobacter mustelae (ATCC 43772) (fragment)
C:Species: Helicobacter mustelae
C:Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 30-May-1997
C:Accession: F49215
R:Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.
Infect. Immun. 60, 5259-5266, 1992
A:Title: Purification and characterization of the urease enzymes of Helicobacter spec
A:Reference number: A49215; MUID:93084378
A:Accession: F49215
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <TUR>
A:Note: sequence extracted from NCBI backbone (NCBIP:119487)
C:Superfamily: urease 26k chain; urease 11k chain homology; urease 12k chain homology
C:Keywords: hydrolase

Query Match 22.9%; Score 25; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LLLHLOGE 8
DB 9 MMLHYAGE 16

RESULT 8
S71592
serine proteinase inhibitor, 31k - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Sep-1998
C:Accession: S71592
R:Rao, C.N.; Liu, Y.Y.; Peavey, C.L.; Woodley, D.T.
Arch. Biochem. Biophys. 317, 311-314, 1995
A:Title: Novel extracellular matrix-associated serine proteinase inhibitors from huma
A:Reference number: S71592; MUID:95177668
A:Accession: S71592
A:Molecule type: protein
A:Residues: 1-18 <RAO>

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:30:04 ; Search time 112.59 Seconds
(without alignments)
11.273 Million cell updates/sec

Title: US-08-934-367-6

Perfect score: 109
Sequence: 1 LLLHLQGEREPGMLKOLFNN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	30	27.5	16	2	PH1790
2	29	26.6	10	2	S39030
3	29	26.6	18	2	G02018
4	27	24.8	15	2	PH1788
5	25	22.9	17	2	PH1802
6	25	22.9	17	2	PH1822
7	25	22.9	18	2	FA9215
8	25	22.9	18	2	S71592
9	24	22.0	4	2	A34626
10	24	22.0	8	2	A61348
11	24	22.0	8	2	A33995
12	24	22.0	8	2	S55310
13	24	22.0	8	2	A58620
14	24	22.0	10	2	A43405
15	24	22.0	10	2	A60421
16	24	22.0	10	2	S08997
17	24	22.0	10	2	S08998
18	24	22.0	10	2	A26381
19	24	22.0	10	2	B33995
20	24	22.0	11	2	PD0442
21	24	22.0	15	2	A26228
22	24	22.0	15	2	PH1329
23	24	22.0	15	2	S38976
24	24	22.0	16	2	PT0282
25	24	22.0	19	2	A41668
26	24	22.0	19	2	S29212
27	24	22.0	20	2	A47687
28	23	21.1	15	2	S67975
29	23	21.1	16	1	A49761

30	23	21.1	17	2	PH0778	T-cell receptor al
31	23	21.1	19	2	PH1339	Ig heavy chain DJ
32	22	20.2	7	4	A58725	virotoxin - destro
33	22	20.2	9	2	G56978	collagen alpha 1(I
34	22	20.2	11	2	D56979	collagen alpha 1(I
35	22	20.2	11	2	A33571	follicstatin - bovl
36	22	20.2	12	2	P00776	NADH dehydrogenase
37	22	20.2	13	2	S09018	hemolytic protein
38	22	20.2	13	2	A28505	neurotensin-like p
39	22	20.2	14	2	PH1347	Ig heavy chain DJ
40	22	20.2	14	2	PH1311	Ig heavy chain DJ
41	22	20.2	14	2	PH1321	Ig heavy chain DJ
42	22	20.2	14	2	PH1305	Ig heavy chain DJ
43	22	20.2	14	2	PH1306	Ig heavy chain DJ
44	22	20.2	15	2	PT0222	Ig heavy chain CDR
45	22	20.2	15	2	PH1314	Ig heavy chain DJ

ALIGNMENTS

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RESULT 1
PH1790
T cell receptor alpha chain V region (clone 2PBL V alpha 24-6) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1790
R:Porcetti, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blo
A:Reference number: PH1754; MUID:93301585
A:Accession: PH1790
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <POR>

Query Match
Best Local Similarity 27.5%; Score 30; DB 2; Length 16;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HLQGEREP 11
DB 1 HLQGERP 8

RESULT 2
S39030
Igsyl-bradykinin - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 19-Apr-1996
C:Accession: S39030
R:Conlon, J.M.; Olson, K.R.
FEBS Lett. 334, 75-78, 1993
A:Title: Purification of a vasoactive peptide related to Igsyl-bradykinin from trout
A:Reference number: S39030; MUID:94039817
A:Accession: S39030
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-10 <CON>

Query Match
Best Local Similarity 26.6%; Score 29; DB 2; Length 10;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 EREP GW 13
DB 1 KREP GW 6

RESULT 3
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OY 12 GWLKOLF 18
||| |||
Db 5 GWLAOLF 11

RESULT 14
PCT-US95-09262-13
; Sequence 13, Application PC/TUS9509262
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09262
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/10040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.38"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: //label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-13

Query Match 32.1%; Score 35; DB 4; Length 14;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWLKOLF 18
||| |||
Db 5 GWLAOLF 11

RESULT 15
US-08-621-803-227
; Sequence 227, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; FUSION PROTEINS AND BPI-DERIVED PEPTIDES
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 227:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.388"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: //label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-227

Query Match 30.3%; Score 33; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWLKOLF 18
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Db 1 GWLAOLF 7

Search completed: December 21, 2000, 08:31:46
Job time: 369 sec

;; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02465
; FILING DATE: 11-JAN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,1133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: "BPI.38"
; PCT-US94-02465-40

Query Match 32.1%; Score 35; DB 4; Length 14;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 GWLQOLF 18
DB 5 GWLQOLF 11

RESULT 12
PCT-US95-00498-40
; Sequence 40, Application PC/TUS9500498
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
; TITLE OF INVENTION: Materials
; NUMBER OF SEQUENCES: 237
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00498
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; INFORMATION FOR SEQ ID NO: 40:

;; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: "XMP.38"
; PCT-US95-00498-40

Query Match 32.1%; Score 35; DB 4; Length 14;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 GWLQOLF 18
DB 5 GWLQOLF 11

RESULT 13
PCT-US95-00656-40
; Sequence 40, Application PC/TUS9500656
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Materials and Methods
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: "XMP.38"
; PCT-US95-00656-40

Query Match 32.1%; Score 35; DB 4; Length 14;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

APPLICANT: Little II, Roger G
APPLICANT: Lim, Edward
APPLICANT: Padem, Mitchell B.
TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES: 252
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,259A
FILING DATE: 21-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/504,841
FILING DATE: 20-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11021US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: "XMP.38"
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: //label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-13

Query Match 32.1%; Score 35; DB 2; Length 14;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GWLKOLF 18
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Db 5 GWLKOLF 11

RESULT 10
US-09-119-263-40
Sequence 40, Application US/09119263
GENERAL INFORMATION:
APPLICANT: Horwitz, Arnold H.
APPLICANT: Lambert, Lewis H.
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
NUMBER OF SEQUENCES: 237
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois

COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,263
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/758,116
FILING DATE:
APPLICATION NUMBER: 08/372,783
FILING DATE:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27129/32415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: "XMP.38"
US-09-119-263-40

Query Match 32.1%; Score 35; DB 3; Length 14;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GWLKOLF 18
111111
Db 5 GWLKOLF 11

RESULT 11
PCT-US94-02465-40
Sequence 40, Application PC/TUS9402465
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Biologically Active Peptides from
TITLE OF INVENTION: Functional Domains of Bactericidal/Permeability-Increasing
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25

TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "BPI.38"
US-08-473-344-40

Query Match 32.1%; Score 35; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWLKOLF 18
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Db 5 GWLAOLF 11

RESULT 7
US-08-621-803-39
Sequence 39, Application US/08621803
Patent No. 5851802
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
NUMBER OF INVENTIONS: Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,803
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.38"
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note="The C-Terminus is Amidated."
US-08-621-803-39

Query Match 32.1%; Score 35; DB 2; Length 14;

Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 12 GWLKOLF 18
||| |||
Db 5 GWLAOLF 11

RESULT 8
US-08-485-445A-40
Sequence 40, Application US/08485445A
Patent No. 5856438
GENERAL INFORMATION:
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Biologically Active Peptides from
TITLE OF INVENTION: Functional Domains of Bactericidal/
TITLE OF INVENTION: Permeability-Increasing Protein and
NUMBER OF SEQUENCES: 226
CORRESPONDENCE ADDRESS:
ADDRESSER: McAndrews, Held & Malloy, Ltd.
STREET: Suite 3400, 500 West Madison Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,445A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11018US08/100-224.P4.C1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-707-8889
TELEFAX: 312-707-9155
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "BPI.38"
US-08-485-445A-40

Query Match 32.1%; Score 35; DB 2; Length 14;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWLKOLF 18
||| |||
Db 5 GWLAOLF 11

RESULT 9
US-08-621-259A-13
Sequence 13, Application US/08621259A
Patent No. 5858974
GENERAL INFORMATION:

: TITLE OF INVENTION: Biologically Active Peptides from
: TITLE OF INVENTION: Functional Domains of Bactericidal/
: TITLE OF INVENTION: Permeability-Increasing Protein and
: TITLE OF INVENTION: Uses Thereof
: NUMBER OF SEQUENCES: 226
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Allegretti & Witcoff, Ltd.
: STREET: Suite 3000, 10 S. Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/306,473A
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/209,762
: FILING DATE: 11-MAR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/183,222
: FILING DATE: 14-JAN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: McDonnell, John J.
: REGISTRATION NUMBER: 26,949
: REFERENCE/DOCKET NUMBER: 93,1133-
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-715-1000
: TELEFAX: 312-715-1234
: INFORMATION FOR SEQ ID NO: 40:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 14 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: "BPI.38"
: US-08-306-473A-40
:
: Query Match 32.1%; Score 35; DB 1; Length 14;
: Best Local Similarity 85.7%; Pred. No. 10;
: Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 12 GWLKOLF 18
DB 5 GWLKOLF 11
:
: RESULT 5
: US-08-209-762-40
: Sequence 40, Application US/08209762
: Patent No. 5733872
: GENERAL INFORMATION:
: APPLICANT: little, Roger G.
: TITLE OF INVENTION: Biologically Active Peptides from
: TITLE OF INVENTION: Functional Domains of Bactericidal/permeability-Increasing
: TITLE OF INVENTION: Protein and Uses Thereof
: NUMBER OF SEQUENCES: 98
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Allegretti & Witcoff, Ltd.
: STREET: 10 South Wacker Drive, Suite 3000
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/209,762
: FILING DATE: 11-JAN-1994
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5733872nan, Kevin E
: REGISTRATION NUMBER: 35,303
: REFERENCE/DOCKET NUMBER: 93,1133
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-715-1000
: TELEFAX: 910-221-5317
: INFORMATION FOR SEQ ID NO: 40:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 14 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: "BPI.38"
: US-08-209-762-40
:
: Query Match 32.1%; Score 35; DB 1; Length 14;
: Best Local Similarity 85.7%; Pred. No. 10;
: Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 12 GWLKOLF 18
DB 5 GWLKOLF 11
:
: RESULT 6
: US-08-473-344-40
: Sequence 40, Application US/08473344
: Patent No. 5763567
: GENERAL INFORMATION:
: APPLICANT: little, Roger G.
: TITLE OF INVENTION: Biologically Active Peptides from
: TITLE OF INVENTION: Functional Domains of Bactericidal/permeability-Increasing
: TITLE OF INVENTION: Protein and Uses Thereof
: NUMBER OF SEQUENCES: 98
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Banner & Allegretti, Ltd.
: STREET: 10 South Wacker Drive, Suite 3000
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/473,344
: FILING DATE: 7-JUN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/306,473
: FILING DATE: 15-SEP-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/209,762
: FILING DATE: 11-MAR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: McDonnell, John J.
: REGISTRATION NUMBER: 26,949
: REFERENCE/DOCKET NUMBER: 93,1133-J
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-715-1000

US-08-311-611A-40

Query Match 32.1%; Score 35; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWLKOLF 18
DB 5 GWLAOLF 11

RESULT 2

US-08-372-783-40
Sequence 40, Application US/08372783
Patent No. 5578572

GENERAL INFORMATION:
APPLICANT: Horwitz, Arnold H.
APPLICANT: Lambert, Lewis H.
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
MATERIALS
NUMBER OF SEQUENCES: 237
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/372,783

FILING DATE:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/273,540

FILING DATE: 11-JUL-1994

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/209,762

FILING DATE: 11-MAR-1994

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/183,222

FILING DATE: 14-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Rin-Laures, Li-Hsien

REGISTRATION NUMBER: 33,547

REFERENCE/DOCKET NUMBER: 27129/32415

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

MOLECULE TYPE: linear

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: "XMP.38"

US-08-372-783-40

Query Match 32.1%; Score 35; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWLKOLF 18
DB 5 GWLAOLF 11

DB 5 GWLAOLF 11

RESULT 3

US-08-372-105-40
Sequence 40, Application US/08372105
Patent No. 5627153

GENERAL INFORMATION:
APPLICANT: Little, Roger G.
APPLICANT: Lim, Edward
APPLICANT: Lambert, Lewis H.
APPLICANT: Scannon, Patrick J.
TITLE OF INVENTION: Anti-Fungal Materials and Methods
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/372,105

FILING DATE:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/273,540

FILING DATE: 11-JUL-1994

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/209,762

FILING DATE: 11-MAR-1994

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/183,222

FILING DATE: 14-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Rin-Laures, Li-Hsien

REGISTRATION NUMBER: 33,547

REFERENCE/DOCKET NUMBER: 27129/32415

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

MOLECULE TYPE: linear

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: "XMP.38"

US-08-372-105-40

Query Match 32.1%; Score 35; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWLKOLF 18
DB 5 GWLAOLF 11

RESULT 4

US-08-306-473A-40

Sequence 40, Application US/08306473A
Patent No. 5652332

GENERAL INFORMATION:
APPLICANT: Little, Roger G.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:31:46 ; Search time 99.91 Seconds
(without alignments)
3.355 Million cell updates/sec

Title: US-08-934-367-6
Perfect score: 109
Sequence: 1 LLLHLOGERPPGLKQLFTN 20

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 1676186 residues

Total number of hits satisfying chosen parameters: 87906

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/prodata/2/1aa/6.COMB.pep: *
4: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	35	32.1	14	1	US-08-306-473A-40
5	35	32.1	14	1	US-08-209-762-40
6	35	32.1	14	1	US-08-473-344-40
7	35	32.1	14	2	US-08-621-803-39
8	35	32.1	14	2	US-08-485-445A-40
9	35	32.1	14	2	US-08-621-259A-13
10	35	32.1	14	3	US-09-119-263-40
11	35	32.1	14	4	PCT-US94-02465-40
12	35	32.1	14	4	PCT-US95-00498-40
13	35	32.1	14	4	PCT-US95-00656-40
14	35	32.1	14	4	PCT-US95-09262-13
15	35	32.1	10	2	US-08-621-803-227
16	35	30.3	10	2	US-08-621-259A-219
17	35	30.3	11	2	US-08-621-803-428
18	35	30.3	11	2	US-08-621-259A-220
19	35	30.3	12	2	US-08-621-803-230
20	35	30.3	12	2	US-08-621-259A-222
21	35	30.3	13	1	US-08-261-660A-33
22	35	30.3	13	1	US-08-261-660A-42
23	35	30.3	13	4	PCT-US94-06931-33
24	35	30.3	13	4	PCT-US94-06931-42
25	35	30.3	14	1	US-08-311-611A-15
26	35	30.3	14	1	US-08-311-611A-33
27	35	30.3	14	1	US-08-311-611A-34
28	35	30.3	14	1	US-08-311-611A-35

29	33	30.3	14	1	US-08-311-611A-36	Sequence 36, App1
30	33	30.3	14	1	US-08-311-611A-44	Sequence 44, App1
31	33	30.3	14	1	US-08-311-611A-45	Sequence 45, App1
32	33	30.3	14	1	US-08-311-611A-46	Sequence 46, App1
33	33	30.3	14	1	US-08-311-611A-81	Sequence 81, App1
34	33	30.3	14	1	US-08-311-611A-89	Sequence 89, App1
35	33	30.3	14	1	US-08-311-611A-91	Sequence 91, App1
36	33	30.3	14	1	US-08-311-611A-106	Sequence 106, App
37	33	30.3	14	1	US-08-311-611A-107	Sequence 107, App
38	33	30.3	14	1	US-08-311-611A-109	Sequence 109, App
39	33	30.3	14	1	US-08-311-611A-110	Sequence 110, App
40	33	30.3	14	1	US-08-311-611A-122	Sequence 122, App
41	33	30.3	14	1	US-08-311-611A-142	Sequence 142, App
42	33	30.3	14	1	US-08-372-783-15	Sequence 15, App1
43	33	30.3	14	1	US-08-372-783-33	Sequence 33, App1
44	33	30.3	14	1	US-08-372-783-34	Sequence 34, App1
45	33	30.3	14	4	PCT-US95-09262-62	Sequence 62, App1

ALIGNMENTS

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RESULT 1
US-08-311-611A-40
; Sequence 40, Application US/08311611A
; Patent No. 5523288
; GENERAL INFORMATION:
; APPLICANT: Cohen, Jonathan
; APPLICANT: Kung, Ada H.C.
; APPLICANT: Lambert, Jr., Lewis H.
; TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial
; TITLE OF INVENTION: Infection by Administration of
; TITLE OF INVENTION: Bactericidal/Permeability-Increasing
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,611A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,401
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/125,651
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 32251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELETYPE: 25-3856
; INFORMATION FOR SEQ. ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "BPI.38"
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Db	6	LFKPFASLHIL	18

Search completed: December 21, 2000, 08:40:02
Job time: 125 sec

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN; TISSUE-WHOLE EMBRYOS;
RX MEDLINE: 98141813.
RA Peale F.V., Mason K., Hunter A.W., Bothwell M.;
RT "Multiplex display polymerase chain reaction amplifies and resolves
  related sequences sharing a single moderately conserved domain.";
RL Anal. Biochem. 256:158-168(1998).
DR EMBL: U34617; AAC36455.1; -.
FT NON-TER 1 1
FT NON-TER 10 10
SQ SEQUENCE 10 AA; 1068 MW; 9A7598276728705A CRC64;

Query Match
Best Local Similarity 18.4%; Score 25; DB 13; Length 10;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 DFGFPHL 17
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Db 3 DGLPKRV 10

RESULT 12
O94554 PRELIMINARY; PRT; 16 AA.
ID O94554;
AC O94554;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE CALMODULIN KINASE 2 (FRAGMENT).
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
  Schizosaccharomycetaceae; Schizosaccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RA Alemnay V., Alligie R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U57982; AAD09466.1; -.
KM Kinase.
FT NON-TER 1 1
FT NON-TER 16 AA; 1846 MW; 4A673B1F4C3288D9 CRC64;
SQ SEQUENCE 16 AA; 1846 MW; 4A673B1F4C3288D9 CRC64;

Query Match
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 FGFP 8

RESULT 13
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ID O9P570;
AC O9P570;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
  Gallus.
RN [1]
RP SEQUENCE.
RA MEDLINE: 92011685.
RA Seltani S., Barber D.L., Aebersold R., Steyer E., Shen X., Nimpf J.;
RT "The laying hen expresses two different low density lipoprotein
  receptor-related proteins.";
RL J. Biol. Chem. 266:19079-19087(1991).

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SQ SEQUENCE 19 AA; 1861 MW; 4EEC931205620608 CRC64;

Query Match
Best Local Similarity 18.4%; Score 25; DB 13; Length 19;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 6 LLOMDFGPKHLVD 20
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Db 1 LLAOLGXPTALD 15

RESULT 14
O9TWH5 PRELIMINARY; PRT; 20 AA.
ID O9TWH5;
AC O9TWH5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 40 KDA GAP JUNCTION PROTEIN (FRAGMENT).
OS Heliothis virescens (Noctuid moth) (Owllet moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
  Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
  Noctuoidea; Noctuidae; Heliothinae; Heliothis.
RN [1]
RP SEQUENCE.
RX MEDLINE: 95347000.
RA Ryerse J.S.;
RT "Immunocytochemical, electrophoresis, and immunoblot analysis of
  Heliothis virescens gap junctions isolated in the presence and absence
  of protease inhibitors.";
RL Cell Tissue Res. 261:179-186(1995).
SQ SEQUENCE 20 AA; 2304 MW; A298D3EB3E89586B CRC64;

Query Match
Best Local Similarity 18.4%; Score 25; DB 5; Length 20;
Matches 5; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 5 LLOMDFGPKHLVD 21
   1 1 1 1 1 1
Db 3 VIFNIDGYLEFLTRDF 19

RESULT 15
O9TIG3 PRELIMINARY; PRT; 20 AA.
ID O9TIG3;
AC O9TIG3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE GALACTOCEREBROSIDASE (FRAGMENT).
OS CALC.
GN Ateles belzebuth chamek.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.
RN [1]
RP SEQUENCE FROM N.A.
RA Canavez F.C.;
RT "Gene mapping in Ateles paniscus chamek.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF099175; AAF21849.1; -.
DR INTERPRO: IPR001286; -.
DR PFM: PF02057; Glyco_hydro_59; 1.
FT NON-TER 1 1
FT NON-TER 20 20
SQ SEQUENCE 20 AA; 2317 MW; EA306655966B58F CRC64;

Query Match
Best Local Similarity 18.4%; Score 25; DB 6; Length 20;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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Query Match 20.6%; Score 28; DB 2; Length 21;
 Best Local Similarity 45.5%; Pred. No. 8e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 5 LILQMDPFGFPK 15
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 Db 3 ILKILDFSDPK 13

RESULT 7
 Q9UGS1 PRELIMINARY; PRT; 12 AA.
 AC Q9UGS1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE DJ796117.4 (NOVEL PROTEIN SIMILAR TO GS2) (FRAGMENT).
 GN DJ796117.4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RP [1]
 RA SEQUENCE FROM N.A.
 RA Batlow K.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL035398; CAB63074.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1430 MW; AF7740ABECB69AA6 CRC64;

Query Match 19.9%; Score 27; DB 4; Length 12;
 Best Local Similarity 44.4%; Pred. No. 6.4e+02;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 5 LILQMDPFG 13
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 Db 1 MILEMDSF 9

RESULT 8
 Q9TRR6 PRELIMINARY; PRT; 19 AA.
 AC Q9TRR6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CALCYCLIN-ASSOCIATED PROTEIN, CAP50-CA2+/PHOSPHOLIPID-BINDING PROTEIN
 DE L-14 FRAGMENT.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RP [1]
 RA MEDLINE: 92250478.
 RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hataka H.;
 RT "A calyculin-associated protein is a newly identified member of the
 RT Ca2+/phospholipid-binding proteins, annexin family.";
 RL J. Biol. Chem. 267:8919-8924(1992).
 SQ SEQUENCE 19 AA; 2018 MW; 9A54062504B8322E CRC64;

Query Match 19.9%; Score 27; DB 6; Length 19;
 Best Local Similarity 37.5%; Pred. No. 1e+03;
 Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 11 FGFPKHLVDPLQSL 26
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 Db 2 FETDEQAIDXLGSR 17

RESULT 9
 P70861 PRELIMINARY; PRT; 21 AA.

AC P70861;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE THDP (FRAGMENT).
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-212;
 RX MEDLINE: 97312006.
 RA Ge Y., Old I.G., Giron S., Charon N.W.;
 RT "The flag motility operon of Borrelia burgdorferi is initiated by a
 RT sigma 70-like promoter.";
 RL Microbiology 143:1681-1690(1997).
 DR EMBL; U62901; AAB62742.1; -.
 FT NON_TER 21 21
 SQ SEQUENCE 21 AA; 2432 MW; F33E1EC548BD5B33 CRC64;

Query Match 19.1%; Score 26; DB 2; Length 21;
 Best Local Similarity 40.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 9 MDFGPKHL 18
 : : : : :
 Db 7 IEFDFEGIL 16

RESULT 10
 P82401 PRELIMINARY; PRT; 25 AA.
 AC P82401;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE AUREIN 5.1.
 OS Litorea raniformis, and Litorea aurea (Australian frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 RN Litorea.
 RN [1]
 RP SEQUENCE.
 RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
 RA Wallace J.C., Tyler M.J.;
 RT "The antibiotic and anticancer aurein peptides from the Australian
 RT bell frogs Litorea aurea and Litorea raniformis.";
 RL Eur. J. Biochem. 0:0-0(2000).
 CC -1- FUNCTION: HAS NO ANTIMICROBIAL OR ANTICANCER ACTIVITY.
 SQ SEQUENCE 25 AA; 2547 MW; 15C6169CD98AFC27 CRC64;

Query Match 19.1%; Score 26; DB 13; Length 25;
 Best Local Similarity 38.9%; Pred. No. 2e+03;
 Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 6 LILQMDPFGPKHLVDPLQ 23
 : : : : :
 Db 2 LLDIVTGLGNLIVYK 19

RESULT 11
 O73594 PRELIMINARY; PRT; 10 AA.
 AC O73594;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE ZAX-2 (FRAGMENT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.

OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 96092035.
 RA Linder D., Freund R., Kadenbach B.:
 RT "Species-specific expression of cytochrome c oxidase isozymes";
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 112:461-469(1995).
 SO SEQUENCE 24 AA; 2795 MW; D49D27C03B61F803 CRC64;

Query Match 24.3%; Score 33; DB 6; Length 24;
 Best Local Similarity 58.3%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 6 LLOMDFGPKHL 17
 Db 11 LFOEDNGIPVHL 22

RESULT 3
 ID 031365 PRELIMINARY; PRT; 13 AA.
 AC 031365;
 DT 01-JAN-1998 (TREMBLREL. 05, Created)
 DT 01-JAN-1998 (TREMBLREL. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLREL. 08, Last annotation update)
 DE GUA (FRAGMENT).
 GN GUA.
 OS Borrelia garinii.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TP90;
 RX MEDLINE: 97426044.
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
 Rosa P.:
 RT "The Borrelia burgdorferi circular plasmid cp26: conservation of
 RT plasmid structure and targeted inactivation of the ospC gene";
 RL Mol. Microbiol. 25:361-374(1997).
 DR EMBL: U03701; AAC45356.1; -.
 FT NON_TER 13 13
 SO SEQUENCE 13 AA; 1382 MW; 08EFB4180E0BC720 CRC64;

Query Match 23.5%; Score 32; DB 2; Length 13;
 Best Local Similarity 55.6%; Pred. No. 1.2e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 CULLOMDFG 12
 Db 4 CALIVLDFG 12

RESULT 4
 ID 092G55 PRELIMINARY; PRT; 21 AA.
 AC 092G55;
 DT 01-MAY-1999 (TREMBLREL. 10, Created)
 DT 01-MAY-1999 (TREMBLREL. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLREL. 10, Last annotation update)
 DE ATP-BINDING PROTEIN (FRAGMENT).
 GN RECF.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-L2 434B;
 RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.:
 RT "Gene identification of Chlamydia trachomatis by random DNA
 RT sequencing.";

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF087306; AAD04082.1; -.
 KW ATP-binding.
 FT NON_TER 1 1
 FT NON_TER 21 21
 SO SEQUENCE 21 AA; 2336 MW; 0185D9AC428276D9 CRC64;

Query Match 22.4%; Score 30.5; DB 2; Length 21;
 Best Local Similarity 50.0%; Pred. No. 3.3e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

OY 6 LLOMDFGPKHL 17
 Db 8 ILQL-ISFPKHI 18

RESULT 5
 ID 046081 PRELIMINARY; PRT; 24 AA.
 AC 046081;
 DT 01-NOV-1996 (TREMBLREL. 01, Created)
 DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
 DT 01-MAY-2000 (TREMBLREL. 13, Last annotation update)
 DE NITROGENASE 3 SUBUNIT H (FRAGMENT).
 GN ANFH.
 OS Clostridium hungatei.
 OC Bacteria; Firmicutes; Bacilli/Clostridium group; Clostridiaceae;
 OC Clostridium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B3B;
 RA Chen T., Leschine S.B.:
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U59415; AAB02934.1; -.
 DR INTERPRO: IPR000392; -.
 DR PFWA: PF00142; fer4_N1FH; 1.
 FT NON_TER 1 1
 SO SEQUENCE 24 AA; 2752 MW; C014801651E11BFC CRC64;

Query Match 22.1%; Score 30; DB 2; Length 24;
 Best Local Similarity 37.5%; Pred. No. 4.5e+02;
 Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 10 DFGPKHLVDFQSL 25
 Db 1 EFVIPKPLTMDQEDM 16

RESULT 6
 ID 09X3D0 PRELIMINARY; PRT; 21 AA.
 AC 09X3D0;
 DT 01-NOV-1999 (TREMBLREL. 12, Created)
 DT 01-NOV-1999 (TREMBLREL. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLREL. 12, Last annotation update)
 DE CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
 GN PETD.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Urbach E., Chisholm S.W.:
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 RT sorted from the Sargasso Sea and Gulf Stream";
 RL Limnol. Oceanogr. 43:1615-1630(1998).
 DR EMBL: AF070133; AAD20742.1; -.
 FT NON_TER 21 21
 SO SEQUENCE 21 AA; 2410 MW; CC947A212386FE23 CRC64;

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:40:02 ; Search time 28.23 Seconds
(without alignments)
85.998 Million cell updates/sec

Title: US-08-934-367-50
Perfect score: 136
Sequence: 1 LDGCLLQMDFGFPKHLVDFLQSL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 6467

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.14:*
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	33	24.3	13	031296	031296 borrelia af
2	33	24.3	6	09TR30	09TR30 ovls aries
3	33	23.5	13	031365	031365 borrelia ga
4	30.5	22.4	21	09ZG55	09ZG55 chlamydia t
5	30	22.4	24	046081	046081 clostridium
6	28	20.6	21	09X3D0	09X3D0 prochloroco
7	27	19.9	12	0490G51	0490G51 homo sapien
8	26	19.9	19	09TRR6	09TRR6 oryctolagus
9	26	19.1	21	P70861	P70861 borrelia bu
10	26	19.1	25	13 P82401	13 P82401 litorea ran
11	25	18.4	10	13 073594	13 073594 gallus gall
12	25	18.4	16	3 094554	3 094554 schistosach
13	25	18.4	19	13 09P570	13 09P570 gallus gall
14	25	18.4	19	13 09TW5	13 09TW5 heliothis v
15	25	18.4	20	6 09TRG3	6 09TRG3 ateles belz
16	25	18.4	21	4 016575	4 016575 homo sapien
17	25	18.4	23	6 09TRZ8	6 09TRZ8 canis faml
18	25	18.4	24	12 069137	12 069137 human herpe
19	25	18.4	25	4 090009	4 090009 homo sapien

20	25	18.4	26	2 09R621	09R621 photobacter
21	24.5	18.0	17	4 09UJH1	09UJH1 homo sapien
22	24.5	18.0	22	13 09PS42	13 09PS42 gallus gall
23	24.5	18.0	25	13 09PS41	13 09PS41 gallus gall
24	24	17.6	12	11 064296	11 064296 mus musculu
25	24	17.6	13	2 031364	2 031364 borrelia ga
26	24	17.6	13	2 034622	13 034622 borrelia bu
27	24	17.6	15	11 092114	11 092114 mus musculu
28	24	17.6	19	5 09W508	5 09W508 drosophila
29	24	17.6	22	12 085460	12 085460 avian myelo
30	24	17.6	25	2 067969	2 067969 prochloroco
31	23.5	17.3	15	2 09R407	2 09R407 acinetobact
32	23	16.9	8	2 085406	8 085406 coxiella bu
33	23	16.9	9	5 096417	5 096417 drosophila
34	23	16.9	10	2 09X534	2 09X534 leclercia a
35	23	16.9	10	2 09X533	2 09X533 escherichia
36	23	16.9	13	2 034770	2 034770 borrelia af
37	23	16.9	13	11 035758	11 035758 rattus norv
38	23	16.9	14	6 09TRQ7	6 09TRQ7 bos taurus
39	23	16.9	17	2 09X313	2 09X313 prochloroco
40	23	16.9	18	13 P82068	13 P82068 litorea gen
41	23	16.9	20	2 09R4F1	2 09R4F1 desulfovibr
42	23	16.9	21	4 09UMU6	4 09UMU6 homo sapien
43	23	16.9	21	8 09ZYB7	8 09ZYB7 spinaria sp
44	23	16.9	21	10 041496	10 041496 solanum tub
45	23	16.9	21	12 080817	12 080817 human t-cel

ALIGNMENTS

RESULT 1
ID 031296 PRELIMINARY; PRT; 13 AA.
AC 031296:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, last annotation update)
DE GUAA (FRAGMENT).
GN GUAA.
OS Borrelia afzelii.
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP21;
RX MEDLINE; 97426044.
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D., Rosa P.;
RT "The Borrelia burgdorferi circular plasmid cp26: conservation of
RT plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-374(1997).
DR EMBL; U93696; AAC45526.1; -.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1412 MW; 08EFA2C20E195720 CRC64;

Query Match 24.3%; Score 33; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 80;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 LDGCLLQMDFG 12
Db 1 MNDCAIILDFG 12
RESULT 2
ID 09TR30 PRELIMINARY; PRT; 24 AA.
AC 09TR30:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT VIIA-L (FRAGMENT).

Query Match 16.2%; Score 22; DB 1; Length 26;
Best Local Similarity 71.4%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 17 LLVDFIQ 23
11111:
Db 13 LLYDVYK 19

Search completed: December 21, 2000, 08:40:18
Job time: 116 sec

RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.:
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 CC Electrophoresis 20:1098-1108(1999).
 CC RT
 CC -1- FUNCTION: ASSOCIATED WITH THE OXYGEN-EVOLVING COMPLEX OF
 CC PHOTOSYSTEM II (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE; ASSOCIATED
 CC WITH THE PHOTOSYSTEM II COMPLEX (BY SIMILARITY).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
 CC (SPOT N179) IS: 5.9, ITS MW IS: 22 KDA.
 CC -1- SIMILARITY: TO OTHER OEE2 SUBUNITS.
 CC Photosynthesis; Photosystem II; Chloroplast; Thylakoid membrane.
 FT NON TER 13 13
 SQ SEQUENCE 13 AA: 1294 MW: C6772BD54D7C44D CRC64;

Query Match 16.2%; Score 22; DB 1; Length 13;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 FGPRK 15
 11 11
 Db 9 FGAPK 13

RESULT 13
 CHH3_BOMMO STANDARD; PRT; 17 AA.
 ID CHH3_BOMMO
 AC P20729;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE CHORION CLASS HIGH-CYSTEINE HCA PROTEIN 13 PRECURSOR (HC-A.13)
 DE (FRAGMENT).
 OS Bombyx mori (Silk moth).
 OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Bombycoidea; Bombycidae; Bombyx.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85083111.
 RA Rodakis G.C., Lecanidou R., Rickbush T.H.;
 RT "Diversity in a chorion multigene family created by tandem
 RT duplications and a putative gene-conversion event.";
 RL J. Mol. Evol. 20:265-273(1984).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF MANY FROM THE EGGSHELL OF THE
 CC SILK MOTH.
 CC -1- SIMILARITY: MEMBER OF THE ALPHA-BRANCH OF CHORION PROTEIN TO WHICH
 CC BELONG CLASSES A, CA AND HCA.
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 CC EMBL: X01068; CAB57790.1; -.
 DR PIR: B23219; B23219.
 DR Eggshell; Chorion; Repeat; Multigene family; Signal.
 FT SIGNAL 1
 FT NON TER 17 17
 SQ SEQUENCE 17 AA: 1913 MW: 5E634508C5355C9C CRC64;

Query Match 16.2%; Score 22; DB 1; Length 17;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LDGCLL 6
 1 1111

Db 11 VOGCLI 16

RESULT 14
 COXN_THUOB STANDARD; PRT; 20 AA.
 ID COXN_THUOB
 AC P80980;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE VIIB-HEART (EC 1.9.3.1) (FRAGMENT).
 OS Thunnus obesus (Bigeye tuna).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
 CC Scombridae; Thunnus.
 RN [1]
 RP SEQUENCE.
 RP TISSUE=HEART;
 RX MEDLINE; 97454291.
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver.";
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
 CC 4 FERRICYTOCHROME C.
 CC Oxidoreductase; Mitochondrion.
 FT NON TER 20 20
 SQ SEQUENCE 20 AA: 2303 MW: 0A33BD34006E5AA6 CRC64;

Query Match 16.2%; Score 22; DB 1; Length 20;
 Best Local Similarity 57.1%; Pred. No. 1.9e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 10 DGFPRKH 16
 1 1111
 Db 14 DNGMPVH 20

RESULT 15
 CT21_LITCI STANDARD; PRT; 26 AA.
 ID CT21_LITCI
 AC P81847; P81848; P81849; P81850;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CITROPIN 2.1.3 [CONTAINS: CITROPIN 2.1.2; CITROPIN 2.1.1; CITROPIN
 DE 2.1].
 OS Litoria citropa (Australian blue mountains tree frog).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 CC Litoria.
 RN [1]
 RP SEQUENCE.
 RP TISSUE=SKIN;
 RX MEDLINE; 99435977.
 RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
 RA Wallace J.C., Tyler M.J.;
 RT "Host defence peptides from the skin glands of the Australian blue
 RT mountains tree-frog Litoria citropa. Solution structure of the
 RT antibacterial peptide citropin 1.1.";
 RL Eur. J. Biochem. 265:627-637(1999).
 CC -1- TISSUE SPECIFICITY: DORSAL AND SUBMENTAL SKIN GLANDS.
 FT PEPTIDE 1 22 CITROPIN 2.1.
 FT PEPTIDE 1 23 CITROPIN 2.1.1.
 FT PEPTIDE 1 25 CITROPIN 2.1.2.
 FT PEPTIDE 1 26 CITROPIN 2.1.3.
 SQ SEQUENCE 26 AA: 2519 MW: 7490C28BB2E4899A CRC64;

OY 14 PKHLV 19
1 1111
DB 7 PFHLV 12

RESULT 9

DCM_PSECF ID DCM_PSECF STANDARD: PRT: 14 AA.
AC P1914;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARBON MONOXIDE DEHYDROGENASE MEDIUM CHAIN (EC 1.2.99.2) (FRAGMENT).
OS Pseudomonas carboxydoflava.
OC Bacteria: Proteobacteria; Beta subdivision; Comamonadaceae;
OC Hydrogenophaga.
RN 11
RP SEQUENCE.
RX MEDLINE: 90055678.
RA Kraut M., Hugendieck I., Herzig S., Meyer O.;
RT "Homology and distribution of Co dehydrogenase structural genes in
RT carboxydoflavobacteria."
RL Arch. Microbiol. 152:335-341(1989).
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
CC ACCEPTOR.
CC -1- COFACTOR: MOLYBDENUM.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR: PL0142; PL0142.
KW Oxidoreductase; Molybdenum.
FT NON_TER 14
FT SEQUENCE 14 AA: 1756 MM: 65583C6D1FB7C25B CRC64:

Query Match 17.6%; Score 24; DB 1; Length 14;
Best Local Similarity 23.1%; Pred. No. 6.3e+02;
Matches 3; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 5 LLLQMDGFPKH 17
1 1111
DB 2 MIPREYHAPKHV 14

RESULT 10

YCXD_ODOSI ID YCXD_ODOSI STANDARD: PRT: 26 AA.
AC P49839;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HYPOTHETICAL 3.2 KDA PROTEIN IN RPOC2-RPS2 INTERGENIC REGION (ORF26B).
OS Odontella sinensis.
OC Chloroplast.
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
OC Bidulphiophycidae; Eupodiscaceae; Odontella.
RN 11
RP SEQUENCE FROM N.A.
RA Kowalik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.;
RT "The chloroplast genome of a chlorophyll a+c-containing alga,
RT Odontella sinensis."
RL Plant Mol. Biol. Rep. 13:336-342(1995).
CC -----
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CC -----
DR EMBL: Z67753; CAA91747.1;
KW Chloroplast; Hypothetical protein.

SO SEQUENCE 26 AA: 3137 MM: 8305B587C0A30B36 CRC64;

Query Match 17.3%; Score 23.5; DB 1; Length 26;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

OY 1 LDG---CLL 7
1 1111
DB 10 LDGFIECLLM 19

RESULT 11

DHE2_THUTH ID DHE2_THUTH STANDARD: PRT: 16 AA.
AC P20016;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE NAD-SPECIFIC GLUTAMATE DEHYDROGENASE (EC 1.4.1.2) (NAD-GDH)
DE (FRAGMENT).
OS Thunnus thynnus (Bluefin tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
RN 11
RP SEQUENCE.
RX TISSUE=LIVER;
RX MEDLINE: 76253947.
RA Veronese F.M., Bevilacqua R., Bocu E., Brown D.M.;
RT "Purification, characteristics and sequence of a peptide containing
RT an essential lysine residue."
RL Biochim. Biophys. Acta 445:1-13(1976).
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE + H(2)O + NAD(+) = 2-OXOGLUTARATE
CC + NH(3) + NADH.
CC -1- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
DR PIR: A12729; A12729.
DR INTERPRO: IPR001625;
DR PROSITE: PS00074; GLFV_DEHYDROGENASE, PARTIAL.
KW Oxidoreductase; NAD.
FT NON_TER 1
FT ACT_SITE 12
FT NON_TER 16
FT SEQUENCE 16 AA: 1518 MM: FF299AA7C5F1062E CRC64:

Query Match 16.9%; Score 23; DB 1; Length 16;
Best Local Similarity 33.3%; Pred. No. 1e+03;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 4 CLLQMDGFPK 15
1 1111
DB 1 CAVVDVFGGAK 12

RESULT 12

PSBP_PINPS ID PSBP_PINPS STANDARD: PRT: 13 AA.
AC P81668;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE OXYGEN-EVOLVING ENHANCER PROTEIN 2 (OEE2) (23 KDA SUBUNIT OF OXYGEN
DE EVOLVING SYSTEM OF PHOTOSYSTEM II) (FRAGMENT).
GN PSBP.
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Coniferales; Coniferales; Pinaceae; Pinus.
RN 11
RP SEQUENCE.
RX TISSUE=NEEDLE;
RX MEDLINE: 99274088.

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
 DR PIR: S43632; S43632.
 KM Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 23
 SQ SEQUENCE 23 AA; 2635 MW; BCBEDA3FBAD9C509 CRC64;

Query Match 19.9%; Score 27; DB 1; Length 23;
 Best Local Similarity 50.0%; Pred. No. 3.6e+02;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 6 LLQMDGFPKHL 17
 | | | | |
 Db 11 LFOAXNGIPVXL 22

RESULT 6
 COX_CANFA STANDARD; PRT; 23 AA.

AC G9TR28;
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-HEART, MITOCHONDRIAL
 DE (EC 1.9.3.1) (CYTOCHROME C OXIDASE SUBUNIT VIIA-H) (COX VIIA-M)
 DE (FRAGMENT).
 GN COX7A1 OR COX7AH.
 OS Canis familiaris (dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN, AND HEART;
 RX MEDLINE: 96092035.
 RA Linder D., Freund R., Kadenbach B.;
 RL "Species-specific expression of cytochrome c oxidase isozymes."; Comp. Biochem. Physiol. 112B:461-469(1995).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERROCYTOCHROME C.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
 KM Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 23
 SQ SEQUENCE 23 AA; 2627 MW; AD3EA34B61FF73CE CRC64;

Query Match 18.4%; Score 25; DB 1; Length 23;
 Best Local Similarity 50.0%; Pred. No. 7.4e+02;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 6 LLQMDGFPKHL 17
 | | | | |
 Db 11 LFOADNGIPVXL 22

RESULT 7
 CH60_DROME STANDARD; PRT; 11 AA.

AC P35380;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MITOCHONDRIAL MATRIX PROTEIN PI (60 KDA CHAPERONIN) (HEAT SHOCK PROTEIN 60) (HSP-60) (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).
 GN MHP-PI OR HSP60.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephyridiidae; Drosophilidae; Drosophila.
 RN [1]

RP SEQUENCE.
 RC STRAIN=VALLECAS; TISSUE=WING IMAGINAL DISK;
 RX MEDLINE: 93272852.
 RA Santaren J.F., van Damme J., Puyse M., Vandekerckhove J.,
 RA Garcia-Bellido A.;
 RT "Identification of Drosophila wing imaginal disc proteins by two-dimensional gel analysis and microsequencing";
 RT Exp. Cell Res. 206:220-226(1993).
 RL Exp. Cell Res. 206:220-226(1993).
 CC -1- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL MATRIX (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
 DR FLTBASE; FBgn0010375; Mmp-P1.
 DR INTERPRO; IPR001844; .
 DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
 KM Chaperone; ATP-binding; Mitochondrion.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1243 MW; 78501A366365A6DB CRC64;

Query Match 17.6%; Score 24; DB 1; Length 11;
 Best Local Similarity 27.3%; Pred. No. 4.9e+02;
 Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 5 LLQMDGFPK 15
 : : : : :
 Db 1 VIIQSGMSPK 11

RESULT 8
 ANGT_HORSE STANDARD; PRT; 14 AA.

AC P01016;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE ANGIOTENSINOGEN (FRAGMENT).
 GN AGT.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 RN [1]
 RP SEQUENCE.
 RA Skeggs L.T., Jr., Kahn J.R., Lentz K., Shumway N.P.;
 RT "The preparation, purification, and amino acid sequence of a rat polypeptide renin substrate."; J. Exp. Med. 106:439-453(1957).
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.
 CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR; A01250; A01250.
 DR INTERPRO; IPR000215; .
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KM Vasoconstrictor; Plasma; Serpin.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 1 8 ANGIOTENSIN II.
 FT NON_TER 14
 FT NON_TER 14
 SQ SEQUENCE 14 AA; 1759 MW; 2E9921F8EEFBDD7 CRC64;

Query Match 17.6%; Score 24; DB 1; Length 14;
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RX MEDLINE: 76081726.
 RA Birken S., Milner G.D., Canfield R.E.;
 RT "Studies of the structure of canine fibrinogen."
 RL Thromb. Res. 7:599-610(1975).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
 CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
 CC (STRONKER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
 CC MONOMERS.
 DR PIR: A05298; A05298.
 DR INTERPRO: IPR002181; .
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
 DR BLOOD COAGULATION; Plasma.
 FT NON_TER 24
 SQ SEQUENCE 24 AA; 2690 MW; D427050783F52628 CRC64;

Query Match 20.6%; Score 28; DB 1; Length 24;
 Best Local Similarity 45.5%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 DGCCLLLQMDFGPKHLL 18
 DB 6 DMCCLIDREFG 16

RESULT 3
 ID IRBP_SHEEP STANDARD: PRT: 24 AA.
 AC P12663;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE INTERPHOTORECEPTOR RETINOID-BINDING PROTEIN (IRBP) (INTERSTITIAL
 DE RETINOL-BINDING PROTEIN) (FRAGMENT).
 GN RBP3.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 RN (1)
 RP SEQUENCE.
 RX MEDLINE: 86301171.
 RA Fong S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A.,
 RA Bridges C.D.B.;
 RT "N-terminal sequence homologies in interstitial retinol-binding
 RT proteins from 10 vertebrate species."
 RL FEBS Lett. 205:309-312(1986).
 CC -1- FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN
 CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
 CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
 CC -1- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
 CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
 CC EPITHELIUM CELLS.
 DR PIR: A24417; A24417.
 DR Vitamin A; Transport.
 FT NON_TER 24
 SQ SEQUENCE 24 AA; 2799 MW; 02DEBEB61A8E4523 CRC64;

Query Match 20.6%; Score 28; DB 1; Length 24;
 Best Local Similarity 33.3%; Pred. No. 2.6e+02;
 Matches 6; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 LDGCLLLQMDFGPKHLL 18

DB 7 LDMAQVLLDNYTPESLIM 24

RESULT 4
 ID IRBP_PIG STANDARD: PRT: 25 AA.
 AC P12662;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE INTERPHOTORECEPTOR RETINOID-BINDING PROTEIN (IRBP) (INTERSTITIAL
 DE RETINOL-BINDING PROTEIN) (FRAGMENT).
 GN RBP3.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN (1)
 RP SEQUENCE.
 RX MEDLINE: 86301171.
 RA Fong S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A.,
 RA Bridges C.D.B.;
 RT "N-terminal sequence homologies in interstitial retinol-binding
 RT proteins from 10 vertebrate species."
 RL FEBS Lett. 205:309-312(1986).
 CC -1- FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN
 CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
 CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
 CC -1- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
 CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
 CC EPITHELIUM CELLS.
 DR PIR: B24417; B24417.
 DR Vitamin A; Transport.
 FT NON_TER 25
 SQ SEQUENCE 25 AA; 2813 MW; 4E751DFA160231B7 CRC64;

Query Match 20.6%; Score 28; DB 1; Length 25;
 Best Local Similarity 33.3%; Pred. No. 2.7e+02;
 Matches 6; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 LDGCLLLQMDFGPKHLL 18
 DB 7 LDFAKILLDNYTPESLIM 24

RESULT 5
 ID COX1_ONCMY STANDARD: PRT: 23 AA.
 AC P80333;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER (EC 1.9.3.1) (VIIIIC)
 DE (FRAGMENT).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 RN (1)
 RP SEQUENCE.
 RX TISSUE=LIVER;
 RC MEDLINE: 94237150.
 RA Freund R., Kadenbach B.;
 RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
 RT of cytochrome c oxidase isolated from rainbow trout."
 RL Eur. J. Biochem. 221:1111-1116(1994).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O +
 CC 4 FERROCYTOCHROME C.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:40:18 ; Search time 12.36 Seconds
(Without alignments)
67.204 Million cell updates/sec

Title: US-08-934-367-50

Perfect score: 136
Sequence: 1 LDGCLLDMDFGFKHLVDVFLQSIS 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 1478

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	33	24.3	24	1	COXJ_SHEEP
2	28	20.6	24	1	FTBG_CANFA
3	28	20.6	24	1	IRBP_SHEEP
4	28	20.6	25	1	IRBP_PIG
5	27	19.9	23	1	COXJ_ONCMW
6	25	18.4	23	1	COXK_CANFA
7	24	17.6	11	1	CH60_DROME
8	24	17.6	14	1	ANGT_HORSE
9	24	17.6	14	1	DCMM_PSECF
10	23.5	17.3	26	1	YCXD_ODOSI
11	23	16.9	16	1	DHE2_THUTH
12	22	16.2	13	1	PSBP_PINS
13	22	16.2	17	1	CHH3_BOMMO
14	22	16.2	20	1	COXN_THIOB
15	22	16.2	26	1	CT21_LITCI
16	21.5	15.8	25	1	ALR_PSEFL
17	21	15.4	9	1	SAMP_MUSCA
18	21	15.4	23	1	IRBP_RABIT
19	21	15.4	24	1	CR17_LITXA
20	21	15.4	24	1	CR18_LITXA
21	21	15.4	25	1	AMP3_MELGA
22	21	15.4	26	1	AMD1_CHICK
23	21	15.4	26	1	AMD1_RABIT
24	21	15.4	26	1	MEL_APIDO
25	20	14.7	11	1	TEML_RANNE
26	20	14.7	16	1	MDH_SYNY4
27	20	14.7	18	1	DRPH_UCAPU
28	20	14.7	21	1	ATPB_PHYPA
29	20	14.7	21	1	OMPI_ACTPL
30	20	14.7	21	1	TRYP_PROATP
31	20	14.7	23	1	SODM_RANCA
32	20	14.7	24	1	CCNA_STRTI
33	19	14.0	10	1	GS15_BACSU

34	19	14.0	12	1	CD11_LITXA	P56245	litorea xan
35	19	14.0	12	1	CD14_LITXA	P56246	litorea xan
36	19	14.0	13	1	SODM_CANFA	P54712	canis fam1l
37	19	14.0	19	1	MDH_SHEPU	P82177	shewanella
38	19	14.0	19	1	UP21_SHEPIN	P82027	uperoletia f
39	19	14.0	19	1	UP25_OPEIN	P82031	uperoletia f
40	19	14.0	20	1	ITRA_ALBUU	P24925	albizzia ju
41	19	14.0	21	1	DCMS_PSECA	P19921	pseudomonas
42	19	14.0	24	1	FEDC_AMYME	P80707	amycolatops
43	19	14.0	24	1	LEC_CROST	P16351	crotalaria
44	19	14.0	24	1	PEPT_ASPNG	P55749	aspergillus
45	19	14.0	25	1	BOTR_BOTJA	P22028	botriops ja

ALIGNMENTS

RESULT	1	STANDARD	PRT	24 AA.
COXJ_SHEEP				
ID	COXJ_SHEEP			
AC	O9TR30;			
DT	01-OCT-2000 (Rel. 40, Created)			
DT	01-OCT-2000 (Rel. 40, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	CYTOCHROME C OXIDASE POLYPEPTIDE VITA-LIVER/HEART, MITOCHONDRIAL			
DE	(EC 1.9.3.1) (CYTOCHROME C OXIDASE SUBUNIT VITA-L) (FRAGMENT).			
GN	COX7A2 OR COX7AL.			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Caprinae; Ovis.			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=LIVER, AND HEART;			
RX	MEDLINE: 96092035.			
RA	Linder D., Freund R., Kadenbach B.;			
RT	"Species-specific expression of cytochrome c oxidase isozymes.";			
RL	Comp. Biochem. Physiol. 112B:461-469(1995).			
CC	-1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE			
CC	CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN			
CC	MITOCHONDRIAL ELECTRON TRANSPORT.			
CC	-1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +			
CC	4 FERRICYTOCHROME C.			
CC	-1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.			
CC	-1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VITA FAMILY.			
KW	Oxidoreductase; Inner membrane; Mitochondrion.			
FT	NON TER 24			
SO	SEQUENCE 24 AA; 2795 MW; D49D27C03B61F803 CRC64;			
Query Match 24.3%; Score 33; DB 1; Length 24;				
Best Local Similarity 58.3%; Pred. No. 43;				
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;				
QY	6	LLQMDFGFKHL 17		
DB	11	LFQEDNGIPVHL 22		
RESULT 2				
FTBG_CANFA		STANDARD:	PRT:	24 AA.
ID	FTBG_CANFA			
AC	P12800;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	FIBRINOGEN GAMMA-CHAIN (FRAGMENT).			
GN	FGG.			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
RN	[1]			
RP	SEQUENCE.			

RESULT 14
 PC4030
 rRNA endonuclease (EC 3.1.27.10) - shiitake mushroom (fragment)
 M:Alternate names: nuclease Le3
 C:Species: Lentinula edodes (shiitake mushroom)
 C:Date: 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 20-Mar-1996
 C:Accession: PC4030
 R:Kobayashi, H.; Inokuchi, N.; Koyama, T.; Tomita, M.; Irie, M.
 Biosci. Biotechnol. Biochem. 59, 1169-1171, 1995
 A:Title: Purification and characterization of the 2nd 5'-nucleotide-forming nuclease fr
 A:Reference number: PC4030; MUID:95337563
 A:Accession: PC4030
 A:Molecule type: DNA
 A:Residues: 1-23 <KOB>
 C:Comment: This enzyme has 3'-nucleotidase activity.
 C:Keywords: endonuclease; hydrolase

Query Match 18.4%; Score 25; DB 2; Length 23;
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 11 FCFPKHLVDFLQS 24
 :| | | | :|
 DB 1 WGMIGHLVGFAS 14

RESULT 15
 B61597
 cytochrome P450 AL-2 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
 C:Accession: B61597
 R:Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.
 Drug Metab. Dispos. 19, 291-297, 1991
 A:Title: Purification and aminopyrine monooxygenase activity of liver microsomal cytochr
 A:Reference number: A61597; MUID:91292910
 A:Accession: B61597
 A:Status: Preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <SHI>

Query Match 18.0%; Score 24.5; DB 2; Length 14;
 Best Local Similarity 47.1%; Pred. No. 9.7e+02;
 Matches 8; Conservative 1; Mismatches 3; Indels 5; Gaps 1;

QY 5 LLLQMDGFRPKHLVDF 21
 |||:| ||| |
 DB 3 LLLSLSF----LVGF 14

Search completed: December 21, 2000, 08:39:30
 Job time: 134 sec

C:Superfamily: mammalian cytochrome-c oxidase chain VIIA
C:Keywords: liver, membrane-associated complex; mitochondrion; oxidoreductase

Query Match 19.9%; Score 27; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 6.7e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 LQMDFGPKHL 17
| | | | |
Db 11 LFOAXNGIPVHL 22

RESULT 9

PC2199 alicyclic amine N-sulfoltransferase (EC 2.8.2.-) - rat (fragment)

N:Alternate names: NST-1

C:Species: Rattus norvegicus (Norway rat)

C>Date: 06-Sep-1994 #sequence_revision 05-Apr-1995 #text_change 03-May-1996

C:Accession: PC2199

R:Naritomi, Y.; Niwa, T.; Shiraga, T.; Iwasaki, K.; Noda, K.

Biol. Pharm. Bull. 17, 1008-1011, 1994

A:Title: Isolation and characterization of an alicyclic amine N-sulfoltransferase from fe

A:Reference number: PC2199; MUID:95119961

A:Accession: PC2199

A:Molecule type: protein

A:Residues: 1-24 <NAR>

A:Experimental source: liver

C:Comment: This enzyme catalyzes sulfonation not only of the alicyclic amine but also de

C:Superfamily: alcohol sulfoltransferase

C:Keywords: sulfoltransferase

Query Match 19.9%; Score 27; DB 2; Length 24;
Best Local Similarity 62.5%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 FGFPKHL 18
| | | | |
Db 14 FGFPKRL 21

RESULT 10

S59492

formate dehydrogenase alpha chain - Alcaligenes eutrophus (fragment)

C:Species: Alcaligenes eutrophus

C>Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999

C:Accession: S59492

R:Friedebold, J.; Mayer, F.; Bill, E.; Trautwein, A.X.; Bowlen, B.

Biol. Chem. Hoppe-Seyler 376, 561-568, 1995

A:Title: Structural and immunological studies on the soluble formate dehydrogenase from

A:Reference number: S59492; MUID:96145736

A:Accession: S59492

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <PRI>

Query Match 19.1%; Score 26; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 6.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 QMDFGFP 14
| | | | |
Db 6 EIDFGFP 12

RESULT 11

PX0078

alanine dehydrogenase (EC 1.4.1.1) - oscillatoriacean cyanobacterium (fragment)

C:Species: oscillatoriacean cyanobacterium

C>Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 07-May-1999

C:Accession: PX0078

R:Sawa, Y.; Tanl, M.; Murata, K.; Shibata, H.; Ochiai, H.

J. Biochem. 116, 995-1000, 1994

A:Title: Purification and characterization of alanine dehydrogenase from a cyanobacte

A:Reference number: PX0078; MUID:95204408

A:Accession: PX0078

A:Molecule type: protein

A:Residues: 1-21 <Saw>

A:Note: The source is designated as Phormidium lapideum

C:Comment: This enzyme catalyzes a reversible oxidative deamination of L-alanine to p

C:Superfamily: alanine dehydrogenase; alanine dehydrogenase homology

C:Keywords: oxidoreductase

Query Match 19.1%; Score 26; DB 2; Length 21;
Best Local Similarity 44.4%; Pred. No. 8.7e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 MDGFPKHL 17
| | | | |
Db 1 MEIGVPKEI 9

RESULT 12

T44936 calmodulin kinase 2 - fission yeast (Schizosaccharomyces pombe) (fragment)

C:Species: Schizosaccharomyces pombe

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000

C:Accession: T44936

R:Alamy, V.; Allague, R.

submitted to the EMBL Data Library, May 1996

A:Reference number: Z2873

A:Accession: T44936

A>Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-16 <ALP>

A:Cross-references: EMBL:U57982; PIDD:AA09466.1

Query Match 18.4%; Score 25; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FGFP 14
| | | | |
Db 5 FGFP 8

RESULT 13

A60743

ornithine carbamoyltransferase (EC 2.1.3.3), anabolic - Aeromonas formicans (fragment

C:Species: Aeromonas formicans

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: A60743

R:Riticol, C.; De Coen, J.L.; Momin, P.; Falmagne, P.; Stalon, V.

J. Gen. Microbiol. 135, 2453-2464, 1989

A:Title: Evolutionary relationships among bacterial carbamoyltransferases.

A:Reference number: A60743; MUID:90188287

A:Accession: A60743

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-17 <TRI>

C:Keywords: transferase

Query Match 18.4%; Score 25; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 KHLVD 20
| | | | |
Db 1 KHLKD 6

A05298
fibrinogen gamma chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 10-Mar-1994
C:Accession: A05298
R:Birken, S.; Walner, G.D.; Canfield, R.E.
Thromb. Res. 7, 599-610, 1975
A:Title: Studies of the structure of canine fibrinogen.
A:Reference number: A94308; MUID:76081726
A:Accession: A05298
A:Molecule type: protein
A:Residues: 1-24 <DIR>
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: blood coagulation; liver; plasma

Query Match 20.6%; Score 28; DB 2; Length 24;
Best Local Similarity 45.5%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 LDGCLLQMDFGPKHLL 18
DB 6 DMCCLILDERFG 16

RESULT 4
A24417
Interphotoreceptor retinoid-binding protein - sheep (fragment)
N:Alternate names: Interstitial retinol-binding protein
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Nov-1997
C:Accession: A24417
R:Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
FEBS Lett. 205, 309-312, 1986
A:Title: N-terminal sequence homologues in interstitial retinol-binding proteins from 10
A:Reference number: A91365; MUID:86301171
A:Accession: A24417
A:Molecule type: protein
A:Residues: 1-24 <RON>
C:Superfamily: Interphotoreceptor retinoid-binding protein
C:Keywords: duplication

Query Match 20.6%; Score 28; DB 2; Length 24;
Best Local Similarity 33.3%; Pred. No. 4.9e+02;
Matches 6; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 LDGCLLQMDFGPKHLL 18
DB 7 LDMAQVLLDNYTFPEMLM 24

RESULT 5
B24417
Interphotoreceptor retinoid-binding protein - pig (fragment)
N:Alternate names: Interstitial retinol-binding protein
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Nov-1997
C:Accession: B24417
R:Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
FEBS Lett. 205, 309-312, 1986
A:Title: N-terminal sequence homologues in interstitial retinol-binding proteins from 10
A:Reference number: A91365; MUID:86301171
A:Accession: B24417
A:Molecule type: protein
A:Residues: 1-25 <RON>
C:Superfamily: Interphotoreceptor retinoid-binding protein
C:Keywords: duplication

Query Match 20.6%; Score 28; DB 2; Length 25;
Best Local Similarity 33.3%; Pred. No. 5.1e+02;
Matches 6; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 LDGCLLQMDFGPKHLL 18
DB 7 LDRAKILLDNYTFPEMLM 24

RESULT 6
S36662
dermorphin (Iys-7) [validated] - two-colored leaf frog
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 31-Mar-2000
C:Accession: S36662
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Espamer, G.; Krell,
FEBS Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of
A:Reference number: S21152; MUID:92339502
A:Accession: S36662
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIC>

Query Match 19.9%; Score 27; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 11 FGPK 15
DB 3 FGPK 7

RESULT 7
A32521
hexokinase (EC 2.7.1.1) I peptide III - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 12-Apr-1995
C:Accession: A32521
R:Schlirch, D.M.; Wilson, J.E.
Arch. Biochem. Biophys. 257, 1-12, 1987
A:Title: Rat brain hexokinase: amino acid sequence at the substrate hexose binding s1
A:Reference number: A90080; MUID:87324917
A:Accession: A32521
A:Molecule type: protein
A:Residues: 1-21 <SCH>
C:Superfamily: human hexokinase I; hexokinase homology
C:Keywords: ATP; glycolysis; phosphotransferase

Query Match 19.9%; Score 27; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 7 LQMDFGPKH 16
DB 3 LGFTFSFPKH 12

RESULT 8
S43632
cytochrome-c oxidase (EC 1.9.3.1) chain VIIa, hepatic - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1997
C:Accession: S43632
R:Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A:Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cyto
A:Reference number: S43624; MUID:94237150
A:Accession: S43632
A:Molecule type: protein
A:Residues: 1-23 <FRE>
A:Note: the source is designated as Salmo gairdneri
C:Genetics:
A:Genome: nuclear

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:39:30 ; Search time 19.49 Seconds
(without alignments)
84.657 Million cell updates/sec

Title: US-08-934-367-50

Perfect score: 136
Sequence: 1 LDGCLLQMDFGFPPKHLVDFLOSLIS 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 5255

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	21.3	26	2	B59018 MUC1 enhancer bind
2	28	20.6	19	2	A39504 octamer-binding pr
3	28	20.6	24	2	A05298 fibrinogen gamma C
4	28	20.6	24	2	A24417 interphotoreceptor
5	28	20.6	25	2	B24417 interphotoreceptor
6	27	19.9	7	2	S36662 dermatophin (lys-7)
7	27	19.9	21	2	A32521 hexokinase (EC 2.7
8	27	19.9	23	2	S43632 cytochrome-c oxida
9	27	19.9	24	2	PC2199 allylcyclic amine N-
10	26	19.1	15	2	S59492 formate dehydrogen
11	26	19.1	21	2	PX0078 alanine dehydrogen
12	25	18.4	16	2	T44936 calmodulin kinase
13	25	18.4	17	2	A60743 ornithine carbamoy
14	25	18.4	23	2	PC4030 rRNA endonuclease
15	24.5	18.0	14	2	B61597 cytochrome P450 AL
16	24	17.6	13	2	S03879 6-phosphofructokin
17	24	17.6	14	2	A01250 angiotensin precur
18	24	17.6	14	2	PL0142 carbon-monoxide de
19	24	17.6	15	2	A60834 angiotensin I prec
20	24	17.6	15	2	D48394 major fat-globule
21	24	17.6	17	2	S71864 glutathione transf
22	24	17.6	17	2	B31769 T-cell receptor de
23	24	17.6	18	2	PN0175 glutathione transf
24	24	17.6	19	2	B60822 cytochrome P450 UT
25	24	17.6	20	2	A37984 ADP-ATP carrier pr
26	24	17.6	21	2	A42762 multicatalytic end
27	24	17.6	22	2	A35418 brain natriuretic
28	23.5	17.3	26	2	S78574 hypothetical prote
29	23	16.9	14	2	PA0104 protein QF200070 -

30	23	16.9	16	2	A12729 glutamate dehydrog
31	23	16.9	19	2	PH1756 T cell receptor al
32	23	16.9	19	2	I46654 T-cell receptor de
33	23	16.9	20	2	A41439 acid ribonuclease
34	23	16.9	21	2	T07683 proteinase inhibit
35	23	16.9	24	2	T42257 phosphoprotein pho
36	23	16.9	24	2	A19828 female protein - h
37	23	16.9	25	2	I51565 protein-tyrosine k
38	23	16.9	26	2	A42218 early protein Sx1
39	22	16.2	7	1	A61324 dermatophin - Rohde
40	22	16.2	10	2	S13324 virg protein - Agr
41	22	16.2	11	2	PT0250 Ig heavy chain CRD
42	22	16.2	12	2	C36201 1-aminocyclopropan
43	22	16.2	14	2	A61002 photosystem II oxy
44	22	16.2	15	2	S71306 heat shock protein
45	22	16.2	17	2	C37520 glutathione transf

ALIGNMENTS

RESULT 1
B59018
MUC1 enhancer binding protein 85k chain MUC1EBP-85 - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998
C:Accession: B59018
R:AbE, M.; Smith, C.J.; Larson, C.J.
Submitted to the Protein Sequence Database, May 1998
A:Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a
A:Reference number: A59018
A:Accession: B59018
A:Molecule type: protein
A:Residues: 1-17:18-26 <RBE>
A:Experimental source: breast cancer cell line MCF-7
C:Keywords: DNA binding; heterodimer

Query Match 21.3%; Score 29; DB 2; Length 26;
Best Local Similarity 37.5%; Pred. No. 3.7e+02;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 5 LLDQMDFGFPPKHLVD 20
DB 9 VVLXMDVGFTLEPLE 24

RESULT 2
A39504
octamer-binding protein, Ku-like, 72k chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: A39504
R:May, G.; Sutton, C.; Gould, H.
J. Biol. Chem. 266, 3052-3059, 1991
A:Title: Purification and characterization of Ku-2, an octamer-binding protein relate
A:Reference number: A39504; MUID:91131605
A:Accession: A39504
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <MAY>

Query Match 20.6%; Score 28; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 LQMDGFG 13
DB 11 LEMDVGF 17

RESULT 3

; FILING DATE: 07 June 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; US-08-482-142-22

Query Match 21.3%; Score 29; DB 2; Length 26;
Best Local Similarity 41.7%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 DCCLLQMDPGF 13
11 : 1 1 1 :
Db 11 DGTRIQDNGY 22

RESULT 15
US-08-478-572-22
; Sequence 22, Application US/08478572
; Patent No. 5968526
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,572
; FILING DATE: 07-June-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/445,307
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017,605
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; US-08-478-572-22

Query Match 21.3%; Score 29; DB 2; Length 26;
Best Local Similarity 41.7%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 DCCLLQMDPGF 13
11 : 1 1 1 :
Db 11 DGTRIQDNGY 22

Search completed: December 21, 2000, 08:39:07
Job time: 141 sec

CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,618A
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,725
FILING DATE: 07-JUN-1995
APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-12/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-618A-22

Query Match 21.3%; Score 29; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 MDGFPKHL 18
Db 9 IDHPYNELL 18

RESULT 13
US-08-483-952A-22
Sequence 22, Application US/08483952A
Patent No. 6011139
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Erlander, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flenr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,952A
FILING DATE: 07-JUN-1995

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,859
FILING DATE: 17-SEP-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-7/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-952A-22

Query Match 21.3%; Score 29; DB 3; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 MDGFPKHL 18
Db 9 IDHPYNELL 18

RESULT 14
US-08-482-142-22
Sequence 22, Application US/08482142
Patent No. 5820862
GENERAL INFORMATION:
APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,142
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/445,307

TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-08-973-225-142

Query Match 21.3%; Score 29; DB 3; Length 18;
Best Local Similarity 36.8%; Pred. No. 99;
Matches 7; Conservative 2; Mismatches 2; Indels 8; Gaps 1;

OY 2 DGCILLQMDFGPKHLVD 20
||| | :|||
Db 3 DGCYL-----RHVLMVD 13

RESULT 10
US-09-244-298A-142
; Sequence 142, Application US/09244298A
; Patent No. 6121238
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Baird, Ronald W.
; APPLICANT: Gwila, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Magstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Depirnce, Randolph B.
; APPLICANT: Poddaturi, Surekha
; APPLICANT: Yin, Qun
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/244,298A
; FILING DATE: 11-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-244-298A-142
Query Match 21.3%; Score 29; DB 3; Length 18;

Best Local Similarity 36.8%; Pred. No. 99;
Matches 7; Conservative 2; Mismatches 2; Indels 8; Gaps 1;

OY 2 DGCILLQMDFGPKHLVD 20
||| | :|||
Db 3 DGCYL-----RHVLMVD 13

RESULT 11
US-08-484-530-22
; Sequence 22, Application US/08484530
; Patent No. 5846740
; GENERAL INFORMATION:
; APPLICANT: Tobin, Allan J
; APPLICANT: Erlander, Mark G
; APPLICANT: Kaufman, Daniel L.
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albrighton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,530
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Treccartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-60780-8/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-530-22

Query Match 21.3%; Score 29; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 9 MDGEPKHL 18
||| :|||
Db 9 IDHVPNELL 18

RESULT 12
US-08-827-618A-22
; Sequence 22, Application US/08827618A
; Patent No. 5998366
; GENERAL INFORMATION:
; APPLICANT: Tobin, Allan J
; APPLICANT: Erlander, Mark G
; APPLICANT: Kaufman, Daniel L.
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albrighton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
US-08-827-618A-22

TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IB/IX
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,597
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timlan, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-556-597-60

Query Match 21.3%; Score 29; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDGCLLL 7
DB 2 LDGCFLL 8

RESULT 8
US-08-764-640-142
Sequence 142, Application US/08764640
Patent No. 5869451
Patent No. 5869451 5837683
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwiria, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palanlappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Deprijnce, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA

ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-764-640-142

Query Match 21.3%; Score 29; DB 2; Length 18;
Best Local Similarity 36.8%; Pred. No. 99;
Matches 7; Conservative 2; Mismatches 2; Indels 8; Gaps 1;

QY 2 DGCILLMDFGFKHLVD 20
DB 3 DGCFL-----RHWMLD 13

RESULT 9
US-08-973-225-142
Sequence 142, Application US/08973225A
Patent No. 6083913
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwiria, Steven E.
APPLICANT: Duffin, David J.
APPLICANT: Gates, Christian
APPLICANT: Haselden, Sherril S.
APPLICANT: Matheakis, Larry C.
APPLICANT: Schatz, Peter J.
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: THROMBOPOIETIN RECEPTOR
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK306505M
TELECOMMUNICATION INFORMATION:

CLASSIFICATION: 422
ATTORNEY/AGENT INFORMATION:
NAME: Shannon, Karen L.
REGISTRATION NUMBER: 36,675
REFERENCE/DOCKET NUMBER: 8597/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-620-151-17

Query Match 21.7%; Score 29.5; DB 2; Length 26;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

OY 4 CILLQMDGFPKHL 18
1 : 11:11:1
DB 4 CKICSRSEFG-KHVL 17

RESULT 5
US-08-765-783A-83
Sequence 83, Application US/08765783A
Patent No. 5994524
GENERAL INFORMATION:
APPLICANT: Matsushima, Kouji
APPLICANT: Yamamoto, Yoshihiro
APPLICANT: Yamada, Yoshiki
APPLICANT: Sato, Koh
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
TITLE OF INVENTION: Interleukin-8
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,783A
FILING DATE: 07-MAR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-765-783A-83

Query Match 21.3%; Score 29; DB 2; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 QMDGFPK 15
1 : 1111:
DB 1 QHHEGFPK 8

RESULT 6
US-08-406-330-60
Sequence 60, Application US/08406330
Patent No. 5817748
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,330
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-330-60

Query Match 21.3%; Score 29; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LDGCLLL 7
1 : 1111:
DB 2 LDGCFLL 8

RESULT 7
US-08-556-597-60
Sequence 60, Application US/08556597
Patent No. 5877155
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2000, 08:39:07 ; Search time 17.58 Seconds
(Without alignments)
24.789 Million cell updates/sec

Title: US-08-934-367-50
Perfect score: 136
Sequence: 1 LDGCLLDQDFGPKHLVDFLOSL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 1676186 residues

Total number of hits satisfying chosen parameters: 99815

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
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5: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	22.8	11	1	US-08-039-778B-3
2	31	22.8	22	1	US-08-039-778B-2
3	30	22.1	20	1	US-08-199-508-2
4	29.5	21.7	26	2	US-08-620-151-17
5	29	21.3	9	2	US-08-765-783A-83
6	29	21.3	12	2	US-08-406-330-60
7	29	21.3	18	2	US-08-556-597-60
8	29	21.3	18	2	US-08-764-640-142
9	29	21.3	18	3	US-08-573-225-142
10	29	21.3	18	3	US-08-573-225-142
11	29	21.3	20	2	US-09-244-298A-142
12	29	21.3	20	2	US-08-484-530-22
13	29	21.3	20	2	US-08-827-618A-22
14	29	21.3	20	2	US-08-483-952A-22
15	29	21.3	26	2	US-08-482-142-22
16	29	21.3	26	2	US-08-478-572-22
17	28	20.6	9	3	US-08-441-018-40
18	28	20.6	17	1	US-08-370-567-7
19	28	20.6	17	1	US-08-438-759-7
20	28	20.6	17	4	PCT-US94-05684-7
21	28	20.6	21	3	US-08-802-981-112
22	28	20.6	21	3	US-08-802-981-113
23	28	20.6	22	3	US-08-940-095-133
24	28	20.6	22	3	US-08-940-093-133
25	28	20.6	26	1	US-08-940-096-133
26	28	20.6	26	1	US-08-475-989-27
27	28	20.6	26	2	US-08-482-142-37
28	28	20.6	26	2	US-08-482-142-134
29	28	20.6	26	2	US-08-482-142-168

29	28	20.6	26	2	US-08-478-572-37	Sequence 37, Appl
30	28	20.6	26	2	US-08-478-572-134	Sequence 134, App
31	28	20.6	26	2	US-08-478-572-168	Sequence 168, App
32	28	20.6	26	2	US-08-475-985-27	Sequence 27, Appl
33	28	20.6	26	2	US-08-256-839-27	Sequence 27, Appl
34	28	20.6	26	4	PCT-US95-04481-13	Sequence 13, Appl
35	28	20.6	26	4	PCT-US95-04481-30	Sequence 40, Appl
36	27.5	20.2	26	3	US-08-630-172-40	Sequence 39, Appl
37	27	19.9	9	2	US-08-482-651-39	Sequence 85, Appl
38	27	19.9	15	2	US-08-482-142-85	Sequence 85, Appl
39	27	19.9	15	2	US-08-478-572-85	Sequence 85, Appl
40	27	19.9	19	1	US-07-977-696C-36	Sequence 36, Appl
41	27	19.9	19	1	US-08-129-930B-36	Sequence 36, Appl
42	27	19.9	20	1	US-08-399-696-88	Sequence 88, Appl
43	27	19.9	20	2	US-08-733-505A-48	Sequence 48, Appl
44	27	19.9	20	2	US-08-934-915-7	Sequence 7, Appl
45	27	19.9	20	2	US-08-706-741B-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1
US-08-039-778B-3
; Sequence 3, Application US/08039778B
; Patent No. 5436137
; GENERAL INFORMATION:
; APPLICANT: Spindel, Eliot R.
; APPLICANT: Vijayaraghavan, Srinivasan
; APPLICANT: Nagalla, Srinivasa R.
; APPLICANT: Li, Kang
; TITLE OF INVENTION: DNA SEQUENCE WHICH ENCODES A
; TITLE OF INVENTION: PEPTIDE CAPABLE OF PROMOTING
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/039,778B
; FILING DATE: 19930323
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/919,731
; FILING DATE: 27 July, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00537/068002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-039-778B-3
Query Match 22.8%; Score 31; DB 1; Length 11;
Best Local Similarity 43.8%; Pred. No. 25;


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OS      Homo sapiens.
XX
PN      M09924836-A1.
XX
PD      20-MAY-1999.
XX
PF      04-NOV-1998; 98WO-US23435.
XX
PR      17-NOV-1997; 97US-0066100.
PR      07-NOV-1997; 97US-0064900.
PR      07-NOV-1997; 97US-0064908.
PR      07-NOV-1997; 97US-0064911.
PR      07-NOV-1997; 97US-0064912.
PR      07-NOV-1997; 97US-0064983.
PR      07-NOV-1997; 97US-0064984.
PR      07-NOV-1997; 97US-0064985.
PR      07-NOV-1997; 97US-0064987.
PR      17-NOV-1997; 97US-0066090.
PR      17-NOV-1997; 97US-0066094.
PR      17-NOV-1997; 97US-0066095.
PR      17-NOV-1997; 97US-0066089.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Carter KC, Ebner R, Endress GA, Feng P, Janat F,
PI      Kyaw H, Lafleur DW, Moore PA, Ni J, Olsen HS, Rosen CA;
PI      Ruben SM, Shi Y, Soppet DR, Wei Y;
XX
DR      MPI: 1999-337740/28.
DR      N-PSDB; X85016.
XX
PT      New human secreted proteins and coding sequences useful for treating
PT      disorders of the immune system and hyperproliferative disorders
XX
PS      Disclosure: Page 119; 507pp; English.
XX
CC      This sequence represents a secreted human protein encoded by the gene
CC      clone detailed in the descriptor line. The gene can be used to generate
CC      fusion proteins by linking to the gene to a human immunoglobulin Fc
CC      portion (e.g. X84924) for increasing the stability of the fused protein
CC      as compared to the human protein only.
CC      The invention relates to 125 novel genes and their fragments (nucleic
CC      acid sequences: X84933-X85057; amino acid sequences Y27567-Y27933) which
CC      are useful for preventing, treating or ameliorating medical conditions
CC      e.g. by protein or gene therapy. Also, pathological conditions can be
CC      diagnosed by determining the amount of the new polypeptides in a sample
CC      or by determining the presence of mutations in the new polynucleotides.
CC      Specific uses are described for each of the 125 polynucleotides, based on
CC      which tissues they are most highly expressed in (see X84933 for described
CC      uses).
XX
SQ      Sequence 14 AA;

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Query Match      23.5%; Score 32; DB 20; Length 14;
Best Local Similarity 61.5%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Db      1 phsrsvsfqlgls 13

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 Job time: 150 sec

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OY 11 FGPKHLVDFLOSLS 26
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 Db 1 fgfpehlivdfqsls 16

RESULT 11
 W24294
 ID W24294 standard; peptide; 11 AA.
 XX
 AC W24294;

XX 17-OCT-1997 (first entry)
 DT
 XX

DE Human/Rabbit CERP common peptide.
 XX

KW Immune response; high density lipoprotein; HDL; cholesterol; human;
 KM Serum; epitope; cholesteryl ester transfer protein; CERP; rabbit.
 XX

OS Oryctolagus cuniculus.
 OS Homo sapiens.

XX W09639168-A1.
 PN

XX 12-DEC-1996.
 PD

XX 05-JUN-1996; 96WO-US09143.
 PF

XX 06-JUN-1995; 95US-0482454.
 PR

XX (IMMU-) IMMUNE RESPONSE CORP.
 PA

XX Brostoff SM, Carlo DJ, Kwoh DY;
 PI

XX WPI: 1997-042849/04.
 DR

XX Stimulating an immune response to increase high density lipoprotein
 PT - avoids repeated administration of toxic drugs to lower cholesteryl
 PT ester transfer protein levels
 XX

XX Claim 5; Page 16; 26pp; English.
 PS

XX The sequences given in W24292-94 were used in the method of the
 CC invention to stimulate an immune response to increase high density
 CC lipoprotein (HDL) cholesterol in a mammal exhibiting low levels of
 CC serum HDL. These peptides represent immunogenic epitopes of
 CC cholesteryl ester transfer protein (CERP). The method utilizes
 CC the body's own immune system to lower CERP levels, thereby increasing
 CC the level of beneficial HDL cholesterol, preferably in serum. The
 CC method avoids the problems associated with the repeated administration
 CC of drugs which have undesirable side effects. This peptide represents
 CC a region of CERP which is common to both human and rabbit proteins.
 XX

XX Sequence 11 AA;
 SQ

Query Match 39.0%; Score 53; DB 18; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLVLDFLOSLS 26
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 Db 1 hlvlvdfqsls 11

RESULT 12
 W38080

ID W38080 standard; Peptide; 21 AA.
 XX

AC W38080;
 XX

DT 23-APR-1998 (first entry)
 XX

DE PPPY motif containing peptide used to bind WW domains.
 XX

XX Peptide recognition unit; WW domain; cell signalling; growth regulation;
 KM Cytoskeleton organisation; targeted drug screening; modulator;
 KW WW domain interaction; YAP protein; dystrophin.
 XX

OS Synthetic.
 OS

XX W09737223-A1.
 PN

XX 09-OCT-1997.
 PD

XX 03-APR-1997; 97WO-US05547.
 PF

XX 03-APR-1996; 96US-0630916.
 PR

XX (CYTO-) CYTOGEN CORP.
 PA

XX (UYNC-) UNIV NORTH CAROLINA.
 XX

PI Fowlkes DM, Kay BK, Pirozzi G;
 XX

DR WPI: 1997-503234/46.
 XX

XX Identifying cell signalling and growth regulatory polypeptides by
 PT reaction with multivalent recognition complex - polypeptides are
 PT useful in targeted drug selection
 XX

PS Disclosure: Fig 15C; 220pp; English.
 XX

XX Peptides W38068-92 contain PPPY-like motifs. The PPP motif is
 CC found in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides
 CC containing this residue have been shown to bind the YAP WW domain, but
 CC not the WW domain from dystrophin or to a panel of SH3 domains. Peptides
 CC W38068-92 were biotinylated and complexed with alkaline streptavidin,
 CC and used in a cross affinity mapping experiment. They were tested for
 CC their ability to bind to the 3 WW domains of WMP4 (W36797), which were
 CC expressed as glutathione-S-transferase expression proteins. The present
 CC peptide, derived from PRKag (sic), binds to some of the WW domains
 CC of the novel protein. The WW domain is a small functional domain. Its
 CC name is derived from the observation that two tryptophan residues, 1 in
 CC the amino terminal portion of the WW domain and 1 in the carboxyl
 CC terminal portion, are conserved. Most proteins containing WW domains
 CC have a function involving cell signalling and growth regulation or the
 CC organisation of the cytoskeleton. Polypeptides containing a WW domain are
 CC identified by treating a multivalent recognition unit complex that has
 CC selective binding affinity for a WW domain, with many polypeptides and
 CC identifying those with selective affinity for the complex. Proteins
 CC containing WW domains are used for targeted drug screening, i.e. to
 CC identify potential modulators of specific WW domain interactions.
 XX

XX Sequence 21 AA;
 SQ

Query Match 24.3%; Score 33; DB 18; Length 21;
 Best Local Similarity 50.0%; Pred. No. 62;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 3 GCILLQMDFGFP 14
 ||:|
 Db 1 gyllyemavqfp 12

RESULT 13
 P30225

ID P30225 standard; Protein; 12 AA.
 XX

AC P30225;
 XX

DT 25-MAY-1992 (first entry)
 XX

DE Sequence of interferon (HuIFN) -alpha-61A around amino acid 40.
 XX

KW Hybrid interferon; antiviral; therapy; cancer; tumour.
 XX

PI Glenn K, Needleman P;
XX
DR WPI: 1999-276984/23.
XX
XX
PT New recombinant DNA vaccines
PS
XX
XX Disclosure; Page 75; 99pp; English.
XX
CC This sequence represents an immunogenic fragment of the rabbit
CC cholesterol ester transferase protein (CERT).
CC The invention relates to recombinant DNA vaccines that contain DNA
CC encoding CERT, which can be used for producing antibodies to lessen the
CC transfer of cholesterol esters from high density lipoprotein (HDL). The
CC method can provide an autogenic immunological process for lessening the
CC transfer of cholesterol esters from HDL particles and for increasing the
CC HDL cholesterol concentration of a mammal whose blood also contains
CC CERT. The method may be useful in treating human pro-atherogenic
CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC short-term effects of the small molecule drugs now available.
XX
SQ Sequence 22 AA:

Query Match	78.7%	Score 107;	DB 20;	Length 22;
Best Local Similarity	95.5%	Pred. No. 6.8e-11;		
Matches	21;	Conservative	1;	Mismatches 0; Indels 0; Gaps 0.
Oy	5	LLLOMDFGPRKHLVDFLOSL	26	
Db	1	lllqmdfgfpehlvdfllqsls	22	
RESULT	8			
Y13821				
ID	Y13821	standard; peptide: 22 AA.		
XX				
AC	Y13821;			
XX				
DT	08-JUL-1999	(first entry)		
XX				
DE	Human CERP immunogenic fragment.			
XX				
KM	CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;			
KW	antibody production; cholesteryl ester transfer; therapy;			
KM	high density lipoprotein; HDL cholesterol concentration;			
KW	pro-atherogenic dyslipoproteinemia.			
XX				
OS	Homo sapiens.			
XX				
PN	W09915655-A1.			
XX				
PD	01-APR-1999.			
XX				
PF	17-SEP-1998;	98WO-US19366.		
XX				
PR	19-SEP-1997;	97US-0934367.		
XX				
PA	(MONS) MONSANTO CO.			
XX				
PI	Glenn K, Needleman P;			
XX				
DR	WPI; 1999-276984/23.			
XX				
PT	New recombinant DNA vaccines			
XX				
PS	Disclosure; Page 88; 99pp; English.			
XX				
CC	This sequence represents an immunogenic fragment of the human			
CC	cholesteryl ester transferase protein (CERP).			
CC	The invention relates to recombinant DNA vaccines that contain DNA			
CC	encoding CERP, which can be used for producing antibodies to lessen the			
CC	transfer of cholesteryl esters from high density lipoprotein (HDL). The			

CC	method can provide an autogenic immunological process for lessening the
CC	transfer of cholesterol esters from HDL particles and for increasing the
CC	HDL cholesterol concentration of a mammal whose blood also contains
CC	CETP. The method may be useful in treating human pro-atherogenic
CC	dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC	method can have an effect that lasts for months as compared to the
CC	short-term effects of the small molecule drugs now available.
xx	
SQ	Sequence 22 AA;
	Query Match 78.7%; Score 107; DB 20; Length 22;
	Best Local Similarity 95.5%; Pred. No. 6.8e-11;
	Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	5 ILLDMDFGPKHLVDFLQSLS 26 1 ILLqmdfgfpehllydfiqsls 22
Ddb	
RESULT	9
ID	Y91230 standard; peptide: 16 AA. Y91230

RESULT	9	
ID	Y91230	standard; peptide: 16 AA.
XX		
AC	Y91230;	
XX		
DT	22-MAY-2000	(first entry)
XX		
DE	Human cholesteryl transport protein (CEP) peptide, SFG ID NO:108.	
XX		
KW	Promiscuous T-cell epitope; measles virus F protein; MWF;	
KW	hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;	
KW	luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;	
KW	somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;	
KW	foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;	
KW	Plasmodium falciparum; circumsporozoite; antimalarial; CEP;	
KW	cholesteryl ester transport protein; anti-arteriosclerotic.	
XX		
OS	Homo sapiens.	
XX		
PN	MO9966957-A2.	
XX		
PD	29-DEC-1999.	
XX		
PF	21-JUN-1999; 99MO-US133975.	
XX		
PR	20-JUN-1998; 98US-0100412.	
XX		
PA	(UNBI-) UNITED BIOMEDICAL INC.	
XX		
PI	Wang CY;	
XX		
DR	WPI; 2000-160564/14.	
XX		
PT	New artificial T helper cell epitope and derived immunogens with target	
PT	antigenic site, for immunization against e.g. malaria, arteriosclerosis	
PT	or human immune deficiency virus	
XX		
XX	Claim 10; Page 62; 129pp; English.	
XX		
CC	The invention relates to novel promiscuous T helper cell epitopes (Th),	
CC	and immunogenic peptides comprising the Th epitopes of the invention	
CC	along with B cell epitopes. The Th epitopes and peptide immunogens	
CC	containing them, are used to induce a T helper cell response,	
CC	specifically against Plasmodium falciparum, cholesteryl ester transport	
CC	protein (CEP) or HIV epitopes, but more generally against any pathogen,	
CC	immunoreactive self-antigen or tumour antigen. The Th epitopes and	
CC	peptide immunogens may be used for prevention and/or treatment of	
CC	infections (HIV, foot-and-mouth disease or malaria); for cancer	
CC	immunotherapy; for inhibition of the action of luteinising hormone	
CC	releasing hormone (LHRH) for contraception, treatment of hormone-	
CC	degrading cancer, prevention of boar taint in meat, and	
CC	immunocastration; for promoting the growth of animals; or for	

CC protein (CEP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy: for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of bear taint in meat, and
 CC immunocastration); for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target antigen.
 CC Th can replace carrier proteins and pathogen-derived T helper epitopes.
 CC Sequence Y9121 represents a promiscuous T helper epitope from the
 CC measles virus F (VWF) protein and sequences Y91122-Y91142, Y91226 and
 CC Y91245-Y91246 represent synthetic Th epitopes based on the MZF Th
 CC epitope. Sequence Y91143 represents a promiscuous Th epitope from
 CC hepatitis B virus (HBV) surface antigen, and sequences Y91144-Y91155 are
 CC synthetic epitopes derived from this HBV epitope. Y91156-Y91196,
 CC Y91227 and Y91242-Y91244 are antigenic peptides comprising an LHRH
 CC sequence joined to a promiscuous Th epitope. Y91197 is the LHRH target
 CC antigenic peptide used in these LHRH antigenic peptides. Y91200 is
 CC somatostatin, and Y91201-Y91207 are antigenic peptides comprising
 CC somatostatin and a Th epitope. Somatostatin immunogens may be used
 CC to promote growth in livestock. Y91208 is a human CD4 CD82-like domain
 CC antigenic site, and Y91209-Y90211 are MZF Th epitope/CD4 CD82
 CC antigenic peptides which may be used to prevent HIV infection of T
 CC cells. Y90212 is a modified version of a human IGE (Immunoglobulin
 CC E) CH3 domain, and Y90213-Y90219 are Th epitope/IGE CH3 antigenic
 CC peptides which may be used in the treatment of allergies. Y91220 is
 CC a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid
 CC protein and Y91221-Y91222 comprise this peptide and a Th epitope. Y91223
 CC is a Plasmodium falciparum circumsporozoite (CS) target antigen, and
 CC Y91224-Y91225 comprise the CS antigen and an MZF Th epitope and may be
 CC used in a malaria vaccine. Y91228-Y91231 represent CEP-derived peptides
 CC and Y91232-Y91241 are immunogens comprising a CEP peptide and a Th
 CC epitope which may be used to prevent or treat arteriosclerosis and
 CC cardiovascular disease. Y91247 and Y91252-Y91257 are HIV-1 neutralising
 CC B-cell epitopes, and Y91248-Y91251 and Y91258-Y91273 are antigenic
 CC peptides comprising MZF Th and HIV-1 B-cell epitope which may be used as
 CC a component in an anti-HIV-1 vaccine. Y91198 and Y91199 are respectively
 CC an immunostimulatory invasive protein epitope from Yersinia species, and
 CC hinge spacer peptide, both of which may optionally be used in the
 CC antigenic peptides of the invention.
 CC Note: Sequence Y91227 is also designated SEQ ID NO:106 in the
 CC specification.

XX Sequence 26 AA;

Query Match 86.0%; Score 117; DB 21; Length 26;
 Best Local Similarity 92.0%; Pred. No. 2e-12;
 Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 DGLLLQMDGFPKHLVDFLQSL 26

Db 2 dglfllqmdfgfpehllvdfllgsls 26

RESULT 6
 Y13809 Y13809 standard; peptide: 22 AA.
 AC Y13809;
 XX
 XX
 DT 08-JUL-1999 (first entry)
 DE Rabbit CEP immunogenic fragment.
 XX
 XX
 KM CEP: cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 KM antibody production; cholesteryl ester transfer; therapy;
 KM high density lipoprotein; HDL cholesterol concentration;
 KM pro-atherogenic dyslipoproteinaemia.

XX
 OS Oryctolagus sp.
 XX
 PN MO9915655-A1.
 XX
 PD 01-APR-1999.
 XX
 XX
 PF 17-SEP-1998; 98WO-US19366.
 XX
 PR 19-SEP-1997; 97US-0934367.
 XX
 PA (MONS) MONSANTO CO.
 PI Glenn K, Needleman P;
 DR WPI; 1999-276984/23.
 PT New recombinant DNA vaccines
 PS Example 1; Page 73; 99pp; English.
 XX
 XX This sequence represents an immunogenic fragment of the rabbit
 CC cholesteryl ester transferase protein (CEP).
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CEP, which can be used for producing antibodies to lessen the
 CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
 CC method can provide an autogenic immunological process for lessening the
 CC transfer of cholesteryl esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CEP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.

XX Sequence 22 AA;

Query Match 81.6%; Score 111; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.5e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLQMDGFPKHLVDFLQSL 26

Db 1 lllqmdfgfpehllvdfllgsls 22

RESULT 7
 Y13815 Y13815 standard; peptide: 22 AA.
 AC Y13815;
 XX
 XX
 DT 08-JUL-1999 (first entry)
 DE Rabbit CEP immunogenic fragment.
 XX
 XX
 KM CEP: cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 KM antibody production; cholesteryl ester transfer; therapy;
 KM high density lipoprotein; HDL cholesterol concentration;
 KM pro-atherogenic dyslipoproteinaemia.
 XX
 XX Oryctolagus sp.
 OS
 PN MO9915655-A1.
 PD 01-APR-1999.
 XX
 XX
 PF 17-SEP-1998; 98WO-US19366.
 XX
 PR 19-SEP-1997; 97US-0934367.
 XX
 PA (MONS) MONSANTO CO.

XX	01-MAY-1996;	96WO-US06147.
XX		
PR	01-MAY-1995;	95US-0432483.
XX		
PA	(TCEL-) T CELL SCI INC.	
XX		
PI	Rittershaus CW, Thomas LJ;	
XX		
DR	WPI; 1996-506103/50.	
XX		
PT	Cholesteryl ester transfer protein B cell epitope linked to T cell	
PT	epitope - used to generate vaccine to regulate CERP activity for	
PT	decreasing the risk of developing a cardiovascular disease e.g.	
PT	atherosclerosis	
XX		
PS		
XX	Claim 5; Page 41; 72pp; English.	
CC		
CC	A B-cell epitope (W06128) comprising the C-terminal 26 amino acids	
CC	of human liver mature cholesteryl ester transfer protein (CERP)	
CC	(see also W06127) is involved in a neutral lipid binding or a	
CC	transfer activity of CERP. It can be linked to a universal or	
CC	broad range immunogenic T-cell epitope, such as that found at amino	
CC	acids 830-843 of tetanus toxoid protein, to produce a synthetic	
CC	vaccine (see also W06129) that elicits an immune response against	
CC	endogenous CERP activity, thereby treating or preventing	
CC	cardiovascular disease, such as atherosclerosis. It may also be	
CC	incorporated into a multivalent vaccine (see also W06131)	
CC	including another CERP B-cell epitope.	
XX		
XX		
Sequence	26 AA;	

Query Match	86.0%	Score 117	DB 17	Length 26
Best Local Similarity	92.0%	Pred. No. 2e-12	1	Indels 0; Gaps 0
Matches 23; Conservative 1; Mismatches 1				
QY	2	DCCLLQMDGFGPKHLVDFIQSL	26	
	11		11	
Db	2	dqflllqmdfgfpehlvdfiqsls	26	
RESULT	4			
Y13801				
ID	Y13801	standard; peptide: 26 AA.		
XX				
AC	Y13801:			
XX				
DT	08-JUL-1999	(first entry)		
XX				
DE		Rabbit CERP immunogenic fragment.		
XX				
KW	CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;			
KW	antibody production; cholesteryl ester transfer; therapy;			
KW	high density lipoprotein; HDL cholesterol concentration;			
KW	pro-atherogenic dyslipoproteinemia.			
XX				
OS	Oryctolagus sp.			
XX				
PN	W09915655-A1.			
XX				
PD	01-APR-1999.			
XX				
PF	17-SEP-1998; 98WO-US19366.			
XX				
PR	19-SEP-1997; 97US-0934367.			
XX				
XX				
PA	(MONS) MONSANTO CO.			
XX				
PI	Glenn K, Needleman P;			
XX				
DR	WPI; 1999-276984/23.			
XX				
PT	New recombinant DNA vaccines			

xx Claim 15; Page 85; 99pp; English.

ps

xx This sequence represents an immunogenic fragment of the rabbit

xx cholesteryl ester transferase protein (CETP).

cc The invention relates to recombinant DNA vaccines that contain DNA

cc encoding CETP, which can be used for producing antibodies to lessen the

cc transfer of cholesteryl esters from high density lipoprotein (HDL). The

cc method can provide an autogenic immunological process for lessening the

cc transfer of cholesteryl esters from HDL particles and for increasing the

cc HDL cholesterol concentration of a mammal whose blood also contains

cc CETP. The method may be useful in treating human pro-atherogenic

cc dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The

cc method can have an effect that lasts for months as compared to the

cc short-term effects of the small molecule drugs now available.

xx

xx Sequence 26 AA;

xx

Query Match	86.0%;	Score 117;	DB 20;	Length 26;
Best Local Similarity	92.0%;	Pred. No. 2e-12;	Indels	0;
Matches 23;	Conservative 1;	Mismatches	1;	Gaps 0
QY	2	DGCLLQMDGFPKHLVDFLOSL	26	
	11			
	2	dGflllqmdtGfpehllvdfllqsls	26	
Db	2	dGflllqmdtGfpehllvdfllqsls	26	
RESULT	5			
ID	Y91228	standard; peptide: 26 AA.		
AC	Y91228;			
DT	22-MAY-2000	(first entry)		
XX	Human cholesterolyl transport protein (CETP) peptide, SEQ ID NO:106.			
XX	Promiscuous T-cell epitope; measles virus F protein; MYF;			
KW	hepatitis B virus surface antigen; HBV; Immunogenic; B-cell epitope;			
KW	luteinizing hormone releasing hormone; LHRH; contraceptive; anticancer;			
KW	somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;			
KW	foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;			
KW	Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;			
KW	cholesteryl ester transport protein; anti-arteriosclerotic.			
XX	Homo sapiens.			
XX	WO966957-A2.			
XX	29-DEC-1999.			
XX	21-JUN-1999;	99WO-US13975.		
XX	20-JUN-1998;	98US-0100412.		
XX	(UNBT-) UNITED BIOMEDICAL INC.			
XX	Wang CY;			
XX	WPI; 2000-160564/14.			
XX	New artificial T helper cell epitope and derived immunogens with target			
XX	antigenic site, for immunization against e.g. malaria, arteriosclerosis			
XX	or human immune deficiency virus			
XX	Claim 10; Page 49; 12pp; English.			
XX	The invention relates to novel promiscuous T helper cell epitopes (Th),			
XX	and immunogenic peptides comprising the Th epitopes of the invention			
XX	along with B cell epitopes. The Th epitopes and peptide immunogens			
XX	containing them, are used to induce a T helper cell response,			
XX	specifically against Plasmodium falciparum, cholesteryl ester transport			

CC This sequence represents an immunogenic fragment of the rabbit
CC cholesterol ester transferase protein (CETP).
CC The invention relates to recombinant DNA vaccines that contain DNA
CC encoding CETP, which can be used for producing antibodies to lessen the
CC transfer of cholesterol esters from high density lipoprotein (HDL). The
CC method can provide an autogenic immunological process for lessening the
CC transfer of cholesterol esters from HDL particles and for increasing the
CC HDL cholesterol concentration of a mammal whose blood also contains
CC CETP. The method may be useful in treating human pro-atherogenic
CC dyslipoproteinemias characterized by low HDL/LDL cholesterol ratios. The
CC method can have an effect that lasts for months as compared to the
CC short-term effects of the small molecule drugs now available.
CC
CC Sequence 26 AA:
SQ
Query Match 100.0%; Score 136; DB 20; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDGCLLLQMDGFPKHLVDFLOSL S 26
Db 1 ldgclllqmdgfpkhlvdflosls 26
RESULT 2
Y91231
ID Y91231 standard; peptide: 26 AA.
XX
AC Y91231:
DT 22-MAY-2000 (first entry)
DE Human cholesterol transport protein (CETP) peptide, SEQ ID NO:109.
XX
KW Promiscuous T-cell epitope; measles virus F protein; MVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW interleukin hormone releasing hormone; IHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KW cholesterol ester transport protein; anti-arteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US13975.
XX
PR 20-JUN-1998; 98US-0100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus
XX
PS Claim 10; Page 62; 129pp; English.
XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesterol ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of

CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of interleukin hormone
CC releasing hormone (IHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration); for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target antigen.
CC Th can replace carrier proteins and pathogen-derived T helper epitopes.
CC Sequence Y91121 represents a promiscuous T helper epitope from the
CC measles virus F (MVF) protein and sequences Y91122-Y91142, Y91226 and
CC Y91245-Y91246 represent synthetic Th epitopes based on the MVF Th
CC epitope. Sequence Y91143 represents a promiscuous Th epitope from
CC hepatitis B virus (HBV) surface antigen, and sequences Y91144-Y91155 are
CC synthetic epitopes derived from this HBV epitope. Y91156-Y91196,
CC Y91227 and Y91242-Y91244 are antigenic peptides comprising an IHRH
CC sequence joined to a promiscuous Th epitope. Y91197 is the IHRH target
CC antigenic peptide used in these IHRH antigenic peptides. Y91200 is
CC somatostatin, and Y91201-Y91207 are antigenic peptides comprising
CC somatostatin and a Th epitope. Somatostatin immunogens may be used
CC to promote growth in livestock. Y91208 is a human CD4 CDR2-like domain
CC antigenic site, and Y91209-Y90211 are MVH Th epitope/CD4 CDR2
CC cells. Y90212 is a modified version of a human IgE (immunoglobulin
CC E) CH3 domain, and Y90213-Y90219 are Th epitope/IgE CH3 antigenic
CC peptides which may be used in the treatment of allergies. Y91220 is
CC a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid
CC protein and Y91221-Y91222 comprise this peptide and a Th epitope. Y91223
CC is a Plasmodium falciparum circumsporozoite (CS) target antigen, and
CC Y91224-Y91225 comprise the CS antigen and an MVF Th epitope and may be
CC used in a malaria vaccine. Y91228-Y91231 represent CETP-derived peptides
CC and Y91232-Y91241 are immunogens comprising a CETP peptide and a Th
CC epitope which may be used to prevent or treat arteriosclerosis and
CC cardiovascular disease. Y91247 and Y91252-Y91257 are HIV-1 neutralising
CC B-cell epitopes, and Y91248-Y91251 and Y91258-Y91273 are antigenic
CC peptides comprising MVH Th and HIV-1 B-cell epitope which may be used as
CC a component in an anti-HIV-1 vaccine. Y91198 and Y91199 are respectively
CC an immunostimulatory invasion protein epitope from Yersinia species, and
CC hinge spacer peptide, both of which may optionally be used in the
CC antigenic peptides of the invention.
XX
SQ Sequence 26 AA:
Query Match 100.0%; Score 136; DB 21; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDGCLLLQMDGFPKHLVDFLOSL S 26
Db 1 ldgclllqmdgfpkhlvdflosls 26
RESULT 3
W06128
ID W06128 standard; peptide: 26 AA.
XX
AC W06128:
DT 07-FEB-1997 (first entry)
DE Human cholesterol ester transfer protein C-terminal B-cell epitope.
XX
KW Cholesterol ester transfer protein; CETP; antigen; vaccine;
KW cardiovascular disease; arteriosclerosis; B-cell epitope.
XX
OS Homo sapiens.
XX
PN WO9634888-A1.
XX
PD 07-NOV-1996.
XX

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:38:46 ; Search time 26.24 Seconds

(without alignments)
33.881 Million cell updates/sec

Title: US-08-934-367-50

Sequence: 1 LDGCLLQMDFGFPKHLVDFLOSL 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 143201

Minimum DB seq length: 0

Maximum DB seq length: 26

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq-36:*

1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT:*
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21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136	100.0	26	20	Y13802
2	136	100.0	26	20	Y13802
3	117	86.0	26	17	W06128
4	117	86.0	26	20	Y13801
5	117	86.0	26	21	Y91228
6	111	81.6	22	20	Y13809
7	107	78.7	22	20	Y13815
8	107	78.7	22	20	Y13821
9	83	61.0	16	21	Y91230
10	79	58.1	16	21	Y91229
11	53	39.0	11	18	W24294
12	33	24.3	21	18	W38080

13	32	23.5	12	4	P30225
14	32	23.5	12	9	P80053
15	32	23.5	14	20	Y27814
16	32	23.5	21	19	W65690
17	31.5	23.2	16	17	R98414
18	31	22.8	11	15	R47611
19	31	22.8	21	19	W65666
20	31	22.8	22	15	R47610
21	31	22.8	22	19	W65669
22	30.5	22.4	15	19	W21149
23	30	22.1	20	15	R61276
24	30	22.1	20	19	W41190
25	30	22.1	25	20	Y12067
26	29	21.3	12	18	W32681
27	29	21.3	12	17	W71811
28	29	21.3	18	18	W36737
29	29	21.3	18	18	W09586
30	29	21.3	18	21	Y52473
31	29	21.3	20	16	R72269
32	29	21.3	20	21	Y59570
33	29	21.3	22	17	R95899
34	29	21.3	22	18	W22196
35	29	21.3	24	20	Y13053
36	29	21.3	25	21	Y51627
37	29	21.3	26	15	R31744
38	29	21.3	26	19	W71924
39	29	21.3	26	20	Y50373
40	28	20.6	9	15	R46908
41	28	20.6	9	15	R55648
42	28	20.6	9	16	R67236
43	28	20.6	9	17	W09354
44	28	20.6	9	17	R96068
45	28	20.6	9	17	R86700

ALIGNMENTS

RESULT 1	
ID Y13802	standard; peptide; 26 AA.
XX Y13802;	
XX 08-JUL-1999	(first entry)
DT	Rabbit CERP immunogenic fragment.
XX	
DE	Rabbit CERP immunogenic fragment.
XX	
KW	CERP: cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
KW	antibody production; cholesteryl ester transfer; therapy;
KW	high density lipoprotein; HDL cholesterol concentration;
KW	pro-atherogenic dyslipoproteinemia.
XX	
OS	Oryctolagus sp.
XX	
PN	W0915655-A1.
XX	
PD	01-APR-1999.
XX	
PF	17-SEP-1998; 98WC-US19366.
XX	
PR	19-SEP-1997; 97US-0934367.
XX	
PA	(MONS) MONSANTO CO.
XX	
PI	Glenn K. Needleman P;
XX	
DR	WPI; 1999-276984/23.
XX	
PT	New recombinant DNA vaccines
XX	
PS	Claim 15; Page 94; 99pp; English.
XX	

Sequence of interf
Sequence of human
Human secreted pro
Fibronectin bindin
Interferon-gamma r
Bombesin-like pept
Fibronectin bindin
Bombesin-like pept
Peptide #13. Synt
Human bc12 proto-o
Transactivating pr
Tax protein fragme
Human 5' EST sece
Human platelet g1y
Mimotope capable o
Thrombopoietin rec
RTS60-1 mutation-c
Glutamic acid deca
GAD65 fragment, pe
Fragment #4 of 7-a
Endogenous TCR alp
Human secreted pro
S. cerevisiae Rad1
Der P I derived pe
Dermatophagoides D
Dermatophagoides S
GGF segment D'. H
GGF segment D'. H
Bovine glial cell
Bovine glial growt
Human glial growt
Bovine glial growt

RT "A novel C-terminal domain in the thyroid hormone receptor selectively
RT mediates thyroid hormone inhibition."
RL J. Biol. Chem. 269:32713-32716(1994).
SQ SEQUENCE 16 AA; 1920 MW; 79A831A4F3C8E22F CRC64;

Query Match 21.0%; Score 21; DB 4; Length 16;
Best Local Similarity 40.0%; Pred. No. 4.1e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 11 KLFLLDDEQ 20
||:| |
Db 4 KLMKVTDLQ 13

Search completed: December 21, 2000, 08:35:36
Job time: 599 sec

DE MAST CELL PROTEASE 5 (FRAGMENT).
 GN MCPT5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
 RN Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ; TISSUE=LIVER;
 RA Lunderius C., Hellman L.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF119364; AAD43901.1; -.
 KW Protease.
 FT NON_TER
 SQ SEQUENCE 19 AA; 2075 MW; 6AA33AA6B28E4B7D CRC64;

Query Match 22.0%; Score 22; DB 11; Length 19;
 Best Local Similarity 83.3%; Pred. No. 3.3e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 LFLHL 17
 1 1 1 1 1
 Db 4 LFLHL 9

RESULT 12
 049448 PRELIMINARY; PRT; 20 AA.
 AC 049448;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE UNCERTAIN (FRAGMENT).
 OS MYCOPLASMA genitalium.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G-37;
 RA Peterson S.N., Hu P., Bott K.F., Hutchison C.A.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G-37;
 RA Peterson S.N.;
 RA Thesis (1992), Microbiology and Immunology,
 RL University of North Carolina Medical School, USA.
 DR EMBL: J01744; AAD10557.1; -.
 FT NON_TER
 SQ SEQUENCE 20 AA; 2424 MW; BFBCE399592F014 CRC64;

Query Match 22.0%; Score 22; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 4 QASYSQKLP 13
 1 1 1 1 1
 Db 4 KAYVMKTLF 13

RESULT 13
 09182 PRELIMINARY; PRT; 7 AA.
 AC 09182;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE CYTOCHROME OXIDASE I (FRAGMENT).
 GN COI.
 OS Pterolebias zonatus.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
 OC Atherinomorpha; Cyprinodontiformes; Aplocheiloidel; Aplocheilidae;
 OC Pterolebias.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Murphy W.J., Thomerson J.E., Collier G.E.;
 RT "A molecular phylogeny of Neotropical aplocheiloid killifishes
 (Cyprinodontiformes, Rivulidae)."
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF002591; AAD01074.1; -.
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 7 AA; 899 MW; 672721F6CB572030 CRC64;

Query Match 21.0%; Score 21; DB 8; Length 7;
 Best Local Similarity 66.7%; Pred. No. 3e+05;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 LFLHL 17
 1 1 1 1 1
 Db 2 LYQHL 7

RESULT 14
 044693 PRELIMINARY; PRT; 10 AA.
 AC 044693;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE AMYLIOQUEFACIENS TRPE GENE (3' END) AND TRPD GENE (5' END)
 DE (FRAGMENT).
 OS Bacillus amyloliquefaciens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/staphylococcus group; Bacillus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 85006754.
 RA Yoshimura K., Uemura J., Seki T., Oshima Y.;
 RT "Construction of a promoter-probe vector for a Bacillus subtilis host
 by using the trpD+ gene of Bacillus amyloliquefaciens."
 RL J. Bacteriol. 159:905-912(1984).
 DR EMBL: K02661; AAB05353.1; -.
 FT NON_TER
 SQ SEQUENCE 10 AA; 1266 MW; D5121FC729D5A416 CRC64;

Query Match 21.0%; Score 21; DB 2; Length 10;
 Best Local Similarity 33.3%; Pred. No. 2.6e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 8 SQKKLFLHL 16
 1 1 1 1 1
 Db 2 SQRSLFPHM 10

RESULT 15
 090D41 PRELIMINARY; PRT; 16 AA.
 AC 090D41;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE BETA-ISOPORN THYROID HORMONE RECEPTOR (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95105146.
 RA Flynn T.R., Hollenberg A.N., Cohen O., Menke J.B., Usala S.J.,
 Tollen S., Hegarty M.K., Wondisford F.E.;

```
RESULT 7
O56610 ID O56610 PRELIMINARY: PRT: 18 AA.
AC O56610:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DE 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE ACCA (FRAGMENT).
GN ACCA.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C6706.
RX MEDLINE: 97074686.
RA Franco A., Pelt-Eh Y., Johnson J., Barry E.M., Guerra H., Maurer R.,
RA Morris J.G.;
RT "Cloning and characterization of dnaE, encoding the catalytic subunit
RT of replicative DNA polymerase III, from Vibrio cholerae strain
RT C6706."
RL Gene 175:281-283(1996).
DR EMBL: U30472; AAC4579.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2153 MW; 18BECAD212842EF CRC64;
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Query Match 23.0%; Score 23; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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OY 14 LHLDFQ 20
DB 3 LNFDFE 9
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```
RESULT 8
O9R506 ID O9R506 PRELIMINARY: PRT: 14 AA.
AC O9R506:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DE 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE 2-HALOGENZATE 1,2-DIOXYGENASE COMPONENT A BETA SUBUNIT.
OS Burkholderia cepacia (Pseudomonas cepacia).
OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
OC Burkholderia.
RN [1]
RP SEQUENCE.
RX MEDLINE: 92104974.
RA Fetzner S., Muller R., Lings F.;
RT "Purification and some properties of 2-halobenzoate 1,2-dioxygenase, a
RT two-component enzyme system from Pseudomonas cepacia 2CBS."
RL J. Bacteriol. 174:279-290(1992).
FT NON_TER 18
SQ SEQUENCE 14 AA; 1544 MW; 0BC0478DE85A33B CRC64;
```

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Query Match 22.0%; Score 22; DB 2; Length 14;
Best Local Similarity 28.6%; Pred. No. 2.4e+03;
Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
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```
OY 1 TTVQASYSQKLEL 14
DB 1 TLESSTYLDVVAFT 14
```

```
RESULT 9
O9U0J2 ID O9U0J2 PRELIMINARY: PRT: 15 AA.
AC O9U0J2:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DE 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
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```
DE PRORELAXIN H2 PRECURSOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Garibay-Tupas J.;
RT "Characterization of the human relaxins H1 and H2 5'-flanking
RT regions."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF104935; AAD21961.1; -.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1806 MW; E9AF622F3A86818 CRC64;
```

```
Query Match 22.0%; Score 22; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 13 FLHL 17
DB 6 FFHL 10
```

```
RESULT 10
O9RLU4 ID O9RLU4 PRELIMINARY: PRT: 19 AA.
AC O9RLU4:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DE 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE NISG PROTEIN (FRAGMENT).
GN NISG.
OS Lactococcus lactis.
OC Plasmid pLEB513.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N8; TRANSPOSON=TN5481;
RA Immonen T., Sairis P.E.J.;
RT "Evidence for a mosaic structure of the tn5481 in Lactococcus lactis
RT N8."
RL DNA Seq. 9:245-261(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=N8; TRANSPOSON=TN5481;
RA Immonen T., Sairis P.E.J.;
RT "Characterization of the nisFG operon of the nlsZ producing
RT Lactococcus lactis subsp. lactis N8 strain."
RL DNA Seq. 9:263-274(1998).
DR EMBL: AJ000993; CAA04441.1; -.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2139 MW; 6A429DC80E673613 CRC64;
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Query Match 22.0%; Score 22; DB 2; Length 19;
Best Local Similarity 33.3%; Pred. No. 3.3e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 1 TTVQASYSQKRL 12
DB 7 TLIVALSKKKI 18
```

```
RESULT 11
O9RLF0 ID O9RLF0 PRELIMINARY: PRT: 19 AA.
AC O9RLF0:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DE 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
```

```

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP MEDLINE: 93015942.
RA Kojima K., Ogawa H.K., Seno N., Yamamoto K., Irimura T., Osawa T.,
RA Matsunaga I.,
RT "Carbohydrate-binding proteins in bovine kidney have consensus amino
RT acid sequences of annexin family proteins."
RL J. Biol. Chem. 267:20536-20539(1992).
SQ SEQUENCE 19 AA; 2294 MW; F025B1E02C50C419 CRC64;

Query Match 25.0%; Score 25; DB 6; Length 19;
Best Local Similarity 41.7%; Pred. No. 9.9e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 7 YSOKRLFLHLD 18
   ||
   ||:|
Db 6 YSXNHLHVF 17

RESULT 3
ID 046963 PRELIMINARY: PRT: 15 AA.
AC 046963:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE SPOT 42 RNA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CP78;
RX MEDLINE: 80074983.
RA Sahagan B.G., Dahlberg J.E.;
RT "A small, unstable RNA molecule of Escherichia coli: spot 42 RNA. I.
RT Nucleotide sequence analysis."
RL J. Mol. Biol. 131:573-592(1979).
DR EMBL: X01895; CAA25985.1; -
SQ SEQUENCE 15 AA; 1725 MW; 5A51DAF170EA61E CRC64;

Query Match 24.0%; Score 24; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 12 LFLHLDF 19
   ||::|
   ||::|
Db 7 LLLHWIGF 14

RESULT 4
ID 095844 PRELIMINARY: PRT: 16 AA.
AC 095844:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 18 KDA COELIAC SERUM-REACTIVE GLYCOPROTEIN (FRAGMENT).
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Secale.
RN [1]
RP SEQUENCE.
RX MEDLINE: 96283789.
RA Rocher A., Calero M., Soriano F., Mendez E.;
RT "Identification of major rye secalins as coeliac immunoreactive
RT proteins."

```

```

RL Biochim. Biophys. Acta 1295:13-22(1996).
SQ SEQUENCE 16 AA; 1787 MW; 4659CA46B2B28861 CRC64;

Query Match 24.0%; Score 24; DB 10; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 TTVOASTSOKKL 12
   ||
   ||:|
Db 3 TTXSQGYGXQL 14

RESULT 5
ID 09R583 PRELIMINARY: PRT: 18 AA.
AC 09R583:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE TRANSFERRIN-BINDING PROTEIN 1 (FRAGMENT).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
RN [1]
RP SEQUENCE.
RX MEDLINE: 93307625.
RA Griffiths E., Stevenson P., Byfield P., Ala'Aldeen D.A.,
RA Borriello S.P., Holland J., Parsons T., Williams P.;
RT "Antigenic relationships of transferrin-binding proteins from
RT Neisseria meningitidis, N. gonorrhoeae and Haemophilus influenzae:
RT cross-reactivity of antibodies to NH2-terminal peptides."
RL FEMS Microbiol. Lett. 109:85-91(1993).
SQ SEQUENCE 18 AA; 1999 MW; FC0F1PB0A86C77C4 CRC64;

Query Match 24.0%; Score 24; DB 2; Length 18;
Best Local Similarity 55.6%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 VOASTSOKK 11
   |||
   |||:|
Db 3 VOAGQADEK 11

RESULT 6
ID 09UQJ1 PRELIMINARY: PRT: 11 AA.
AC 09UQJ1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE PROELAXIN HI PRECURSOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Garibay-Tupas J.;
RT "Characterization of the human HI relaxin 5'-flanking region."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF104934; AAD21967.1; -
FT NON_TER 11
SQ SEQUENCE 11 AA; 1416 MW; 40C86818E9C729C7 CRC64;

Query Match 23.5%; Score 23.5; DB 4; Length 11;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 6; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 11 KLFL-HLDD 18
   :|||
   :|||:
Db 3 RLFLPHLE 11

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:35:34 ; Search time 157.2 Seconds
(without alignments)
11.880 Million cell updates/sec

Title: US-08-934-367-5
Perfect score: 100
Sequence: 1 TTVOASYSOKKLFLLHDFQ 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organellar:*
9: SP-plant:*
10: SP-protist:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	25.0	18	3 Q02414	Q02414 aspergillus
2	25	25.0	19	6 Q9TRL8	Q9TRL8 bos taurus
3	24	24.0	15	2 Q46963	Q46963 escherichia
4	24	24.0	16	10 Q9S8A4	Q9S8A4 secale cere
5	24	24.0	18	2 Q9R583	Q9R583 neisseria m
6	23.5	23.5	11	4 Q9U0J1	Q9U0J1 homo sapien
7	23	23.0	18	2 Q56610	Q56610 vibrio chol
8	22	22.0	14	2 Q9R506	Q9R506 burkholderi
9	22	22.0	15	4 Q9U0J2	Q9U0J2 homo sapien
10	22	22.0	19	2 Q9RLU4	Q9RLU4 lactococcus
11	22	22.0	19	11 Q9R1F0	Q9R1F0 mus musculu
12	22	22.0	20	2 Q49448	Q49448 mycoplasma
13	22	22.0	7	8 Q99182	Q99182 pterolebias
14	21	21.0	10	2 Q44693	Q44693 bacillus am
15	21	21.0	16	4 Q9UD41	Q9UD41 homo sapien
16	21	21.0	18	2 Q06514	Q06514 escherichia
17	21	21.0	18	11 P97522	P97522 rattus norv
18	21	21.0	19	2 Q87732	Q87732 streptomyce
19	21	21.0	19	3 Q92321	Q92321 saccharomyc

20	21	21.0	19	12 Q86583	Q86583 murine hepa
21	21	21.0	20	2 Q9R4W5	Q9R4W5 helicobacte
22	21	21.0	20	9 Q37868	Q37868 bacterioph
23	21	21.0	20	12 Q86935	Q86935 human herpe
24	21	21.0	20	12 Q86936	Q86936 human herpe
25	21	21.0	20	12 Q86937	Q86937 human herpe
26	21	21.0	20	12 Q86938	Q86938 human herpe
27	21	21.0	20	12 Q86939	Q86939 human herpe
28	21	21.0	20	12 Q86940	Q86940 human herpe
29	21	21.0	20	12 Q86941	Q86941 human herpe
30	21	21.0	20	12 Q86942	Q86942 human herpe
31	20.5	20.5	14	2 Q9R274	Q9R274 campylobact
32	20	20.0	7	12 Q9Y010	Q9Y010 porcine tra
33	20	20.0	9	2 Q45852	Q45852 clostridium
34	20	20.0	14	5 Q18502	Q18502 schistosoma
35	20	20.0	15	2 Q9R542	Q9R542 mycobacteri
36	20	20.0	15	4 Q9UCH4	Q9UCH4 homo sapien
37	20	20.0	16	2 Q47605	Q47605 escherichia
38	20	20.0	16	2 Q9R557	Q9R557 bacillus sp
39	20	20.0	16	12 Q79458	Q79458 human immun
40	20	20.0	18	2 P97166	P97166 streptococ
41	20	20.0	18	4 Q9U781	Q9U781 homo sapien
42	20	20.0	18	13 Q91380	Q91380 gallus gall
43	20	20.0	19	4 Q07603	Q07603 homo sapien
44	20	20.0	19	4 Q9UMM9	Q9UMM9 homo sapien
45	20	20.0	19	10 Q9S901	Q9S901 vigna sinen

ALIGNMENTS

RESULT 1
002414 PRELIMINARY: PRT: 18 AA.
AC 002414:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE OROTIDINE-5'-MONOPHOSPHATE DECARBOXYLASE (FRAGMENT).
GN PYRG.
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Eurotiiales; Trichocomaceae;
OC anamorphic Trichocomaceae; Aspergillus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96031709.
RA Gouka R.J., Hessing J.G., Stam H., Musters W., Hondel C.A.;
RT "A novel strategy for the isolation of defined pyrg mutants and the
development of a site-specific integration system for Aspergillus
RT development of a site-specific integration system for Aspergillus
RT awamori.";
RT Curr. Genet. 27:536-540(1995).
DR EMBL: S79674; AAB5350.1; -.
FT NON_TER 1
SQ SEQUENCE 18 AA; 1891 MW; E1A0E3AC7D23688E CRC64;

Query Match 25.0%; Score 25; DB 3; Length 18;
Best Local Similarity 41.2%; Pred. No. 9.4e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 2 TTVOASYSOKKLFLLHDFQ 18
DB 2 TVSADVTTKELLDLAD 18
RESULT 2
Q9TRL8 PRELIMINARY: PRT: 19 AA.
AC 09TRL8:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CA(2+)-DEPENDENT CARBOHYDRATE-BINDING PROTEIN (FRAGMENT).

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DR EMBL: X64731; CAA45966.1; -.
DR PIR: S23423; S23423.
DR MENDEL: 2272; PAVlu.atp1.1.
DR INTERPRO: IPR000568; -.
DR PROSITE: PS00449; ATPASE_A; PARTIAL.
KW Hydrogen ion transport; CF(0); Chloroplast; Transmembrane.
FT NON_TER 1 13
SQ SEQUENCE 17 AA: 1753 MW: F313DCE74C23CF2E CRC64;

Query Match 18.0%; Score 18; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVQASY 7
: : : : :
DB 6 TLSAVY 11

RESULT 14
SP51_BACLI STANDARD; PRT; 17 AA.
AC P27642;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE STAGE V SPOULATION PROTEIN AA (FRAGMENT).
GN SPOVAA.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91237317.
RA Moldover B., Pigot P.J., Yuckin M.D.;
RT "Identification of the promoter and the transcriptional start site of
RT the spoVA operon of Bacillus subtilis and Bacillus licheniformis";
RL J. Gen. Microbiol. 137:527-531(1991).
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DR EMBL: X53991; CAA37938.1; -.
DR PIR: S16144; S16144.
KW Sporulation.
FT NON_TER 17
SQ SEQUENCE 17 AA: 2167 MW: 17505DA08BEF133B CRC64;

Query Match 18.0%; Score 18; DB 1; Length 17;
Best Local Similarity 23.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 9 OKKFLHL 16
: : : : :
DB 2 ERVDFRL 9

RESULT 15

AL22_HORSE
ID AL22_HORSE STANDARD; PRT; 19 AA.
AC P81217;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DANDER MAJOR ALLERGEN EQU C 2.0102 (FRAGMENT).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE: 98237590.
RA Bulone V., Kroghstad-Johnsen T., Smestad-Paulsen B.;
RT "Separation of horse dander allergen proteins by two-dimensional
RT electrophoresis - molecular characterization and identification of
RT Equ c 2.0101 and Equ c 2.0102 as lipocalin proteins";
RL Eur. J. Biochem. 253:202-211(1998).
CC -1- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
CC -1- PTM: N-GLYCOSYLATED.
CC -1- MISCELLANEOUS: PREDOMINANT ALLERGEN OF HORSE DANDER.
CC -1- SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY.
CC -1- CAUTION: C 2.0101 AND C 2.0102 MIGHT BE TWO VARIANTS OF THE
CC SAME PROTEIN.
DR INTERPRO: IPR000566; -.
DR PROSITE: PS00213; LIPOCALIN; PARTIAL.
KW Transport; Lipocalin; Glycoprotein; Allergen.
FT NON_TER 19
SQ SEQUENCE 19 AA: 2195 MW: A8E6EFAFC922C26 CRC64;

Query Match 18.0%; Score 18; DB 1; Length 19;
Best Local Similarity 50.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 QASYQ 9
: : : : :
DB 7 ETDYSQ 12

Search completed: December 21, 2000, 08:32:55
Job time: 438 sec

Db 8 SOKK 11

RESULT 10
AMP_FUSNU STANDARD; PRT; 20 AA.
ID P81207;
AC 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE AMINOPEPTIDASE (EC 3.4.11.-) (AF) (FRAGMENT).
OS Fusobacterium nucleatum.
OC Bacteria; Fusobacteria; Fusobacterium.
RN (1)
RP SEQUENCE.
RC STRAIN-ATCC 10953;
RA MEDLINE: 98361026.
RT Rogers A.H., Gunadi A., Gully N.J., Zilm P.S.;
"An aminopeptidase nutritionally important to Fusobacterium nucleatum".
RL Microbiology 144:1807-1813(1998).
CC -1- FUNCTION: CLEAVES A WIDE RANGE OF DIPEPTIDES AND TRIPEPTIDES.
CC -1- COFACTOR: COBALT.
CC -1- SUBCELLULAR LOCATION: CELL ENVELOPE-ASSOCIATED.
CC Hydrolase; Aminopeptidase; Metalloprotease; Cobalt.
FT NON_TER 20
SO SEQUENCE 20 AA; 2585 MW; 97095B948262C71B CRC64;

Query Match 19.0%; Score 19; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 10 KRLFLHLDF 19
DB 10 KERFLRYVKF 19

RESULT 11
DCMS_PSECF STANDARD; PRT; 20 AA.
ID P1915;
AC 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE CARBON MONOXIDE DEHYDROGENASE SMALL CHAIN (EC 1.2.99.2) (FRAGMENT).
OS Pseudomonas carboxydoflava.
OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
RN (1)
RP SEQUENCE.
RX MEDLINE: 90055678.
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in carboxydoflavobacteria".
RL Arch. Microbiol. 152:335-341(1989).
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED ACCEPTOR.
CC -1- COFACTOR: MOLYBDENUM.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND SMALL.
PIR: P10145; P10145.
KW Oxidoreductase; Molybdenum.
FT NON_TER 20
SO SEQUENCE 20 AA; 2155 MW; 9C7BD676A6C558AA CRC64;

Query Match 19.0%; Score 19; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 TVQASYSOKK 11

Db 7 TVNKGAKOEK 16

RESULT 12
FIBA_HORSE STANDARD; PRT; 14 AA.
ID P14452;
AC 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DE FIBRINOPEPTIDE A.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
RN (1)
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
"Studies on fibrinopeptides from mammals".
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES.
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT NON_TER 14
SO SEQUENCE 14 AA; 1517 MW; 4E998EB63C2A15E7 CRC64;

Query Match 18.0%; Score 18; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FLH 15
DB 6 FLH 8

RESULT 13
ATPL_PAVLU STANDARD; PRT; 17 AA.
ID P28529;
AC 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE ATP SYNTHASE A CHAIN (EC 3.6.1.34) (SUBUNIT IV) (FRAGMENT).
GN ATP1.
OS Pavlova lutheri (Monochrysis lutheri).
OG Chloroplast.
OC Eukaryota; Haptophyceae; Pavlovales; Pavlova.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 92316212.
RA Scaramuzzi C.D., Stokes H.W., Hiller R.G.;
"Characterisation of a chloroplast-encoded secy homologue and atpH from a chromophytic alga. Evidence for a novel chloroplast genome organisation".
RL FEBS Lett. 304:119-123(1992).
CC -1- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL. IT MAY PLAY A DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE.
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CHLOROPLAST THYLAKOID MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.

CC TETRAHYDROCANNABINOL (THC) AND STRYCHNINE.
CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND, ENDOPLASMIC RETICULUM.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR PIR: A36154; A36154.
DR INTERPRO: IPR001128; -.
DR PROSITE: PS00086; CYTOCHROME_P450; PARTIAL.
KM Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2259 MW; 78DC81280C970A55 CRC64;

Query Match 20.0%; Score 20; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 LFALL 17
DB 7 LFALL 12

RESULT 7
NUHM_CANFA STANDARD; PRT; 11 AA.
AC P49820:
ID NUHM_CANFA
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NADH-UBIQUINONE OXIDOREDUCTASE 24 KDA SUBUNIT (EC 1.6.5.3)
DE (EC 1.6.99.3) (FRAGMENT).
GN NDUUF2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE.
RC TISSUE=HEART;
RX MEDLINE: 98163340.
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
CC FRAGMENT OF THE ENZYME.
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -1- COFACTOR: 2FE-2S IRON-SULFUR CLUSTER N 1B.
CC -1- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
CC THIS IS A COMPONENT OF THE MATRIX AND CYTOPLASMIC SIDE OF THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 24 KDA SUBUNIT FAMILY.
DR HSC-2DPAGE; P49820; DOG.
DR INTERPRO: IPR002023; -.
DR PROSITE: PS01099; COMPLEX1_24K; PARTIAL.
KM Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Iron-sulfur.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match 19.0%; Score 19; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LFALL 15
DB 6 LFVH 9

RESULT 8

PA21_MICFM STANDARD; PRT; 12 AA.
ID PA21_MICFM
AC P25072:
DT 01-MAY-1992 (Rel. 22, Created)
DT 15-DEC-1998 (Rel. 22, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PHOSPHOLIPASE A2 ISOZYME 1 (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE
DE 2-ACYLHYDROLASE) (FRAGMENT).
OS Micrurus fulvius microurabineus (Mexican coral snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubridae;
OC Elapidae; Elapinae; Micrurus.
RN [1]
RP SEQUENCE.
RC TISSUE=VENOM;
RX MEDLINE: 79255521.
RA Possant L.D., Alagon A.C., Fletcher P.L. Jr., Varela M.J., Julia J.Z.;
RT "Purification and characterization of a phospholipase A2 from the
RT venom of the coral snake, Micrurus fulvius microurabineus (Brown and
RT Smith).";
RL Biochem. J. 179:603-606(1979).
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-
CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
DR INTERPRO: IPR001211; -.
DR PROSITE: PS00118; PA2_HIS; PARTIAL.
DR PROSITE: PS00119; PA2_ASP; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Venom.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1398 MW; CC21992A899F0339 CRC64;

Query Match 19.0%; Score 19; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 16 LIDFQ 20
DB 2 LIDBF 6

RESULT 9
TX3_PHONI STANDARD; PRT; 19 AA.
ID TX3_PHONI
AC P31010:
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE NEUROTOXIN TX3 (FRAGMENT).
OS Phonteuria nigriyenter (Brazilian armed spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phonteuria.
RN [1]
RP SEQUENCE.
RC TISSUE=VENOM;
RX MEDLINE: 92196803.
RA Rezende L. Jr., Cordeiro M.N., Oliveira E.B., Diniz C.R.;
RT "Isolation of neurotoxic peptides from the venom of the 'armed'
RT spider Phonteuria nigriyenter.";
RL Toxicon 29:1225-1233(1991).
DR PIR: C39305; C39305.
KW Venom; Neurotoxin.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2244 MW; 3214B89CF10F7587 CRC64;

Query Match 19.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SOKK 11

RA Passerini de Rossi B.N., Friedman L.E., Gonzalez Fleche F.L.,
 RA Castello P.R., Franco M.A., Rossi J.P.F.C.,
 RT "Identification of Bordetella pertussis virulence-associated outer
 RT membrane proteins.";
 RL FEMS Microbiol. Lett. 172:9-13(1999).
 KW Outer membrane: Virulence.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2116 MW; D24E1CDCA655206C CRC64;

Query Match 22.0%; Score 22; DB 1; Length 20;
 Best Local Similarity 57.1%; Pred. No. 8.8e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 TVQASYS 8
 Db 11 TVEGEYS 17

RESULT 3
 MAST_POLJA STANDARD; PRT; 14 AA.
 AC POLS17;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE POLISTES MASTOPARAN.
 OS Polistes jadwigae (Paper wasp).
 OS Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Vespoidea; Vespidae; Polistinae; Polistes.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=VENOM;
 RA Hiral Y., Ueno Y., Yasuhara T., Yoshida H., Nakajima T.;
 RT "A new mast cell degranulating peptide, polistes mastoparan, in the
 RT venom of Polistes jadwigae.";
 RL Biomed. Res. 1:185-187(1980).
 CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
 CC THAT COUPLE TO PHOSPHOLIPASE C.
 DR PIR: A01780; QMAPP.
 KW Mast cell degranulation; Venom; Amidation.
 FT MOD.RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA; 1636 MW; 26472A53BF477808 CRC64;

Query Match 21.0%; Score 21; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 9e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 10 KRFLHL 17
 Db 4 KRIGHIL 11

RESULT 4
 TIL8_SPIOL STANDARD; PRT; 20 AA.
 AC P82536;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE THYLAKOID LUMENAL 18 KDA PROTEIN (P18) (FRAGMENT).
 OS Spinacia oleracea (Spinach).
 OS Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
 OC Caryophyllales; Chenopodiaceae; Spinacia.
 RN [1]
 RP SEQUENCE.
 RA Kieselbach T., Bystedt M., Schroeder W.P.;
 RL Submitted (MAY-2000) to the SWISS-PROT data bank.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
 KW Chloroplast; Thylakoid membrane.

FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2192 MW; 752C21963F49FA64 CRC64;

Query Match 21.0%; Score 21; DB 1; Length 20;
 Best Local Similarity 30.8%; Pred. No. 1.3e+03;
 Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 TVQASYSORKLF 13
 Db 5 TPLOSKVTNKVFE 17

RESULT 5
 XYNB_DICB4 STANDARD; PRT; 10 AA.
 ID XYNB_DICB4
 AC P80717;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE ENDO-1,4-BETA-XYLANASE B (EC 3.2.1.8) (XYLANASE B)
 DE (1,4-BETA-D-XYLAN XYLANOXYDOLASE B) (FRAGMENT).
 OS Dictyoglomus sp. (strain B4A).
 OC Bacteria; Dictyoglomus group; Dictyoglomus.
 RN [1]
 RP SEQUENCE.
 RA Adamsen A.K., Jacobsen S., Ahring B.K.;
 RL Submitted (OCT-1996) to the SWISS-PROT data bank.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL
 CC HYDROLASES).
 DR INTERPRO: IPR001000;
 DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; PARTIAL.
 KW Xylan degradation; Hydrolase; Glycosidase.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1144 MW; 4554322AA72041A3 CRC64;

Query Match 20.0%; Score 20; DB 1; Length 10;
 Best Local Similarity 55.6%; Pred. No. 9.3e+02;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 10 KRFLHL 18
 Db 2 KRTILDLDK 10

RESULT 6
 CPBX_CAVPO STANDARD; PRT; 20 AA.
 ID CPBX_CAVPO
 AC P34033;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CYTOCHROME P4501B (EC 1.14.14.1) (FRAGMENT).
 OS Cavia porcellus (Guinea pig).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathli; Cavidae; Cavia.
 RN [1]
 RP SEQUENCE AND CHARACTERIZATION.
 RC STRAIN=HARTLEY; TISSUE=LIVER.
 RX MEDLINE: 91054472.
 RA Narimatsu S., Akutsu Y., Matsunaga T., Watanabe K., Yamamoto I.,
 RA Yoshimura H.;
 RT "Purification of a cytochrome P450 isozyme belonging to a subfamily
 RT of P450 11B from liver microsomes of guinea pigs.";
 RL Biochem. Biophys. Res. Commun. 172:607-613(1990).
 CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
 CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ISOZYME IS INVOLVED IN AN
 CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. THIS ISOZYME IS ACTIVE
 CC UPON P-NITROANISOLE, ANILINE, D-BENZPHETAMINE, DELTA(9)-

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:32:54 ; Search time 62.7 Seconds

(without alignments)
10.191 Million cell updates/sec

Title: US-08-934-367-5

Perfect score: 100

Sequence: 1 TTYQASYSQKLFLLHLDFO 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	24	22.0	18 1 UC21_MAIZE	P80627 zea mays (m
2	22	22.0	20 1 VR90_BORPE	P81549 bordetella
3	21	21.0	14 1 MAST_POLJA	P01517 polistes ja
4	21	21.0	20 1 TL18_SPIOL	P82536 spinacia ol
5	20	20.0	10 1 XYNB_DIC84	P80717 dictyoglomu
6	20	20.0	20 1 CPBX_CAVPO	P34033 cavia porce
7	19	19.0	11 1 NUHM_CANFA	P48820 canis famli
8	19	19.0	12 1 PA21_MICFM	P23072 micrurus fu
9	19	19.0	19 1 TX3_PHONT	P31010 phoneutria
10	19	19.0	20 1 AMP_FUSNU	P81207 fusbacteri
11	19	19.0	20 1 DCMS_PSECF	P19915 pseudomonas
12	18	18.0	14 1 FIBA_HORSE	P14452 equus cabal
13	18	18.0	17 1 APPI_PAVLU	P28529 pavlova lut
14	18	18.0	17 1 SP51_BACLI	P27642 bacillus li
15	18	18.0	19 1 AL22_HORSE	P81217 equus cabal
16	18	18.0	19 1 UP24_UPEIN	P82030 uperoleia i
17	18	18.0	20 1 CRP_MUSCA	P19094 mustelus ca
18	17	17.0	9 1 HUTU_KIEAE	P12381 klebsiella
19	17	17.0	9 1 UAE_HUMAN	P31931 homo sapien
20	17	17.0	10 1 PNEU_RAT	P21996 rattus norv
21	17	17.0	12 1 NC40_SOYBN	P55960 glycyine max
22	17	17.0	15 1 CBPB_PROAT	P19628 protoplerus
23	17	17.0	18 1 AL13_CARMA	P81816 carcinus ma
24	17	17.0	18 1 NODD_CHIIO	O52838 rhizobium l
25	17	17.0	20 1 CARA_ACIRA	P81422 achinetobact
26	17	17.0	20 1 R1PX_CUCPE	P80750 cucurbita p
27	16	16.0	8 1 AKH_MEIML	P25423 melolontha
28	16	16.0	8 1 ANG2_BOTJA	O10582 botriops ja
29	16	16.0	8 1 COXG_RAT	P80430 rattus norv
30	16	16.0	10 1 TRXB_RANRI	P29135 rana rididu
31	16	16.0	11 1 ANGT_CRIGE	P09037 crinia geor
32	16	16.0	12 1 PA2B_VIPBO	P31859 vipera beru
33	16	16.0	13 1 MLA_CAMDR	P01198 camelus dfo

34	16	16.0	14 1 ANGT_HORSE	P01016 equus cabal
35	16	16.0	14 1 LEGB_PSOSE	P22584 psophocarpu
36	16	16.0	14 1 RS19_CLOPP	O46228 clover prol
37	16	16.0	14 1 RS19_LOMBA	O48878 loofah wlc
38	16	16.0	14 1 TKNM_RANMA	P40951 rana margar
39	16	16.0	15 1 COXJ_THIOB	P80979 thunnus obe
40	16	16.0	15 1 FGFI_CANFA	P18651 canis famli
41	16	16.0	15 1 PGKH_PHYPA	P80659 physcomilitre
42	16	16.0	16 1 IBP4_PIG	P24854 sus scrofa
43	16	16.0	16 1 R1PK_TRIKI	P16093 trichosanthe
44	16	16.0	17 1 UP41_UPEIN	P82035 uperoleia i
45	16	16.0	18 1 PHPT_PSESE	P25271 pseudaleteria

ALIGNMENTS

RESULT	ID	UC21_MAIZE	STANDARD:	PRT:	18 AA.
AC	P80627:				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 443)				
DE	(FRAGMENT).				
OS	Zea mays (Maize).				
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;				
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=COLEOPTILE;				
RA	Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,				
RA	Penollet J.-C., Zivy M., de Vienne D.;				
RT	"The maize two dimensional gel protein database: towards an integrated				
RT	genome analysis program."				
RL	Theor. Appl. Genet. 93:997-1005(1996).				
CC	-1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN				
CC	PROTEIN IS: 5.9, ITS MW IS: 26.5 KDA.				
CC	-1- SIMILARITY: TO L-ASCORBATE PEROXIDASES.				
DR	HSSP: P48534; IAPX				
DR	MAIZE-2DPAGE: P80627; COLEOPTILE.				
DR	MAIZEEDB: 123953; -				
FT	NON-TER	1	1		
FT	NON-TER	18	18		
SO	SEQUENCE	18 AA; 1938 MW; F32P6FEF038BAB8A CRC64;			
Query Match					
Best Local Similarity 24.0%; Score 24; DB 1; Length 18;					
Matches 5; Conservativity 71.4%; Pred. No. 3.5e+02;					
Matches 5; Conservativity 0; Mismatches 2; Indels 0; Gaps 0;					
QY	2 TTYQASY 8				
DB	6 TVSAEYS 12				
RESULT 2					
VR90_BORPE	STANDARD:	PRT:	20 AA.		
AC	P81549:				
DT	15-JUL-1999 (Rel. 38, Created)				
DT	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	VIRULENCE-ASSOCIATED OUTER MEMBRANE PROTEIN VIR90 (FRAGMENT).				
GN	VIR90.				
OS	Bordetella pertussis.				
OC	Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;				
OC	Bordetella.				
RN	[1]				
RP	SEQUENCE.				
RC	STRAIN=TOHAMMA I;				
RX	MEDLINE: 99179239.				

A:Cross-references: GDB:119297; OMIM:141900
A:Map position: 11p15.4-11p15.4

Query Match 22.0%; Score 22; DB 4; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 VOASYSQ 9
|||||
DB 3 VOAAVQK 9

RESULT 13

BA5895
T-cell surface glycoprotein CD28 short form - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Feb-1994
C:Accession: BA5895
R:Lee, K.P.; Taylor, C.; Petryniak, B.; Turka, L.A.; June, C.H.; Thompson, C.B.
J. Immunol. 145: 344-352, 1990
A:Title: The genomic organization of the CD28 gene. Implications for the regulation of C
A:Reference number: A45895; MUID:90293482
A:Accession: BA5895
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <LEF>
A:Cross-references: GB:M37813
C:Keywords: glycoprotein

Query Match 22.0%; Score 22; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 VOASYSQ 10
|||||
DB 2 VNLSYNEK 9

RESULT 14

S00493
hemocyanin chain III - Japanese spiny lobster (fragment)
C:Species: Panulirus japonicus (Japanese spiny lobster)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 01-Aug-1997
C:Accession: S00493
R:Makino, N.; Kimura, S.
Eur. J. Biochem. 173, 423-430, 1988
A:Title: Subunits of Panulirus japonicus hemocyanin. 1. Isolation and properties.
A:Reference number: S00492; MUID:88196131
A:Accession: S00493
A:Molecule type: protein
A:Residues: 1-19 <MAK>
C:Superfamily: hemocyanin
C:Keywords: copper; hemolymph; hexamer; oxygen carrier

Query Match 22.0%; Score 22; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 HLDD 18
|||||
DB 16 HLDD 19

RESULT 15

S00493
hemocyanin chain Ib - Japanese spiny lobster (fragment)
C:Species: Panulirus japonicus (Japanese spiny lobster)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 01-Aug-1997
C:Accession: S00493
R:Makino, N.; Kimura, S.

Eur. J. Biochem. 173, 423-430, 1988
A:Title: Subunits of Panulirus japonicus hemocyanin. 1. Isolation and properties.
A:Reference number: S00492; MUID:88196131
A:Accession: S00493
A:Molecule type: protein
A:Residues: 1-20 <MAK>
C:Superfamily: hemocyanin
C:Keywords: copper; hemolymph; hexamer; oxygen carrier

Query Match 22.0%; Score 22; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 HLDD 18
|||||
DB 16 HLDD 19

Search completed: December 21, 2000, 08:30:04
Job time: 268 sec

C:Species: Aspergillus niger
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1997
C:Accession: S10452
R:van Gorcom, R.F.M.; Boschloo, J.G.; Kuijvenhoven, A.; Lange, J.; Bos, C.J.; van Baalen
submitted to the EMBL Data Library, March 1990
A:Reference number: S10452
A:Accession: S10452
A:Molecule type: DNA
A:Residues: 1-18 <VAN>
A:Cross-references: EMBL:X52521; NID:923336; PID:92337

Query Match 23.0%; Score 23; DB 2; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 2 TVQASYSOKLFLH 15
| | | | | | | | | | | | | | | | | |
Db 2 TDQPLSRQETLFTH 15

RESULT 8
S54272
CTC 75 protein - human
C:Species: Homo sapiens (man)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C:Accession: S54272
R:Gensch, E.; Eckerskorn, C.; Lottspeich, F.; Herzog, C.; Kuehn, K.; Poeschl, E.
EMBO J. 14, 791-800, 1995
A:Title: Purification of the sequence-specific transcription factor CTCBF, involved in
A:Reference number: S54272; MUID:95188883
A:Accession: S54272
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <GEN>

Query Match 23.0%; Score 23; DB 2; Length 18;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 TTVOASYSOKKL 12
| | | | | | | | | | | | | | | | | |
Db 6 STGKVEYSEEL 17

RESULT 9
PH0786
T-cell receptor alpha chain (I7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0786
R:Cananova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-T
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846
A:Accession: PH0786
A:Molecule type: mRNA
A:Residues: 1-13 <CAS>
A:Cross-references: EMBL:X60889
A:Experimental source: T lymphocyte
A:Keywords: T-cell receptor

Query Match 22.0%; Score 22; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 5 ASYSOKLFL 13
| | | | | | | | | | | | | | | | | |
Db 4 SAYANKMIF 12

RESULT 10
S29209
avenin alpha-2 - oat (fragment)
N:Alternate names: CIP-3; coeliac immunoreactive protein 3
C:Species: Avena sativa (oat)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C:Accession: S29209
R:Roche, A.; Collia, F.; Ortiz, M.L.; Mendez, E.
FEBS Lett. 310, 37-40, 1992
A:Title: Identification of the three major coeliac immunoreactive proteins and one al
A:Reference number: S29207; MUID:92405739
A:Accession: S29209
A:Molecule type: protein
A:Residues: 1-14 <ROC>
A:Experimental source: endosperm
C:Superfamily: gliadin
C:Keywords: prolamin; seed

Query Match 22.0%; Score 22; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTVOASYSOK 10
| | | | | | | | | | | | | | | | | |
Db 2 TTVOYNPSEQ 11

RESULT 11
A44920
2-halobenzoate 1,2-dioxygenase component A beta chain - Pseudomonas cepacia (fragment)
C:Species: Pseudomonas cepacia
C:Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
C:Accession: A44920
R:Feltner, S.; Muller, R.; Lings, F.
J. Bacteriol. 174, 279-290, 1992
A:Title: Purification and some properties of 2-halobenzoate 1,2-dioxygenase, a two-co
A:Reference number: A44920; MUID:92104974
A:Contents: 2CS8
A:Accession: A44920
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <FET>
A:Note: sequence extracted from NCBI backbone (NCBIP:75379)

Query Match 22.0%; Score 22; DB 2; Length 14;
Best Local Similarity 28.6%; Pred. No. 1.7e+03;
Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 TTVOASYSOKLFL 14
| | | | | | | | | | | | | | | | | |
Db 1 TLESSTLDVAVFI 14

RESULT 12
I52618
hemoglobin beta chain thalassemia mutant Portuguese - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 11-Jul-1996 #text_change 20-Apr-2000
C:Accession: I52618
R:Onier, R.; Onier, C.; Wilson, J.B.; Tamagnini, G.P.; Ribeiro, L.M.; Huismar, T.H.
Br. J. Haematol. 79, 306-310, 1991
A:Title: Dominant beta-thalassemia trait in a Portuguese family is caused by a delet
A:Reference number: I52618; MUID:92068764
A:Accession: I52618
A:Status: translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14 <ONE>
A:Cross-references: GB:S68042; NID:9239717; PIDN:AA820440.1; PID:9239718
C:Genetics:
A:Gene: GDB:HBB

RESULT 3
S14560
Probable heme-binding protein - garden pea chloroplast (fragment)
C:Species: chloroplast Pisum sativum (garden pea)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 11-Jan-2000
C:Accession: S14560
R:Smith, A.G.; Wilson, R.J.; Kaetner, T.M.; Willey, D.L.; Gray, J.C.
Submitted to the EMBL Data Library, October 1990
A:Reference number: S14557
A:Accession: S14560
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18 <SMI>
A:Cross-references: EMBL:X54750; NID:g12194; PID:g12198
C:Genetics:
A:Genome: chloroplast
C:Superfamily: maize chloroplast protein cema
C:Keywords: chloroplast; heme; transmembrane protein

Query Match 25.0%; Score 25; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 6,6e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 8 SOKKFLHL 17
DB 2 AKKATPPL 11

RESULT 4
A26228
Spot 42 protein - Escherichia coli
C:Species: Escherichia coli
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 08-Oct-1999
C:Accession: A26228; A37586; Q00551
R:Joyce, C.M.; Grindley, N.D.F.
J. Bacteriol. 152, 1211-1219, 1982
A:Title: Identification of two genes immediately downstream from the *polA* gene of *Escherichia coli*
A:Reference number: A26228; MUID:83056713
A:Accession: A26228
A:Molecule type: DNA
A:Residues: 1-15 <JOY2>
R:Sahagan, B.G.; Dahlberg, J.E.
J. Mol. Biol. 131, 573-592, 1979
A:Title: A small, unstable RNA molecule of *Escherichia coli*: spot 42 RNA.
A:Reference number: A37586; MUID:80074983
A:Accession: A37586
A:Molecule type: DNA
A:Residues: 1-15 <SMH>
A:Cross-references: GB:X01895; NID:g40868; PIDN:CAA25985.1; PID:g40869
C:Genetics:
A:Gene: *spf*
A:Map position: 87 min

Query Match 24.0%; Score 24; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 8,1e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 12 LFLHLDF 19
DB 7 LLLHVGIF 14

RESULT 5
S70331
Endosperm protein, 18k - rye (fragment)
C:Species: Secale cereale (rye)
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C:Accession: S70331
R:Roche, A.; Calero, M.; Soriano, F.; Mendez, E.

Biochim. Biophys. Acta 1295, 13-22, 1996
A:Title: Identification of major rye *secalins* as coeliac immunoreactive proteins.
A:Reference number: S70327; MUID:96283789
A:Accession: S70331
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <ROC>

Query Match 24.0%; Score 24; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 8,7e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 TTVQASTSQ 12
DB 3 TTVSQGYGQXOL 14

RESULT 6
S47365
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47365; S47375; S47396; S47398; S47355
R:Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of Influenza A is dominated by
A:Reference number: S47355
A:Accession: S47365
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35690; NID:g527471; PIDN:CAA84759.1; PID:g527472; EMBL:Z356

A:Accession: S47375
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE2>
A:Cross-references: EMBL:Z35700; NID:g527493; PIDN:CAA84769.1; PID:g527494
A:Accession: S47379
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE3>
A:Cross-references: EMBL:Z35708; NID:g527509; PIDN:CAA84777.1; PID:g527510
A:Accession: S47396
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE4>
A:Cross-references: EMBL:Z35674; NID:g527527; PIDN:CAA84743.1; PID:g527528
A:Accession: S47397
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE5>
A:Cross-references: EMBL:Z35675; NID:g527529; PIDN:CAA84744.1; PID:g527530
A:Accession: S47398
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE6>
A:Cross-references: EMBL:Z35676; NID:g527531; PIDN:CAA84745.1; PID:g527532
C:Keywords: T-cell receptor

Query Match 23.0%; Score 23; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 1e+03;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTVQASTSQ 9
DB 3 SIRSSEYEQ 11

RESULT 7
S10452
Hypothetical protein (bpha 5' region) - *Aspergillus niger*

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:30:03 ; Search time 112.59 Seconds
(without alignments)
11.273 Million cell updates/sec

Title: US-08-934-367-5
Perfect score: 100
Sequence: 1 TTVQASYSQKLFLLHLDQ 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.65:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28.0	14	2	S13864	methyl coenzyme M
2	26.0	15	2	S65717	prostaglandin D-sy
3	25.0	18	2	S14560	probable heme-bind
4	24.0	15	2	A26228	spot 42 protein -
5	24.0	16	2	S70331	endospore protein,
6	23.0	13	2	S47365	T-cell antigen rec
7	23.0	18	2	S10452	hypothetical prote
8	23.0	18	2	S54272	CDC 75 protein - h
9	22.0	13	2	PH0786	T-cell receptor al
10	22.0	14	2	S29209	avenin alpha-2 - o
11	22.0	14	2	A44920	2-halobenzoate 1,2
12	22.0	14	4	I52618	hemoglobin beta ch
13	22.0	16	2	B45895	T-cell surface gly
14	22.0	19	2	S00495	hemocyanin chain I
15	22.0	20	2	S00493	hemocyanin chain I
16	22.0	20	2	S00494	hemocyanin chain I
17	21.0	6	2	A61411	ameletin - rat
18	21.0	10	2	I40032	tripe protein - Bac
19	21.0	12	2	S65136	kalikrein K2 - hu
20	21.0	13	2	S47374	T-cell antigen rec
21	21.0	13	2	PH1479	T-cell receptor be
22	21.0	14	1	OMWAPP	polistes mastopara
23	21.0	16	2	A36889	leu operon leader
24	21.0	16	2	S34444	blaz protein - Stra
25	21.0	17	2	U02320	hypothetical 2.1k
26	21.0	19	2	A48354	nonstructural prot
27	21.0	19	2	S59717	hypothetical prote
28	21.0	20	2	H49034	nuclear antigen EB
29	20.0	12	2	S26556	T-cell receptor be

30	20	20.0	13	2	S47372	T-cell antigen rec
31	20	20.0	15	2	PN0164	hyoscyamine (6S)-d
32	20	20.0	15	2	S36890	ribosomal protein
33	20	20.0	15	2	PH0770	T-cell receptor be
34	20	20.0	16	2	PC1299	subtilisin (EC 3.4
35	20	20.0	17	2	B49404	T-cell receptor be
36	20	20.0	17	2	I49593	cytic fibrosis tr
37	20	20.0	17	2	I84733	gene CTR protein
38	20	20.0	17	2	A35550	adrenocortical cel
39	20	20.0	19	2	A60459	aminopeptidase, 30
40	20	20.0	19	2	I39327	pre-T/NK cell-asso
41	20	20.0	20	2	A60372	pollen allergen po
42	20	20.0	20	2	S46479	retinoid-X-recepto
43	19	19.0	13	2	A44818	extracellular lipa
44	19	19.0	14	2	A47421	leukorrhe B-4 12
45	19	19.0	15	2	PA0046	protein QM100044 -

ALIGNMENTS

RESULT 1
S13864 methyl coenzyme M reductase (EC 1.8.-.-) II alpha chain - Methanobacterium thermoauto
C:Species: Methanobacterium thermoautotrophicum
A:Variety: strain Marburg
C:Date: 19-Mar-1997 #sequence_revision 13-Sep-1998 #text_change 30-Oct-1998
C:Accession: S13864
R:Rospert, S.; Linder, D.; Ellermann, J.; Thauer, R.K.
Eur. J. Biochem. 194, 871-877, 1990
A:Title: Two genetically distinct methyl-coenzyme M reductases in Methanobacterium th
A:Reference number: S13864; MUID:91099370
A:Accession: S13864
A:Molecule type: protein
A:Residues: 1-14 <ROS>
A:Experimental source: strain Marburg
A:Keywords: methanogenesis; oxidoreductase

Query Match 28.0%; Score 26; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 OKKLFLL 17
DB 3 EKKLFLL 11

RESULT 2
S65717 prostaglandin D-synthase - rat (fragment)
N:Alternate names: prostaglandin-H2 D-isomerase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 31-Oct-1997
C:Accession: S65717
R:Giacomelli, S.; Leone, M.G.; Grima, J.; Silvestrini, B.; Cheng, C.Y.
Biochim. Biophys. Acta 1310, 269-276, 1996
A:Title: Astrocytes synthesize and secrete prostaglandin D synthetase in vitro.
A:Reference number: S65716; MUID:96177373
A:Accession: S65717
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <GIA>
C:Superfamily: lipocalin; lipocalin homology

Query Match 26.0%; Score 26; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTVQASYSQK 11
DB 3 TTVQPNFQDK 12

LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-383-753-57

Query Match 27.0%; Score 27; DB 1; Length 18;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 8 SOKKFLHL 16
: 1 1 1 1
DB 10 AOKMLYQHL 18

RESULT 14
US-08-586-772-57
; Sequence 57, Application US/08586772
; Patent No. 5874239
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; TITLE OF INVENTION: Bioclinylation of Proteins
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,772
; FILING DATE: 03-FEB-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/099,991
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-586-772-57

Query Match 27.0%; Score 27; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 8 SOKKFLHL 16
: 1 1 1 1
DB 10 AOKMLYQHL 18

RESULT 15
US-08-959-512-57
; Sequence 57, Application US/08959512

; Patent No. 5932433
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; TITLE OF INVENTION: Bioclinylation of Proteins
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,512
; FILING DATE:
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/383,753
; FILING DATE: 03-FEB-1995
; APPLICATION NUMBER: US 08/099,991
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 1038.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-959-512-57

Query Match 27.0%; Score 27; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 8 SOKKFLHL 16
: 1 1 1 1
DB 10 AOKMLYQHL 18

Search completed: December 21, 2000, 08:31:46
Job time: 369 sec

Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 HLDFQ 20

Db 2 YLDFQ 7

RESULT 11

US-09-100-414B-2

; Sequence 2, Application US/09100414B

; Patent No. 6023468

; GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi

; TITLE OF INVENTION: NOVEL LHRH PEPTIDE

; TITLE OF INVENTION: IMMUNOGENS

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morgan & Finnegan, L.L.P.

; STREET: 345 Park Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10154-0054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC Windows

; SOFTWARE: Word 97

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/100.414B

; FILING DATE: 20-JUNE-1998

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Maria H. Lin

; REGISTRATION NUMBER: 29,323

; REFERENCE/DOCKET NUMBER: 1151-4157

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-758-4800

; TELEFAX: 212-751-6849

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-09-100-414B-2

Query Match 27.0%; Score 27; DB 3; Length 16;

Best Local Similarity 66.7%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 10 KKLFLHLD 18

Db 6 KGLLHKLD 14

RESULT 12

US-09-100-409A-61

; Sequence 61, Application US/09100409A

; Patent No. 6090388

; GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi

; TITLE OF INVENTION: PEPTIDE COMPOSITION FOR

; PREVENTION AND TREATMENT OF HIV INFECTION AND

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN

; STREET: 345 Park Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10154-0054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version

; SOFTWARE: #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/100.409A

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME:

; REGISTRATION NUMBER:

; REFERENCE/DOCKET NUMBER: 1151-4154

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-758-4800

; TELEFAX: 212-751-6849

; INFORMATION FOR SEQ ID NO: 61:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-09-100-409A-61

Query Match 27.0%; Score 27; DB 3; Length 16;

Best Local Similarity 66.7%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 10 KKLFLHLD 18

Db 6 KGLLHKLD 14

RESULT 13

US-08-383-753-57

; Sequence 57, Application US/08383753

; Patent No. 5723584

; GENERAL INFORMATION:

; APPLICANT: Schatz, Peter J.

; TITLE OF INVENTION: Biotinylation of Proteins

; NUMBER OF SEQUENCES: 102

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: One Market Plaza, Steuart Tower

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/383,753

; FILING DATE: 03-FEB-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/099,991

; FILING DATE: 30-JUL-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 1038.1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 57:

; SEQUENCE CHARACTERISTICS:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,029
FILING DATE: 2 MAY 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-019.08
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1242
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-854-029-28

Query Match 28.0%; Score 28; DB 2; Length 14;
Best Local Similarity 71.4%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 7 YSOKKLF 13
||:|:|
Db 8 YSOEELF 14

RESULT 8
5266328-11
Patent No. 5266328
APPLICANT: SKUBITZ, AMY P.N.; FURCHT, LEO T.
TITLE OF INVENTION: LAMININ CHAIN POLYPEPTIDES FROM
THE CARBOXY TERMINAL GLOBULAR DOMAIN
NUMBER OF SEQUENCES: 14
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/573,672
FILING DATE: 27-AUG-1990
SEQ ID NO: 11:
LENGTH: 17
5266328-11

Query Match 28.0%; Score 28; DB 5; Length 17;
Best Local Similarity 41.7%; Pred. No. 73;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 TWOASYSOKRLF 13
||:|:|
Db 6 YVKEIKKKRAF 17

RESULT 9
US-07-654-839-5
Sequence 5, Application US/07654839
Patent No. 5372933
GENERAL INFORMATION:
APPLICANT: zamarron, Concepcion
APPLICANT: Plow, Edward F.
APPLICANT: Ginsberg, Mark H.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST
TITLE OF INVENTION: RECEPTOR-INDUCED BINDING SITES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSER: Patent Counsel
STREET: 10666 No. 5372933th Torrey Pines Road., Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/654,839
FILING DATE: 19910213
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,753
FILING DATE: 03-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/415,029
FILING DATE: 29-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Blingham, Douglas A.
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: SCRO367P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
US-07-654-839-5

Query Match 28.0%; Score 28; DB 1; Length 19;
Best Local Similarity 38.5%; Pred. No. 83;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 7 YSOKKLFHLDF 19
||:|:|
Db 1 YSMKTTMKIIF 13

RESULT 10
PCT-US94-01234-47
Sequence 47, Application PC/TUS9401234
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE
TITLE OF INVENTION: BINDING SITES
NUMBER OF SEQUENCES: 76
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01234
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,542
FILING DATE: 28-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,566
FILING DATE: 02-FEB-1993
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
PCT-US94-01234-47

Query Match 27.0%; Score 27; DB 4; Length 13;

14
FILING DATE: 18-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0183
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-454-207A-43

Query Match 29.0%; Score 29; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.2e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 YSOKKLF 14
11111111
DB 1 SKKKLFL 7

RESULT 5
US-08-428-415-28
Sequence 28, Application US/08428415
Patent No. 5756335
GENERAL INFORMATION:
APPLICANT: Cold Spring Harbor Laboratory
TITLE OF INVENTION: No. 5756335el Human cdc25 Genes, Encoded
TITLE OF INVENTION: Products and Uses Thereof
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,415
FILING DATE: 24 April 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-019CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-227-7400
TELEFAX: 617-227-5941
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-428-415-28

Query Match 28.0%; Score 28; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 YSOKKLF 13
11111111
DB 8 YSQEELF 14

RESULT 6
US-08-379-685-28
Sequence 28, Application US/08379685
Patent No. 5770423
GENERAL INFORMATION:
APPLICANT: Cold Spring Harbor Laboratory
TITLE OF INVENTION: No. 5770423el Human cdc25 Genes, Encoded
TITLE OF INVENTION: Products and Uses Thereof
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,685
FILING DATE: 26 January 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-019-DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-227-7400
TELEFAX: 617-227-5941
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-379-685-28

Query Match 28.0%; Score 28; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 YSOKKLF 13
11111111
DB 8 YSQEELF 14

RESULT 7
US-08-854-029-28
Sequence 28, Application US/08854029
Patent No. 5994074
GENERAL INFORMATION:
APPLICANT: Cold Spring Harbor Laboratory
TITLE OF INVENTION: No. 5994074el Human cdc25 Genes, Encoded
TITLE OF INVENTION: Products and Uses Thereof
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)

OY 11 KLFHL 17
111111
DB 6 KLFPHL 12

```

RESULT 2
US-08-871-355A-355
; Sequence 355, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,355A
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 355:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; US-08-871-355A-355

Query Match 31.0%; Score 31; DB 3; Length 14;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 KLFHL 17
111111
DB 6 KLFPHL 12

RESULT 3
US-08-454-207A-36
; Sequence 36, Application US/08454207A
; Patent No. 5710123
; GENERAL INFORMATION:
; APPLICANT: Heavener, George A.
; APPLICANT: Kruszyński, Marian
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123rls LLP
; STREET: One Liberty Place - 46th Floor
```

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; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,207A
; FILING DATE: 09-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12110
; FILING DATE: 13-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/997,771
; FILING DATE: 18-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Eldertin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0183
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-454-207A-36
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Query Match 29.0%; Score 29; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1,2e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 SKKKLH 15
111111
DB 1 SKKKLH 8
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RESULT 4
US-08-454-207A-43
; Sequence 43, Application US/08454207A
; Patent No. 5710123
; GENERAL INFORMATION:
; APPLICANT: Heavener, George A.
; APPLICANT: Kruszyński, Marian
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123rls LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,207A
; FILING DATE: 09-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12110
; FILING DATE: 13-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/997,771
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Thu Dec 21 08:51:32 2000

us-08-934-367-5.ra1

Page 1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:31:45 ; Search time 99.91 seconds
(without alignments)
3.355 Million cell updates/sec

Title: US-08-934-367-5
Perfect score: 100
Sequence: 1 TTVQASYSKKFLHLDFQ 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 87906

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	31	31.0	14	2 US-08-637-759B-355	Sequence 355, App
2	31	31.0	14	3 US-08-871-335A-355	Sequence 355, App
3	29	29.0	9	1 US-08-454-207A-36	Sequence 36, App
4	29	29.0	9	1 US-08-454-207A-43	Sequence 43, App
5	28	28.0	14	1 US-08-428-415-28	Sequence 28, App
6	28	28.0	14	1 US-08-379-685-28	Sequence 28, App
7	28	28.0	14	2 US-08-854-029-28	Sequence 28, App
8	28	28.0	17	5 5266328-11	Patent No. 5266328
9	28	28.0	19	1 US-07-654-839-5	Sequence 5, App
10	27	27.0	13	4 PCT-US94-01234-47	Sequence 47, App
11	27	27.0	16	3 US-09-100-414B-2	Sequence 2, App
12	27	27.0	16	3 US-09-100-409A-61	Sequence 61, App
13	27	27.0	18	1 US-08-383-753-57	Sequence 57, App
14	27	27.0	18	2 US-08-586-772-57	Sequence 57, App
15	27	27.0	18	2 US-08-959-512-57	Sequence 49, App
16	26	26.0	19	1 US-08-267-092A-49	Sequence 49, App
17	26	26.0	19	4 PCT-US95-08156-50	Sequence 50, App
18	26	26.0	19	4 US-08-540-412-50	Sequence 50, App
19	26	26.0	20	1 US-08-218-025A-81	Sequence 81, App
20	26	26.0	20	1 US-08-482-228-208	Sequence 208, App
21	25	25.0	6	3 US-08-482-528-208	Sequence 208, App
22	25	25.0	10	2 US-08-482-528-209	Sequence 209, App
23	25	25.0	10	3 US-08-482-528-209	Sequence 209, App
24	25	25.0	10	3 US-08-946-329A-42	Sequence 42, App
25	25	25.0	11	1 US-08-464-531-53	Sequence 53, App
26	25	25.0	11	2 US-08-461-598-53	Sequence 53, App
27	25	25.0	11	2 US-08-322-137-53	Sequence 53, App
28	25	25.0	14	3 US-08-844-031-23	Sequence 23, App

29	25	25.0	15	2 US-08-726-464B-35	Sequence 35, App
30	25	25.0	17	3 US-09-192-048-16	Sequence 16, App
31	25	25.0	18	3 US-09-100-414B-26	Sequence 26, App
32	25	25.0	20	1 US-07-678-974D-16	Sequence 30, App
33	25	25.0	20	2 US-08-934-915-179	Sequence 179, App
34	25	25.0	20	2 US-08-945-168-21	Sequence 15, App
35	25	25.0	10	2 US-08-967-999-15	Sequence 117, App
36	24	24.0	11	2 PCT-US95-04589-117	Sequence 117, App
37	24	24.0	11	4 PCT-US95-04589-117	Sequence 117, App
38	24	24.0	16	1 US-08-158-232-44	Sequence 44, App
39	24	24.0	16	2 US-08-611-928-44	Sequence 44, App
40	24	24.0	16	3 US-09-100-437-1	Sequence 1, App
41	24	24.0	16	3 US-09-173-891-44	Sequence 44, App
42	24	24.0	17	1 US-08-518-474-9	Sequence 9, App
43	24	24.0	17	1 US-08-518-474-9	Sequence 11, App
44	24	24.0	17	1 US-08-518-474-11	Sequence 11, App
45	24	24.0	2	2 US-08-248-839C-144	Sequence 144, App

ALIGNMENTS

RESULT 1
US-08-637-759B-355
; Sequence 355, Application US/08637759B
; Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637/759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ. ID NO.: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-637-759B-355

Query Match 31.0%; Score 31; DB 2; Length 14;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE: 20196006.
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegem C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Styrikas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-T., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE002927; AAF45430.1; -;
 DR FLYBASE: FBgn0040023; CG12575.
 FT NON TER 19
 SO SEQUENCE 19 AA: 2039 MW: FAF4913F8360228A CRC64;

Query Match 21.6%; Score 24; DB 5; Length 19;
 Best Local Similarity 80.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 HLVD 16
 11:11
 DB 4 HLVD 8

Search completed: December 21, 2000, 08:37:54
 Job time: 287 sec

OY 6 DFGPKHL 13
1 1 1 1
Db 3 DIGLPRV 10

RESULT 7
ID 094554 PRELIMINARY; PRT; 16 AA.
AC 094554;

DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
DE 01-MAY-1999 (TREMBlrel. 10, last annotation update)
DE CALMODULIN KINASE 2 (FRAGMENT).
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomyces.
RN [1]

RP SEQUENCE FROM N.A.
RA Alemany V., Alique R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U57982; AAD09466.1; -
KW Kinase.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1846 MW; 4A673B1F4C3288D9 CRC64;

Query Match 22.5%; Score 25; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FGFP 10
1 1 1 1
Db 5 FGFP 8

RESULT 8
ID 09PS70 PRELIMINARY; PRT; 19 AA.
AC 09PS70;

DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, last annotation update)
DE LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]

RP SEQUENCE.
RX MEDLINE: 92011695.
RA Stifani S., Barber D.L., Aebbersold R., Steyrer E., Shen X., Nimpf J.,
RA Schneider W.J.;
RT "The laying hen expresses two different low density lipoprotein
RT receptor-related proteins.";
RL J. Biol. Chem. 266:19079-19087(1991).
SQ SEQUENCE 19 AA; 1861 MW; 4EEC931205620608 CRC64;

Query Match 22.5%; Score 25; DB 13; Length 19;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 2 LIQMDFGPKHLVD 16
1 1 1 1 1 1
Db 1 LIAQGLGXPTALAD 15

RESULT 9
ID 09TWH5 PRELIMINARY; PRT; 20 AA.
AC 09TWH5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, last annotation update)
DE 40 KDA GAP JUNCTION PROTEIN (FRAGMENT).
OS Heliothis virescens (Noctuid moth) (Owllet moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Heliothinae; Heliothis.
RN [1]

RP SEQUENCE.
RX MEDLINE: 95347000.
RA Ryerse J.S.;
RT "Immunocytochemical, electrophoresis, and immunoblot analysis of
RT Heliothis virescens gap junctions isolated in the presence and absence
RT of protease inhibitors.";
RL Cell Tissue Res. 281:179-186(1995).
SQ SEQUENCE 20 AA; 2304 MW; A298D3B3E8586B CRC64;

Query Match 22.5%; Score 25; DB 5; Length 20;
Best Local Similarity 29.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 LIQMDFGPKHLVD 17
1 1 1 1 1 1
Db 3 VIFNIDGGYLEFTRDF 19

RESULT 10
ID 09TTG3 PRELIMINARY; PRT; 20 AA.
AC 09TTG3;

DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, last annotation update)
DE GALACTOCEREBROSIDASE (FRAGMENT).
GN CALC.

OS Ateles belzebuth chamek.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateles.
RN [1]

RP SEQUENCE FROM N.A.
RA Canavez F.C.;
RT "Gene mapping in Ateles paniscus chamek.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF099175; AAF21849.1; -
DR INTERPRO: IPR001286; -
DR PFWA; PF02057; Glyco_hydro_59; 1.
FT NON_TER 1 1
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2317 MW; EA306655966B58F CRC64;

Query Match 22.5%; Score 25; DB 6; Length 20;
Best Local Similarity 38.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 LIQMDFGPKHL 14
1 1 1 1 1 1
Db 6 LRPNFGASLHL 18

RESULT 11
ID 09PS42 PRELIMINARY; PRT; 22 AA.
AC 09PS42;

DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, last annotation update)
DE PHENOBARBITAL-INDUCED 48 KDA CYTOCHROME P-450 (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

GN PETD.
OC Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.:
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070133; AAD20742.1; -.
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2410 MW; CC947A212386FE23 CRC64;

Query Match 25.2%; Score 28; DB 2; Length 21;
Best Local Similarity 45.5%; Pred. No. 5.5e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 LLLQMDGFGPK 11
Db 3 ILKKLDFSPDK 13

RESULT 3
09UGS1 PRELIMINARY: PRT; 12 AA.
AC 09UGS1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE DJ796117.4 (NOVEL PROTEIN SIMILAR TO GS2) (FRAGMENT).
GN DJ796117.4.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL033398; CAB63074.1; -.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1430 MW; AF7740ABECB69AA6 CRC64;

Query Match 24.3%; Score 27; DB 4; Length 12;
Best Local Similarity 44.4%; Pred. No. 4.4e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLLQMDGFG 9
Db 1 MILEMDMSF 9

RESULT 4
09TRR6 PRELIMINARY: PRT; 19 AA.
AC 09TRR6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CALCYCLIN-ASSOCIATED PROTEIN, CAP50-CA2+/PHOSPHOLIPID-BINDING PROTEIN
L-14 FRAGMENT.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE.
RX MEDLINE; 92250478.
RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;
RT "A calyculin-associated protein is a newly identified member of the
Ca2+/phospholipid-binding proteins, annexin family.";
RL J. Biol. Chem. 267:8919-8924(1992).

SQ SEQUENCE 19 AA; 2018 MW; 9A54062504B8322E CRC64;

Query Match 24.3%; Score 27; DB 6; Length 19;
Best Local Similarity 37.5%; Pred. No. 7.2e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 7 GFEPKLLVDFLOSLS 22
Db 2 FGTEDECAIIDXGSR 17

RESULT 5
P70861 PRELIMINARY: PRT; 21 AA.
ID P70861
AC P70861;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE THDF (FRAGMENT).
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-212:
RX MEDLINE; 97312006.
RA Ge Y., Old I.G., Girones I.S., Charon N.W.;
RT "The flag motility operon of Borrelia burgdorferi is initiated by a
sigma 70-like promoter.";
RL Microbiology 143:1681-1690(1997).
DR EMBL; U62901; AAB67742.1; -.
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2432 MW; F33E1EC548BD5B33 CRC64;

Query Match 23.4%; Score 26; DB 2; Length 21;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 MDFGPRHLL 14
Db 7 IEFDFEGIL 16

RESULT 6
073594 PRELIMINARY: PRT; 10 AA.
ID 073594
AC 073594;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ZAX-2 (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEHORN; TISSUE-WHOLE EMBRYOS;
RX MEDLINE; 98141813.
RA Peale F.V., Mason K., Hunter A.W., Bothwell M.;
RT "Multiple display polymerase chain reaction amplifies and resolves
related sequences sharing a single moderately conserved domain.";
RL Anal. Biochem. 256:158-168(1998).
DR EMBL; U34617; AAC36435.1; -.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1068 MW; 9A7598276728705A CRC64;

Query Match 22.5%; Score 25; DB 13; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:33:07 ; Search time 37.32 Seconds
(without alignments)
55.044 Million cell updates/sec

Title: US-08-934-367-4

Perfect score: 111
Sequence: 1 LLLQMDFGPPKHLVDFLQSL 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4962

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_14:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_mammal:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_protist:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30.5	27.5	21	2	Q9ZG55
2	28	25.2	21	2	Q9X3D0
3	27	24.3	12	4	Q9UGS1
4	27	24.3	19	6	Q9RRR6
5	26	23.4	21	2	P70861
6	25	22.5	10	13	Q73594
7	25	22.5	16	3	Q94554
8	25	22.5	19	13	Q9PS70
9	25	22.5	20	5	Q9TWH5
10	25	22.5	20	6	Q9TTC3
11	24.5	22.1	22	13	Q9PS42
12	24	21.6	13	2	Q31364
13	24	21.6	13	2	Q31365
14	24	21.6	13	2	Q34622
15	24	21.6	19	5	Q9W508
16	23.5	21.2	15	2	Q9R4U7
17	23	20.7	8	2	Q85406
18	23	20.7	9	5	Q96417
19	23	20.7	10	2	Q9X534

20	23	20.7	10	2	Q9X533	Q9X533 escherichia
21	23	20.7	13	2	Q31296	Q31296 borrelia af
22	23	20.7	13	2	Q34770	Q34770 borrelia af
23	23	20.7	13	11	Q35758	Q35758 rattus norv
24	23	20.7	14	6	Q9TRQ7	Q9TRQ7 bos taurus
25	23	20.7	17	2	Q9X313	Q9X313 prochloroco
26	23	20.7	18	13	P82068	P82068 litorea gen
27	23	20.7	20	2	Q9RAF1	Q9RAF1 desulfovibr
28	23	20.7	21	8	Q9ZVB7	Q9ZVB7 spinaria sp
29	23	20.7	21	10	Q41496	Q41496 solanum tub
30	23	20.7	21	12	Q80817	Q80817 human t-cel
31	23	20.7	22	1	P71537	P71537 methanosaer
32	23	20.7	22	10	Q9S8E1	Q9S8E1 capsicum an
33	22.5	20.3	17	6	Q9TR11	Q9TR11 bos taurus
34	22	19.8	13	4	Q9UPE7	Q9UPE7 homo sapien
35	22	19.8	14	2	Q56945	Q56945 versinia ps
36	22	19.8	17	11	Q9QUU4	Q9QUU4 mus sp. mep
37	22	19.8	20	6	Q9TRA1	Q9TRA1 bos taurus
38	22	19.8	20	12	Q85096	Q85096 punta loro
39	22	19.8	22	6	Q02830	Q02830 oryctolagus
40	21.5	19.4	22	2	Q52009	Q52009 pseudomonas
41	21	18.9	9	2	Q51765	Q51765 pseudomonas
42	21	18.9	15	11	Q9Z114	Q9Z114 mus musculu
43	21	18.9	17	8	Q9ZKWO	Q9ZKWO betrylobraco
44	21	18.9	18	1	Q9UYK7	Q9UYK7 pyrococcus
45	21	18.9	18	6	Q97668	Q97668 equus caball

ALIGNMENTS

RESULT 1
Q9ZG55 PRELIMINARY: PRT: 21 AA.
AC Q9ZG55:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE ATP-BINDING PROTEIN (FRAGMENT).
GN RECF.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L2 43AB;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RT "Gene identification of Chlamydia trachomatis by random DNA
sequencing." (Aug-1998) to the EMBL/GenBank/DBJ databases.
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF087306; AAD04082.1; -.
KW ATP-binding.
FT NON-TER 1 1
FT 21
FT 21
SQ SEQUENCE 21 AA: 2336 MW: 0185D9AC428276D9 CRC64;

Query Match 27.5%; Score 30.5; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 2 LLLQMDFGPPKHL 13
Db 8 LLLQMDFGPPKHL 18
RESULT 2
Q9X3D0 PRELIMINARY: PRT: 21 AA.
AC Q9X3D0:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).

DR SUBMITLIST: BG?????; ????.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 994 MW; E89C07772042C051 CRC64;

Query Match 17.1%; Score 19; DB 1; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.8e+03;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 11 KHLV 15
 : : : : :
 Db 2 KHIYI 6

RESULT 13
 SODM_CANFA STANDARD; PRT; 13 AA.
 ID SODM_CANFA
 AC P54712;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL (EC 1.15.1.1) (FRAGMENT).
 GN SOD2.
 OS Canis familiaris (dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP TISSUE=HEART.
 RC MEDLINE; 98163340.
 RX Dunn M.J., Cordell J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
 CC -1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) -> O(2) + H(2)O(2).
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR HSSP; P04179; 1MSD.
 DR HSC-2DPAGE; P54712; DOG.
 DR INTERPRO; IPR001189; .
 DR PFAM; PF00081; sodef; 1.
 DR PROSITE; PS00088; SOD_MN; PARTIAL.
 KW Oxidoreductase; Manganese; Mitochondrion.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1476 MW; 9C9651DE8BE0672A CRC64;

Query Match 17.1%; Score 19; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 KHLVD 16
 : : : : :
 Db 1 KHSLLD 6

RESULT 14
 UP21_UPEIN STANDARD; PRT; 19 AA.
 ID UP21_UPEIN
 AC P82027;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE UPERIN 2.1.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 OC Uperoleia.
 RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=SKIN SECRETION;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the Australian
 RT floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -1- FUNCTION: SHOWS A MEDIUM ANTIBACTERIAL ACTIVITY AGAINST
 CC L. MENSENTERIODES, M. LUTENS AND S. UBERIS.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=1926; METHOD=FAB.
 KW Amphibian skin; Antibiotic.
 SQ SEQUENCE 19 AA; 1927 MW; 328834D77BA353D2 CRC64;

Query Match 17.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 37.5%; Pred. No. 3.6e+03;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 14 LVDFLOSL 21
 : : : : :
 Db 2 LVDFAKKV 9

RESULT 15
 UP25_UPEIN STANDARD; PRT; 19 AA.
 ID UP25_UPEIN
 AC P82031;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE UPERIN 2.5.
 OS Uperoleia inundata (Floodplain toadlet).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 CC Uperoleia.
 RN [1]
 RP TISSUE=SKIN SECRETION;
 RC SEQUENCE, AND MASS SPECTROMETRY.
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the Australian
 RT floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -1- FUNCTION: SHOWS A MEDIUM ANTIBACTERIAL ACTIVITY AGAINST M. LUTENS,
 CC L. MENSENTERIODES AND S. UBERIS.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=1940; METHOD=FAB.
 KW Amphibian skin; Antibiotic.
 SQ SEQUENCE 19 AA; 1941 MW; 5E94C6C757B463D9 CRC64;

Query Match 17.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 37.5%; Pred. No. 3.6e+03;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 14 LVDFLOSL 21
 : : : : :
 Db 2 LVDFAKKV 9

Search completed: December 21, 2000, 08:38:16
 Job time: 149 sec

RA Johnson L., Norton S., Landau M., Semmes O.J., Sattlerberg R.M.,
 RA Jorenbj W.H., Hintz M.F.;
 RT "Characterization of a pigment-dispersing hormone in eyestalks of the
 RT fiddler crab *Uca pugnator*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5319-5322(1985).
 RN [2]

RP MEDLINE: 93230895.
 RA Loehr J., Klein J., Webster S.G., Dirksen H.;
 RT "Quantification, immunofluorescent purification and sequence analysis of
 RT a pigment-dispersing hormone of the shore crab, *Carcinus maenas*
 RT (L.)".
 RL Comp. Biochem. Physiol. 104B:699-706(1993).
 CC -1- FUNCTION: CAUSES THE MIGRATION OF THE DISTAL RETINAL PIGMENT
 CC INTO THE PROXIMAL END OF THE PIGMENT CHROMATOPHORE CELLS AND
 CC THUS DECREASES THE AMOUNT OF LIGHT ENTERING THE RETINULAS.
 CC -1- SIMILARITY: TO THE PDH OF OTHER ARTHROPODS.
 DR PIR: A25144; DRUFPD.
 KW Hormone; Amidation.
 FT DOMAIN 6 9
 FT MOD_RES 18 18
 FT SEQUENCE 18 AA: 1928 MW: 2505C8BD016F544E CRC64;

Query Match 18.0%; Score 20; DB 1; Length 18;
 Best Local Similarity 40.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 LQMDGCFPK 11
 DB 4 LINSIGLKP 13

RESULT 10
 ATPB_PHYPA STANDARD: PRT: 21 AA.
 AC P80658;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) (FRAGMENT).
 GN ATPB.
 OS Physcomitrella patens (Moss).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
 OC Funariidae; Funariales; Funariaceae; Physcomitrellia.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=PROTONEMA;
 RX MEDLINE: 97275459.
 RA Kasten B., Buck F., Nuske J., Reski R.;
 RT "Cytochrome *b6* affects nuclear- and plastome-encoded energy-converting
 RT plastid enzymes.";
 RL Planta 201:261-272(1997).
 CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
 CC GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
 CC SUBUNIT.
 CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 CC HAS THREE MAIN SUBUNITS: A, B AND C.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE.
 CC MENDEL: 13023; PHYPA:atpb1.
 DR INTERPRO: IPR000194;
 DR PROSITE: PS00152; ATPASE_ALPHA_BETA; PARTIAL.
 KW ATP synthase; Chloroplast; Thylakoid membrane; CF(1);
 KM Hydroxylase; ATP-binding; Hydrogen ion transport.
 FT NON_TER 21
 FT SEQUENCE 21 AA: 2298 MW: 95584F5AC89D81A CRC64;

Query Match 18.0%; Score 20; DB 1; Length 21;

Best Local Similarity 50.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 MDEGFP 10
 DB 16 LDXIFP 21

RESULT 11
 TRYP_PROAT STANDARD: PRT: 21 AA.
 AC P35051;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE TRYPSIN PRECURSOR (EC 3.4.21.4) (FRAGMENT).
 OS *Protopterus aethiops* (Marbled lungfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Dipnoi; Lepidosteiiformes; Protopteridae; Protopterus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=PANCREAS;
 RA Hermodson M.A., Tye R.W., Reeck G.R., Neurath H., Walsh K.A.;
 RT "Comparison of the amino terminal sequences of bovine, dogfish, and
 RT lungfish trypsins.";
 RL FEBS Lett. 14:222-224(1971).
 CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR PIR: A27719; A27719.
 DR HSSP: P07288; 1PFA.
 DR INTERPRO: IPR001254;
 DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
 DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
 KW Hydroxylase; Serine protease; Zymogen.
 FT PROPEP 1 7
 FT CHAIN 8 >21
 FT NON_TER 21
 FT SEQUENCE 21 AA: 2454 MW: 88E2FB1D130729D CRC64;

Query Match 18.0%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 PKH 12
 DB 15 PKH 17

RESULT 12
 GS15_BACSU STANDARD: PRT: 10 AA.
 AC P80861;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE GLUCOSE STARVATION-INDUCIBLE PROTEIN 5 (GS15) (FRAGMENT).
 OS *Bacillus subtilis*.
 OC Bacteria; Firmicutes; *Bacillus*/Clostridium group;
 OC *Bacillus*/Staphylococcus group; *Bacillus*.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=IS58;
 RX MEDLINE: 97443988.
 RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
 RA Hecker M.;
 RT "First steps from a two-dimensional protein index towards a response-
 RT regulation map for *Bacillus subtilis*.";
 RL Electrophoresis 18:1451-1463(1997).
 CC -1- INDUCTION: BY GLUCOSE STARVATION.
 CC -1- SIMILARITY: HIGH, TO GLUTAMYL-T-KINA REDUCTASE.

KM Oxidoreductase; Mitochondrion.
 RT NON_TER 20
 SQ SEQUENCE 20 AA: 2303 MW: 0A33BD34006E5A6 CRC64:

Query Match 19.8%; Score 22; DB 1; Length 20;
 Best Local Similarity 57.1%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 DFGPKH 12
 1 1 1 1
 DB 14 DNGMPVH 20

RESULT 6
 SAMP_MUSCA STANDARD: PRT; 9 AA.
 ID SAMP_MUSCA
 AC P19095;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SERUM AMYLOID P-COMPONENT (SAP) (FRAGMENT).
 OS Mustelus canis (Smooth dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeidae; Carcharhiniformes; Triakidae;
 OC Mustelus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 83160932.
 RA Robey F.A., Tanaka T., Liu T.-Y.;
 RT "Isolation and characterization of two major serum proteins from the
 RT dogfish, Mustelus canis, C-reactive protein and amyloid P
 RT component.";
 RT component.";
 RL J. Biol. Chem. 258:3889-3894(1983).
 CC -1 SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOLD
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -1 DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
 CC IN BASALMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
 CC -1 SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
 CC PIR: B20569; B20569.
 DR INTERPRO: IPR001759; .
 DR PROSITE: PS00289; PENTAXIN; PARTIAL.
 KM Amyloid; Glycoprotein; Plasma; Pentaxin.
 FT DOMAIN 1
 FT NON_TER 9
 FT SEQUENCE 9 AA: 965 MW: D05B5735B386769 CRC64:

Query Match 18.9%; Score 21; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 8.8e+04;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 8 GFPHLLV 15
 1 1 1 1
 DB 1 GFPHKSLI 8

RESULT 7
 TEML_RANTE STANDARD: PRT; 11 AA.
 ID TEML_RANTE
 AC P56923;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TEMPORIN L.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=SKIN.
 RX MEDLINE: 97175050.
 RX Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,

RA Barra D.;
 RT "temporins, antimicrobial peptides from the European red frog Rana
 RT temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -1 FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
 CC GRAM-POSITIVE BACTERIA.
 CC -1 SUBCELLULAR LOCATION: SECRETED.
 CC -1 SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAECURIN/RUGOSIN
 CC FAMILY.
 KM Amphibian skin; Antibiotic; Amidation; Multigene family.
 FT MOD_RES 11
 FT SEQUENCE 11 AA: 1194 MW: 1E990549B372724 CRC64:

Query Match 18.0%; Score 20; DB 1; Length 11;
 Best Local Similarity 55.6%; Pred. No. 1.4e+03;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 13 LLVDFLOSL 21
 1 1 1 1
 DB 1 LLPNLKSL 9

RESULT 8
 MDH_SYNY4 STANDARD: PRT; 16 AA.
 ID MDH_SYNY4
 AC P80460;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE MALATE DEHYDROGENASE (EC 1.1.1.37) (FRAGMENT).
 GN MDH.
 OS Synechocystis sp. (strain PCC 6714).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 RN [1]
 RP SEQUENCE.
 RA Naterstad K., Synstad B., Sirevag R.;
 RL Submitted (SEP-1996) to the SWISS-PROT data bank.
 CC -1 CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALACETATE + NADH.
 CC -1 SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1 SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
 CC INTERPRO: IPR001252; .
 DR PROSITE: PS00068; MDH; PARTIAL.
 KM Oxidoreductase; Tricarboxylic acid cycle; NAD.
 FT NON_TER 16
 FT SEQUENCE 16 AA: 1780 MW: 61D1896F14E81984 CRC64:

Query Match 18.0%; Score 20; DB 1; Length 16;
 Best Local Similarity 66.7%; Pred. No. 2.1e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LOMDFG 8
 1 1 1 1
 DB 9 LTTDFG 14

RESULT 9
 DRPH_UCAPU STANDARD: PRT; 18 AA.
 ID DRPH_UCAPU
 AC P08871;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE PIGMENT-DISPERSING HORMONE (PDH) (LIGHT ADAPTING DISTAL RETINAL
 DE PIGMENT HORMONE) (DRPH).
 OS Uca pugnator (Atlantic sand fiddler crab) (Celuca pugnator).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Ocypodidae; Ocypodidae; Celucae.
 RN [1]
 RP SEQUENCE.
 RA Rao K.R., Riehm J.P., Zahnow C.A., Kleinholz L.H., Tarr G.E.,

DE ANGIOTENSINOGEN (FRAGMENT).
 GN AGT.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 RP SEQUENCE.
 RA Skeggs L.T., Kahn J.R., Lentz K., Shumway N.P.;
 RT "The preparation, purification, and amino acid sequence of a
 RL polypeptide renin substrate.";
 CC J. Exp. Med. 106:439-453(1957).
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR INTERPRO: IPR000215; -
 DR PIR: A01250; A01250.
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KM Vasoconstrictor; Plasma; Serpin.
 FT PEPTIDE 1 10
 FT NON_TER 14 14 ANGIOTENSIN I.
 FT SEQUENCE 14 AA; 1759 MW; 269921F8EEFBD7 CRC64;
 SO

Query Match 21.6%; Score 24; DB 1; Length 14;
 Best Local Similarity 83.3%; Pred. No. 4.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 10 PKHLV 15
 Db 7 PFHLV 12

RESULT 3
 DCM_PSECF STANDARD; PRT; 14 AA.
 AC P19914;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE CARBON MONOXIDE DEHYDROGENASE MEDIUM CHAIN (EC 1.2.99.2) (FRAGMENT).
 OS Pseudomonas carboxydoflava.
 OC Bacteria; Proteobacteria; Beta subdivision; Comamonadaceae;
 OC Hydrogenophaga.
 RN SEQUENCE.
 RP MEDLINE: 90055678.
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RL carboxydotrophic bacteria.";
 CC Arch. Microbiol. 152:335-341(1989).
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
 CC ACCEPTOR.
 CC -1- COFACTOR: MOLYBDENUM.
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR: P10142; P10142.
 KM Oxidoreductase; Molybdenum.
 FT NON_TER 14 14
 FT SEQUENCE 14 AA; 1756 MW; 65583C6D1F87C25B CNC64;
 SO

Query Match 21.6%; Score 24; DB 1; Length 14;
 Best Local Similarity 23.1%; Pred. No. 4.1e+02;
 Matches 3; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 LLLMDFGPKHL 13
 Db 1111

Db 2 MIPREYHARKV 14
 RESULT 4
 PSBP_PINPS STANDARD; PRT; 13 AA.
 AC P81668;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE OXYGEN-EVOLVING ENHANCER PROTEIN 2 (OEE2) (23
 DE KDA SUBUNIT OF OXYGEN
 DE EVOLVING SYSTEM OF PHOTOSYSTEM II) (FRAGMENT).
 GN PSBP.
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Coniferales; Coniferales; Pinaceae; Pinus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-NEEDLE;
 RX MEDLINE: 99274088.
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrmann N., Kremer A.,
 RA Figerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 RL Electrophoresis 20:1098-1108(1999)
 CC -1- FUNCTION: ASSOCIATED WITH THE OXYGEN-EVOLVING COMPLEX OF
 CC PHOTOSYSTEM II (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE; ASSOCIATED
 CC WITH THE PHOTOSYSTEM II COMPLEX (BY SIMILARITY).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
 CC (SPOT M179) IS: 5.9, ITS MW IS: 22 KDA.
 CC -1- SIMILARITY: TO OTHER OEE2 SUBUNITS.
 KM Photosynthesis; Photosystem II; Chloroplast; Thylakoid membrane.
 FT NON_TER 13 13
 FT SEQUENCE 13 AA; 1294 MW; C6772B0D54D7C44D CRC64;
 SO

Query Match 19.8%; Score 22; DB 1; Length 13;
 Best Local Similarity 80.0%; Pred. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 7 FGPK 11
 Db 9 FGAPK 13

RESULT 5
 COXN_THUOB STANDARD; PRT; 20 AA.
 ID COXN_THUOB
 AC P80980;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE VIIb-HEART (EC 1.9.3.1) (FRAGMENT).
 OS Thunus obesus (Bigeye tuna).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-HEART;
 RX MEDLINE: 97454291.
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver.";
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
 CC 4 FERROCYTOCHROME C.

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:35:47 ; Search time 18.39 Seconds
(without alignments)
38.219 Million cell updates/sec

Title: US-08-934-367-4

Sequence: 1 LLLQMDGFPKHLVDFLQSL S 22

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 1213

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	21.6	11	1	CH60_DROME
2	24	21.6	11	1	ANGT_HORSE
3	24	21.6	14	1	DCM_PSECA
4	22	19.8	13	1	PSBP_PIPPS
5	22	19.8	20	1	COXN_THOIB
6	21	18.9	9	1	SAMP_MUSCA
7	20	18.0	11	1	TEML_RANTE
8	20	18.0	16	1	MDH_SYNY4
9	20	18.0	18	1	DRPH_UCAPU
10	20	18.0	21	1	ATPB_PHYPA
11	20	18.0	21	1	TRYP_PROAT
12	19	17.1	10	1	GSIS_BACSU
13	19	17.1	13	1	SODM_CANFA
14	19	17.1	19	1	UP21_UPEIN
15	19	17.1	19	1	UP25_UPEIN
16	19	17.1	21	1	DCMS_PSECA
17	18	16.2	7	1	ALL7_CYPBO
18	18	16.2	8	1	ALL5_CALVO
19	18	16.2	8	1	ALL5_CYPBO
20	18	16.2	10	1	PNEU_RAT
21	18	16.2	12	1	GRAR_RANRU
22	18	16.2	13	1	ORCK_ORCLI
23	18	16.2	15	1	FLA2_LOCHI
24	18	16.2	17	1	FLA2_BARBA
25	18	16.2	20	1	CAOS_RAT
26	18	16.2	21	1	CSPS_STRFR
27	18	16.2	21	1	OMP4_PASHA
28	18	16.2	21	1	YD90_HAETN
29	18	16.2	21	1	FUCL_RAT
30	18	16.2	22	1	FUCL_RAT
31	18	16.2	22	1	CCRN_MACEU
32	17	15.3	9	1	FAR1_CALVO
33	17	15.3	9	1	FAR1_CALVO

34	17	15.3	10	1	CAER_LITXA
35	17	15.3	12	1	OPS3_DROVI
36	17	15.3	12	1	PSP3_PHYPA
37	17	15.3	13	1	UP71_LITFM
38	17	15.3	15	1	DCM_PSECA
39	17	15.3	15	1	LPE_ECOLI
40	17	15.3	16	1	MMX_SOLMU
41	17	15.3	17	1	GAST_MACMU
42	17	15.3	19	1	IRBP_CAVPO
43	17	15.3	19	1	NIO6_SOLMU
44	17	15.3	19	1	UP24_UPEIN
45	17	15.3	20	1	CPA7_PAPSP

ALIGNMENTS

RESULT	ID	CH60_DROME	STANDARD	PRT	11 AA.
1	AC	P35380			
DT	01-JUN-1994	(Rel. 29, Created)			
DT	01-JUN-1994	(Rel. 29, Last sequence update)			
DT	15-DEC-1998	(Rel. 37, Last annotation update)			
DE	MITOCHONDRIAL MATRIX PROTEIN P1 (60 KDA CHAPERONIN) (HEAT SHOCK				
DE	PROTEIN 60) (HSP-60) (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT)				
GN	MMF-P1 OR HSP60.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydroidea; Drosophilidae; Drosophila.				
RM	[1]				
RP	SEQUENCE.				
RC	STRAIN=VALLECAS; TISSUE=WING IMAGINAL DISK;				
RX	MEDLINE: 93272852.				
RA	Sanareen J.F., van Damme J., Puype M., Vandekerckhove J.,				
RT	Garcia-Bellido A.;				
RT	"Identification of Drosophila wing imaginal disc proteins by two-				
RT	dimensional gel analysis and microsequencing.";				
RL	Exp. Cell Res. 206:220-226(1993).				
CC	-1- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND				
CC	MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF				
CC	IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE				
CC	REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED				
CC	UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL MATRIX (BY				
CC	SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.				
DR	FLYBASE: Fgn0010375; Mmp-P1.				
DR	INTERPRO: IPR001844; .				
DR	PROSITE: PS00296; CHAPERONINS_CP60; PARTIAL.				
KW	Chaperone; ATP-binding; Mitochondrion.				
FT	NON_TER				
FT	NON_TER				
FT	SEQUENCE				
FT	11 AA; 1243 MW; 78501A36365A6DB CRC64;				
QY	1 LLLQMDGFPK 11				
DB	1 VILQSWGSPK 11				
Query Match	21.6%;	Score 24;	DB 1;	Length 11;	
Best local Similarity	27.3%;	Pred. No. 3.2e+02;			
Matches	3;	Conservative	5;	Mismatches	3;
				Indels	0;
				Gaps	0;
RESULT	2				
ID	ANGT_HORSE	STANDARD;	PRT;	14 AA.	
AC	P01016;				
DT	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DT	01-FEB-1996	(Rel. 33, Last annotation update)			

C>Date: 22-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 15-Jun-1996
C:Accession: PN0175
R:Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
submitted to JIPIID, December 1995
A:Description: Two dimensional electrophoresis of plant proteins and standardization of
A:Reference number: PN0173
A:Accession: PN0175
A:Molecule type: Protein
A:Residues: 1-18 <TSU>
A:Experimental source: leaf
C:Keywords: transferase

Query Match 21.6%; Score 24; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 DFGFP 10
|||
|||
Db 5 DFGFP 9

RESULT 15
A37984
ADP/ATP carrier protein - yeast (Candida parapsilosis) (fragment)
C:Species: Candida parapsilosis
C>Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 07-Jun-1996
C:Accession: A37984
R:Guertin, B.; Bukusoglu, C.; Rakotomanana, F.; Wohlrab, H.
J. Biol. Chem. 265, 19736-19741, 1990
A:Title: Mitochondrial phosphate transport. N-ethylmaleimide insensitivity correlates with
A:Reference number: A37984; M0ID:91060585
A:Accession: A37984
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-20 <GUE>

Query Match 21.6%; Score 24; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 12 HLLVDPL 18
: |||||
Db 5 NFLIDPL 11

Search completed: December 21, 2000, 08:37:13
Job time: 317 sec

hexokinase (EC 2.7.1.1) I peptide III - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 12-Apr-1995

C:Accession: A32521

R:Schirch, D.M.; Wilson, J.E.

Arch. Biochem. Biophys. 257, 1-12, 1987

A:Title: Rat brain hexokinase: amino acid sequence at the substrate hexose binding site

A:Reference number: A90080; MUID:87324917

A:Accession: A32521

A:Molecule type: protein

A:Residues: 1-21 <SCH>

C:Superfamily: human hexokinase I; hexokinase homology

C:Keywords: ATP; glycolysis; phosphotransferase

Query Match 24.3%; Score 27; DB 2; Length 21;

Best Local Similarity 50.0%; Pred. No. 3.7e+02;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 LQMDFGPKH 12

Db 3 LGFTSFPPXH 12

RESULT 4

S59492

formate dehydrogenase alpha chain - Alcaligenes eutrophus (fragment)

C:Species: Alcaligenes eutrophus

C>Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999

C:Accession: S59492

R:Friedebold, J.; Mayer, F.; Bill, E.; Trautwein, A.X.; Bowlen, B.

Biol. Chem. Hoppe-Seyler 376, 561-568, 1995

A:Title: Structural and immunological studies on the soluble formate dehydrogenase from

A:Reference number: S59492; MUID:96145736

A:Accession: S59492

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <FRI>

Query Match 23.4%; Score 26; DB 2; Length 15;

Best Local Similarity 57.1%; Pred. No. 3.8e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 QMDFGP 10

Db 6 EIDFGP 12

RESULT 5

PX0078

alanine dehydrogenase (EC 1.4.1.1) - oscillatoriacean cyanobacterium (fragment)

C:Species: Oscillatoriacean cyanobacterium

C>Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 07-May-1999

C:Accession: PX0078

R:Sawa, Y.; Tan, M.; Murata, K.; Shibata, H.; Ochiai, H.

J. Biochem. 116, 995-1000, 1994

A:Title: Purification and characterization of alanine dehydrogenase from a cyanobacterium

A:Reference number: PX0078; MUID:95204408

A:Accession: PX0078

A:Molecule type: protein

A:Residues: 1-21 <SAM>

A>Note: the source is designated as Phormidium lapideum

C:Comment: This enzyme catalyzes a reversible oxidative deamination of L-alanine to pyru

C:Superfamily: alanine dehydrogenase; alanine dehydrogenase homology

C:Keywords: oxidoreductase

Query Match 23.4%; Score 26; DB 2; Length 21;

Best Local Similarity 44.4%; Pred. No. 5.4e+02;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 MDGFPKHL 13

4 5

Db 1 MEICVPEKI 9

RESULT 6

T44936

calmodulin kinase 2 - fission yeast (Schizosaccharomyces pombe) (fragment)

C:Species: Schizosaccharomyces pombe

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000

C:Accession: T44936

R:Alamy, V.; Allague, R.

submitted to the EMBL Data Library, May 1996

A:Reference number: 222873

A:Accession: T44936

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-16 <ALE>

A:Cross-references: EMBL:U57982; PIDN:AAD09466.1

Query Match 22.5%; Score 25; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 5.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FGFP 10

Db 5 FGFP 8

RESULT 7

A60743

ornithine carbamoyltransferase (EC 2.1.3.3), anabolic - Aeromonas formicans (fragment)

C:Species: Aeromonas formicans

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: A60743

R:Tricot, C.; De Coen, J.L.; Momin, P.; Falmagne, P.; Stalon, V.

J. Gen. Microbiol. 135, 2453-2464, 1989

A:Title: Evolutionary relationships among bacterial carbamoyltransferases.

A:Reference number: A60743; MUID:90188287

A:Accession: A60743

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-17 <FRI>

C:Keywords: transferase

Query Match 22.5%; Score 25; DB 2; Length 17;

Best Local Similarity 83.3%; Pred. No. 6.3e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 KHLVD 16

Db 1 KHLKD 6

RESULT 8

B61597

cytochrome P450 AL-2 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C:Accession: B61597

R:Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.

Drug Metab. Dispos. 19, 291-297, 1991

A:Title: Purification and aminopyrine monooxygenase activity of liver microsomal cyto

A:Reference number: A61597; MUID:91929210

A:Accession: B61597

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <SHI>

Query Match 22.1%; Score 24.5; DB 2; Length 14;

Best Local Similarity 47.1%; Pred. No. 6.1e+02;

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:31:56 ; Search time 26.84 Seconds
(without alignments)
52.017 Million cell updates/sec

Title: US-08-934-367-4
Perfect score: 111
Sequence: 1 LLLQMDFGFPKHLVDFLOSLIS 22

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 182106 seqs, 63460219 residues
Total number of hits satisfying chosen parameters: 4315

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	28	25.2	19	2	A39504	octamer-binding pr
2	27	24.3	7	2	S36662	dermorphin (lys-7)
3	27	24.3	21	2	A32521	hexokinase (EC 2.7
4	26	23.4	15	2	S59492	formate dehydrogen
5	26	23.4	21	2	PK0078	alanine dehydrogen
6	25	22.5	16	2	T44936	calmodulin kinase
7	25	22.5	17	2	A60743	ornithine carbamoy
8	25	22.5	14	2	B61597	cytochrome P450 AL
9	24	21.6	13	2	S03879	6-phosphofructokin
10	24	21.6	14	2	A01250	angiotensin precur
11	24	21.6	14	2	PL0142	carbon-monoxide de
12	24	21.6	15	2	A60834	angiotensin I prec
13	24	21.6	17	2	B31769	T-cell receptor de
14	24	21.6	18	2	PN0175	glutathione transf
15	24	21.6	20	2	A37984	ADP,ATP carrier pr
16	23	20.7	14	2	PA0104	T-cell receptor de
17	23	20.7	19	2	I46554	protein QP200070-
18	23	20.7	20	2	A41439	acid ribonuclease
19	23	20.7	21	2	T07683	proteinase inhibit
20	23	20.7	7	1	A61324	dermorphin - Rohde
21	22	19.8	10	2	SI3224	viig protein - Agr
22	22	19.8	11	2	PT0250	Ig heavy chain CRD
23	22	19.8	12	2	C36201	I-aminocyclopropan
24	22	19.8	14	2	A61002	photosystem II oxy
25	22	19.8	15	2	S71306	heat shock protein
26	22	19.8	20	2	S72501	protein kinase C 1
27	22	19.8	20	2	S77989	cytochrome-c oxida
28	22	19.8	20	2	S50203	zona pellucida gly
29	21	18.9	9	2	B45796	dihydrolipoamide S

30	21	18.9	9	2	B20569	serum amyloid P-co
31	21	18.9	13	2	S14995	photosystem II oxy
32	21	18.9	14	2	PA0013	photosystem II oxy
33	21	18.9	17	2	C24166	photosystem II ext
34	21	18.9	18	2	H75063	hypothetical prote
35	21	18.9	19	2	B60822	cytochrome P450 UT
36	21	18.9	19	2	D32071	T-cell receptor de
37	21	18.9	20	2	A60822	cytochrome P450 PB
38	21	18.9	20	2	F56046	urinary tract ston
39	21	18.9	20	2	A54077	cytochrome b558 -
40	20	18.0	9	2	T46023	growth hormone rec
41	20	18.0	12	2	S56122	type I DNA methyl
42	20	18.0	13	2	PC1008	40k extracellular
43	20	18.0	14	2	PO0152	18k iron-sulfur pr
44	20	18.0	15	2	PH1788	T cell receptor al
45	20	18.0	16	2	I57530	gene c-fms protein

ALIGNMENTS

RESULT 1
A39504
octamer-binding protein, Ku-like, 72K chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: A39504
R:May, G.; Sutton, C.; Gould, H.
J. Biol. Chem. 266, 3052-3059, 1991
A:Title: Purification and characterization of Ku-2, an octamer-binding protein relate
A:Reference number: A39504; MUID:91131605
A:Accession: A39504
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <MAY>

Query Match 25.2%; Score 28; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LQMDRFG 9
DB 11 LQMDRFG 17
RESULT 2
S36662
dermorphin (lys-7) [validated] - two-colored leaf frog
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 31-Mar-2000
R:Magnuson, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erpanmer, G.; Krell, F.E.B. Lett. 307, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of
A:Reference number: S21152; MUID:92339502
A:Accession: S36662
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIG>

Query Match 24.3%; Score 27; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 FGPK 11
DB 3 FGPK 7
RESULT 3
A32521

TOPOLOGY: linear
MOLECULE TYPE: No. 6046166e
US-08-940-096-133

Query Match 25.2%; Score 28; DB 3; Length 22;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 11 KHLVDFLOSL 22
: 11 1 11 :
Db 7 ERLLEDLQALN 18

RESULT 15
US-07-977-696C-36
; Sequence 36, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and diagnostic Vaccination
; TITLE OF INVENTION: and Therapeutic Methods.
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLANSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07977,696C
; APPLICATION NUMBER: US/07977,696C
; FILING DATE: 11-16-92
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 748-6868
; TELEFAX: (510) 748-6688
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-977-696C-36

Query Match 24.3%; Score 27; DB 1; Length 19;
Best Local Similarity 41.2%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 5 MDGFPKHLVDFLOSL 21
: 1111 1 1 :
Db 1 MDGSLVFLVILKGV 17

Search completed: December 21, 2000, 08:36:43
Job time: 387 sec

STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6004925e
US-08-940-095-133

Query Match 25.2%; Score 28; DB 3; Length 22;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 11 KHLVDFLOSLS 22
: || | || :
DB 7 ERLEDDLQALN 18

RESULT 13
US-08-940-093-133
Sequence 133, Application US/08940093
Patent No. 6037333
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,093
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6037323e
US-08-940-093-133

Query Match 25.2%; Score 28; DB 3; Length 22;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 11 KHLVDFLOSLS 22
: || | || :
DB 7 ERLEDDLQALN 18

RESULT 14
US-08-940-096-133
Sequence 133, Application US/08940096
Patent No. 6046166
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single

RESULT 10
US-08-802-981-112
; Sequence 112, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/802,981
; APPLICATION NUMBER: 435
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-0003000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /product= "Aib"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Acp"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /product= "Acp"
US-08-802-981-112

Query Match 25.2%; Score 28; DB 3; Length 21;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LQMDGFPR 11
| :|||
DB 10 LDAEFGXPK 18

RESULT 11
US-08-802-981-113
; Sequence 113, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof

NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-0003000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /product= "Aib"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Acp"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /product= "Acp"
US-08-802-981-113

Query Match 25.2%; Score 28; DB 3; Length 21;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LQMDGFPR 11
| :|||
DB 10 LDAEFGXPK 18

RESULT 12
US-08-940-095-133
; Sequence 133, Application US/08940095
; Patent No. 6004925
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,567
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/061,514
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0941.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-370-567-7

Query Match 25.2%; Score 28; DB 1; Length 17;
Best Local Similarity 46.2%; Pred. No. 96;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 LOMDFGPKHLV 15
1 1 1 1 1 1
DB 4 LFMDLWHRKHL 16

RESULT 8
US-08-438-759-7
Sequence 7, Application US/08438759
Patent No. 5679782
GENERAL INFORMATION:
APPLICANT: Rosenberg, Steven
APPLICANT: Doyle, Michael
APPLICANT: Goodson, Robert
TITLE OF INVENTION: Peptide Inhibitors of Urokinase Receptor
NUMBER OF INVENTIONS: 37
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,759
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/370,567
FILING DATE:
APPLICATION NUMBER: US/08/061,514
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259

REFERENCE/DOCKET NUMBER: 0941.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-438-759-7

Query Match 25.2%; Score 28; DB 1; Length 17;
Best Local Similarity 46.2%; Pred. No. 96;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 LOMDFGPKHLV 15
1 1 1 1 1 1
DB 4 LFMDLWHRKHL 16

RESULT 9
PCT-US94-05684-7
Sequence 7, Application PC/TUS9405684
GENERAL INFORMATION:
APPLICANT: Chiron Corporation
TITLE OF INVENTION: Peptide Inhibitors of Urokinase Receptor
NUMBER OF INVENTIONS: 37
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05684
FILING DATE: 19 MAY 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0941.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
PCT-US94-05684-7

Query Match 25.2%; Score 28; DB 4; Length 17;
Best Local Similarity 46.2%; Pred. No. 96;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 LOMDFGPKHLV 15
1 1 1 1 1 1
DB 4 LFMDLWHRKHL 16

FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-12/RET/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-618A-22

Query Match 26.1%; Score 29; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 78;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 MDGFPKHL 14
DB 9 IDHYPNELL 18

RESULT 5
US-08-483-952A-22

Sequence 22, Application US/08483952A
Patent No. 6011139

GENERAL INFORMATION:

APPLICANT: Tobin, Allan J

APPLICANT: Erlander, Mark G

APPLICANT: Kaufman, Daniel L.

TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hobach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

COUNTRY: US

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,952A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/123,859

FILING DATE: 17-SEP-1993

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/716,909

FILING DATE: 18-JUN-1991

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/586,536

FILING DATE: 21-SEP-1990

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Treccartin, Richard F.

REGISTRATION NUMBER: 31,801

REFERENCE/DOCKET NUMBER: A-60780-7/RET/MTK

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-952A-22

Query Match 26.1%; Score 29; DB 3; Length 20;
Best Local Similarity 50.0%; Pred. No. 78;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 MDGFPKHL 14
DB 9 IDHYPNELL 18

RESULT 6
US-08-341-018-40

Sequence 40, Application US/08341018A
Patent No. 6087323

GENERAL INFORMATION:

APPLICANT: Gwynne, David I.

APPLICANT: Mahanthappa, Nagesh K.

APPLICANT: Marchionni, Mark A.

APPLICANT: Birmingham, McDonogh, Olivia

APPLICANT: Goldin, Stanley M.

APPLICANT: McBurney, Robert N.

TITLE OF INVENTION: USE OF NEUREGULINS AS MODULATORS OF

FILE REFERENCE: 04585/041001

CURRENT APPLICATION NUMBER: US/08/341,018A

NUMBER OF SEQ ID NOS: 87

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 40

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

US-08-341-018-40

Query Match 25.2%; Score 28; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 1,2e+05;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 11 KHLVDPLQ 19
DB 1 KHLGIEFM 9

RESULT 7
US-08-370-567-7

Sequence 7, Application US/08370567
Patent No. 5656726

GENERAL INFORMATION:

APPLICANT: Rosenberg, Steven

APPLICANT: Doyle, Michael

APPLICANT: Goodson, Robert

TITLE OF INVENTION: Peptide Inhibitors of Urokinase Receptor

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chilton Corporation

STREET: 4560 Horton Street

CITY: Emeryville

STATE: CA

COUNTRY: USA

ZIP: 94608

Db 1 FGYPVYEGDCVQ 13

RESULT 2
US-08-765-783A-83
Sequence 83, Application US/08765783A
Patent No. 5994524
GENERAL INFORMATION:
APPLICANT: Matsushima, Kouji
APPLICANT: Matsunoto, Yoshihiro
APPLICANT: Yamada, Yoshiaki
APPLICANT: Sato, Koh
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
TITLE OF INVENTION: Interleukin-8
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORESTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,783A
FILING DATE: 07-MAR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-765-783A-83

Query Match 26.1%; Score 29; DB 2; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 OMDFGPPK 11
Db 1 OMDFGPPK 8

RESULT 3
US-08-484-530-22
Sequence 22, Application US/08484530
Patent No. 5846740
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Erlanger, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,530
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-8/RT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-530-22

Query Match 26.1%; Score 29; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 78;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 MDGFPKHL 14
Db 9 IDFPYRNELL 18

RESULT 4
US-08-827-618A-22
Sequence 22, Application US/08827618A
Patent No. 5996366
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Erlanger, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,618A
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,725
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:30:16 ; Search time 25.87 Seconds
(without alignments)
14.254 Million cell updates/sec

Title: US-08-934-367-4

Perfect score: 111
Sequence: 1 LLLQMDGFPKHLVDLQSL 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 92835

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-AA: *
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/prodata/2/1aa/6.COMB.pep: *
4: /cgn2_6/prodata/2/1aa/PCITUS.COMB.pep: *
5: /cgn2_6/prodata/2/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	27.0	20	1	US-08-199-508-2
2	29	26.1	9	2	US-08-765-783A-83
3	29	26.1	20	2	US-08-484-530-22
4	29	26.1	20	2	US-08-827-618A-22
5	29	26.1	20	3	US-08-483-952A-22
6	28	25.2	9	3	US-08-341-018-40
7	28	25.2	17	1	US-08-370-567-7
8	28	25.2	17	1	US-08-438-759-7
9	28	25.2	17	4	PCT-US94-05684-7
10	28	25.2	21	3	US-08-802-981-112
11	28	25.2	21	3	US-08-802-981-113
12	28	25.2	22	3	US-08-940-093-133
13	28	25.2	22	3	US-08-940-093-133
14	28	25.2	22	3	US-08-940-096-133
15	27	24.3	19	1	US-07-977-696C-36
16	27	24.3	19	1	US-08-129-930B-36
17	27	24.3	20	2	US-08-733-505A-48
18	27	24.3	20	2	US-08-706-741B-83
19	27	24.3	20	2	US-08-924-695A-83
20	26	23.4	7	1	US-07-923-724-47
21	26	23.4	7	2	US-08-609-426A-47
22	26	23.4	7	2	US-08-374-652C-37
23	26	23.4	11	3	US-08-039-778B-6
24	26	23.4	12	3	US-08-329-799-21
25	26	23.4	15	1	US-08-208-181A-16
26	26	23.4	15	1	US-08-208-181A-22
27	26	23.4	15	3	US-08-596-257A-10
28	26	23.4	15	3	US-08-860-339-10

29	26	23.4	16	1	US-08-346-455B-52	Sequence 52, Appl
30	26	23.4	16	3	US-08-802-981-71	Sequence 71, Appl
31	26	23.4	16	3	US-08-977-221-52	Sequence 52, Appl
32	26	23.4	16	4	PCT-US95-06613-52	Sequence 52, Appl
33	26	23.4	19	1	US-08-238-163-20	Sequence 20, Appl
34	26	23.4	21	3	US-08-802-981-114	Sequence 114, App
35	26	23.4	21	3	US-08-802-981-116	Sequence 116, App
36	26	23.4	22	5	US-08-039-778B-5	Sequence 5, Appl
37	26	23.4	22	5	5248607-2	Patent No. 5248607
38	25.5	23.0	12	1	US-08-467-940-18	Sequence 18, Appl
39	25.5	23.0	12	1	US-08-633-772-18	Sequence 18, Appl
40	25	22.5	6	1	US-08-487-006-65	Sequence 65, Appl
41	25	22.5	6	1	US-08-487-006-76	Sequence 76, Appl
42	25	22.5	6	2	US-08-488-659A-65	Sequence 65, Appl
43	25	22.5	6	2	US-08-488-659A-76	Sequence 76, Appl
44	25	22.5	8	3	US-08-582-776C-29	Sequence 29, Appl
45	25	22.5	8	3	US-08-434-631B-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-199-508-2
; Sequence 2, Application US/08199508
; Patent No. 5717058
; GENERAL INFORMATION:
; APPLICANT: Matthews, Maura-Ann H.
; APPLICANT: Stetler, Gary L. Spencer J.
; APPLICANT: Anthony-Cahill, David C.
; TITLE OF INVENTION: Modulators of Gene Expression
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 5797 Central Avenue
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/199, 508
; FILING DATE: February 18, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/021, 536
; FILING DATE: February 23, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5717058ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 121 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3322
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; TOPOLOGY: unknown to applicant
; MOLECULE TYPE: peptide
; HYPOTHEICAL: yes
; US-08-199-508-2

Query Match 27.0%; Score 30; DB 1; Length 20;
Best Local Similarity 38.5%; Pred. No. 53;
Matches 5; Conservative 4; Mismatches 0; Gaps 0;

OY 7 FGPKHLVDLQ 19

PT Phosphorylated receptor peptide binds STAT transcription factor -
PT has a Tyr-contg. region of an intracellular domain of, e.g. a
PT cytokine, for screening for agents which bind to the receptor
XX
XX Claim 4; Page 39; 55pp; English.

CC This sequence represents the fragment Lys433 to Asp448 of the
CC intracellular region of the interferon-gamma receptor protein. This
CC peptide represents a Tyr-containing region which is capable of being
CC phosphorylated, and can then bind a cytoplasmic transcription factor
CC of the signal transducers and activators of transcription (STAT)
CC family. This peptide specifically binds to STAT1alpha. Receptor
CC peptides such as this, may be used to screen for molecules which
CC interact with it, and for molecules which inhibit or promote an
CC interaction between the receptor peptide and the identified molecule.

Sequence 16 AA;

Query Match	28.48;	Score 31.5;	DB 17;	Length 16;
Best Local Similarity	63.68;	Pred. No. 62;		
Matches 7; Conservative	2;	Mismatches	1;	Gaps 1;

QY	7	ECFPK-HLLVD	16
		: :	
Db	6	fgydkphvld	16

RESULT	12
W65666	
ID	W65666 standard; peptide; 21 AA.

DT	16-OCT-1998 (first entry)
XX	
DE	Fibronectin binding protein-derived peptide #10

microbial surface components recognising adhesive matrix molecule;
 MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope;
 antibiotic; bacterial infection; antibiotic-resistant strain.

05 Synthetic.
05 *Staphylococcus aureus*.

PN WO9831389-A2

PD 23-JUL-1998.

PF 21-JAN-1998; 98WO-US01222.

PR 21-JAN-1997; 97US-0036139.

PA (TEXA) UNIV TEXAS A & M SYSTEM.

PI Hoeoek M, House-pompeo KL, Joh D, Mcgavin MJ, Patti JM;

XX

PT Antibody that binds to fibronectin-binding protein, preventing its binding to fibronectin - used to treat or prevent bacterial infection, especially by *Staphylococci* and *Streptococci*

.....
PS Example 2; Page 92; 201pp; English.

CC The invention relates to antibodies that bind to a fibronectin-binding
CC domain of a fibronectin-binding protein, and inhibit binding of the
CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
CC protein containing at least one peptide of a fibronectin-binding protein
CC linked to a second amino acid sequence; (3) nucleic acid encoding
CC the isolated peptide of (1). Antibodies, the isolated peptides of

CC (1) and the nucleic acids are all useful for immunisation (active or
CC passive) and (by inhibiting binding of bacteria to fibrinectin) for
CC preventing or treating infection in humans or other animals, particularly
CC by staphylococci or streptococci, e.g. meningitis, otitis media,
CC pneumonia, endocarditis, mastitis in cattle, abortion in horses and many
CC others. Since the antibodies block binding of bacteria, they should be
CC effective against antibiotic-resistant strains, and may replace
CC antibiotic therapy or increase its effectiveness. Sequences W6565-68
CC represent synthetic epitopes from the fibrinectin binding domains DU and
CC D1-D4 of the *S. aureus* fmbA gene.

Sequence	21 AA
SQ	

Query Match	27.9%	Score 31	DB 19	Length 21
Best Local Similarity	54.5%	Pred. No. 1e+02		
Matches 6, Conservative		1, Mismatches	4, Indels	0, Gaps 0

QY	7	E	G	F	P	K	H	L	V	D	F	17
		:										
Db	4	y	q	f	p	q	h	n	s	v	d	14

RESULT	13
W65669	
ID	W65669 standard; peptide; 22 AA.

AC W65669;

DT 16-OCT-1998 (first entry)

DE Peptide #13.

KW microbial surface components recognising adhesive matrix molecule;
KW MSCRAMM; fibronectin; fibronectin-binding protein; antibody; epitope
KW antibiotic; bacterial infection; antibiotic-resistant strain.

OS Synthetic

PN W09831389-A2

PD 23-JUL-1998

PF 21-JAN-1998; 98WO-US01222

PR 21-JAN-1997; 97US-0036139

PA (TEXA) UNIV TEXAS A & M SYSTEM

PI Hoeoek M, House-pompeo KL, Joh D, Mcgavin MJ, Patti JM;

XX

XX

PT binding to fibronectin - used to treat or prevent bacterial

XX

The invention relates to antibodies that bind to a fibronectin-binding domain of a fibronectin-binding protein, and inhibit binding of the protein to fibronectin. Also claimed are: (1) isolated peptides of a fibronectin-binding protein that do not bind to fibronectin; (2) fusion protein containing at least one peptide of a fibronectin-binding protein linked to a second amino acid sequence; (3) nucleic acid encoding the isolated peptide of (1). Antibodies, the isolated peptides of (1) and the nucleic acids are all useful for immunisation (active or passive) and (by inhibiting binding of bacteria to fibronectin) for preventing or treating infection in humans or other animals, particularly by staphylococci or streptococci, e.g. meningitis, otitis media, pneumonia, endocarditis, mastitis in cattle, abortion in horses and many others. Since the antibodies block binding of bacteria, they should be

PR 17-NOV-1997: 97US-0066090.
 PR 17-NOV-1997: 97US-0066094.
 PR 17-NOV-1997: 97US-0066095.
 PR 17-NOV-1997: 97US-0066089.
 XX
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Carter KC, Edner R, Endress GA, Feng P, Janat F;
 PI Kyaw H, Lafleur DW, Moore PA, Ni J, Olsen HS, Rosen CA;
 PI Ruben SM, Shi Y, Soppet DR, Wei Y;
 XX
 DR WPI: 1999-337740/28.
 DR N-PSDB: X85016.
 XX
 PT New human secreted proteins and coding sequences useful for treating
 PT disorders of the immune system and hyperproliferative disorders
 XX
 PS Disclosure: Page 119; 507pp; English.
 XX
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. X84924) for increasing the stability of the fused protein
 CC as compared to the human protein only.
 CC The invention relates to 125 novel genes and their fragments (nucleic
 CC acid sequences: X84933-X85057; amino acid sequences Y27567-Y27933) which
 CC are useful for preventing, treating or ameliorating medical conditions
 CC e.g. by protein or gene therapy. Also, pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the 125 polynucleotides, based on
 CC which tissues they are most highly expressed in (see X84933 for described
 CC uses).
 XX
 SQ Sequence 14 AA:
 Query Match 28.8%; Score 32; DB 20; Length 14;
 Best Local Similarity 61.5%; Pred. No. 44;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 10 PKHLVDPLQSLQSL 22
 DB 1 pnsrvsflqsls 13
 RESULT 10
 ID W65690 standard; peptide: 21 AA.
 AC W65690;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Fibronectin binding protein-derived peptide #34.
 XX
 DE Microbial surface components recognising adhesive matrix molecule;
 KM MSCRAMM: fibronectin; fibronectin-binding protein; antibody; epitope;
 KM antibiotic; bacterial infection; antibiotic-resistant strain;
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN MO9831389-A2.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US01222.
 XX
 PR 21-JAN-1997; 97US-0036139.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX

PI Hoeck M, House-Pompeo KL, Joh D, McGavin MJ, Patti JM;
 PI Speziale P;
 XX
 DR WPI: 1998-413816/35.
 XX
 PT Antibody that binds to fibronectin-binding protein, preventing its
 PT binding to fibronectin - used to treat or prevent bacterial
 PT infection, especially by Staphylococci and Streptococci
 XX
 PS Example 8; Page 101; 201pp; English.
 XX
 CC The invention relates to antibodies that bind to a fibronectin-binding
 CC domain of a fibronectin-binding protein, and inhibit binding of the
 CC protein to fibronectin. Also claimed are: (1) isolated peptides of a
 CC fibronectin-binding protein that do not bind to fibronectin; (2) fusion
 CC protein containing at least one peptide of a fibronectin-binding protein
 CC linked to a second amino acid sequence; (3) nucleic acid encoding
 CC the isolated peptide of (1). Antibodies, the isolated peptides of
 CC (1) and the nucleic acids are all useful for immunisation (active or
 CC passive) and (by inhibiting binding of bacteria to fibronectin) for
 CC preventing or treating infection in humans or other animals, particularly
 CC by staphylococci or streptococci, e.g. meningitis, otitis media,
 CC pneumonia, endocarditis, mastitis in cattle, abortion in horses and many
 CC others. Since the antibodies block binding of bacteria, they should be
 CC effective against antibiotic-resistant strains, and may replace
 CC antibiotic therapy or increase its effectiveness. Sequences W65670-90
 CC represent a series of synthetic peptides based on the D3 repeat of
 CC S. aureus fibronectin binding protein A. They were synthesised to contain
 CC a proline residue at each position through the sequence (le a proline
 CC scan).
 XX
 SQ Sequence 21 AA:
 Query Match 28.8%; Score 32; DB 19; Length 21;
 Best Local Similarity 54.5%; Pred. No. 70;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 7 FGPKHLVDPL 17
 DB 4 yqfphpsvdf 14
 RESULT 11
 ID R98414 standard; peptide: 16 AA.
 AC R98414;
 XX
 DT 18-FEB-1997 (first entry)
 XX
 DE Interferon-gamma receptor peptide, Lys433-Asp448.
 XX
 DE Interferon-gamma; IFN; receptor protein; phosphorylated;
 KM cytoplasmic transcription factor; STAT1alpha; STAT2;
 KM signal transducers and activators of transcription; STAT.
 XX
 OS Homo sapiens.
 XX
 PN WO9620211-A1.
 XX
 PD 04-JUL-1996.
 XX
 PF 22-DEC-1995; 95WO-US16988.
 XX
 PR 23-DEC-1994; 94AU-0000249.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Harpur AG, Lackmann M, Oates AC, Wilks AF;
 XX
 DR WPI: 1996-321801/32.
 XX

PI Mark DF, Creasey AA;
 XX WPI: 1983-723186/30.
 DR N-PSDB; N30158.
 XX
 PT Multi-class hybrid interferon poly:peptide(s) - with restricted
 PT antiviral and cell growth regulatory activities
 XX
 PS Example: Fig 17; 61pp; English.
 CC The inventors claim a multiclass hybrid interferon polypeptide and a
 CC DNA unit having a nucleotide sequence which encodes it. Pref. the
 CC AA sequence consists of alpha and beta interferons. Pref. IF1 is
 CC (1) the 1-73 AA seq. of HuIFN-alpha-1 (and IF2 is the 74-166 AA seq.
 CC of HuIFN-beta-1) (see N30155, P30222); or (II) the 1-41 AA seq. of
 CC HuIFN-alpha-61A (and IF2 is the 43-166 AA seq. of HuIFN-beta-1) (see
 CC N30160, P30227). Alternatively IF1 is the amino terminal end of a
 CC beta-IF and IF2 is the carboxy terminal of an alpha-IF (esp. the
 CC 1-73 seq. of HuIFN-beta-1 and the 74-167 seq. of HuIFN-alpha-1
 CC resp.) (see N30156, P30223). In the examples plasmids pCM5 and
 CC pDM101/trp/beta-1 and p-alpha-61A were used (see N30151, N30152,
 CC N30157). HinfI was used to digest the DNA sequences in the region
 CC of significant handicaps (see N30153, N30154, N30158, N30159), and
 CC the restriction fragments were ligated to form hybrid DNA.
 CC
 SQ Sequence 12 AA;
 OY 6 DFGFPK 11
 |||||:
 Db 2 dfgfpq 7
 Query Match 28.8%; Score 32; DB 4; Length 12;
 Best Local Similarity 83.3%; Pred. No. 37;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 P80053
 ID P80053 standard; protein; 12 AA.
 AC P80053;
 XX
 DT 17-NOV-1990 (first entry)
 DE Sequence of human interferon (huIFN) alpha-61A gene around AA 40.
 XX
 KW Alpha-beta hybrid interferon; multi-class hybrid interferon;
 KW antitumour; antiviral; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 7 /note="Residue 40"
 FT
 XX
 XX US4758428-A.
 PN
 XX
 PD 19-JUL-1988.
 PD
 PF 15-JUL-1985; 85US-0755265.
 PF
 PR 15-JUL-1985; 85US-0755265.
 PR
 PR 19-JAN-1983; 83CA-0419758.
 PR
 PA (CETU) CETUS CORP.
 PA
 PI Mark DF, Creasey AA;
 XX
 XX WPI: 1988-219882/31.
 DR
 DR N-PSDB; n80050.
 DR
 PT Multi-class hybrid interferon polypeptide(s) -

PT having sequence from interferon-alpha-1 and sequence from
 PT interferon-beta-1 for restricted activity
 XX
 XX
 PS Example: Fig 17; 24pp; English.
 CC Multi-class hybrid IFN polypeptides having an AA sequence composed
 CC of 2 distinct subsequences are claimed. The plasmids used in the
 CC construction of huIFN-alpha-61A-beta-1 hybrid are plasmids palpa61A and
 CC pDM101/trp/beta-1. Assembly of the palpa61A plasmid involved replacing
 CC the DNA fragment encoding the 23 AA signal polypeptide of preinterferon
 CC with a 120BP EcoRI/Sau3A promoter fragment E.coli trp promoter, operator,
 CC and trp leader ribosome binding site preoperator, encoding an ATG
 CC initiation codon and using HindIII site that was inserted, 59 nucleotides
 CC 3'-end of the TGA translational stop codon, to insert the gene into the
 CC plasmid pDM1 (a deriv of pBR322 having a deletion between the HindIII
 CC and PvuII sites). The complete DNA sequence of the promoter and gene
 CC fragments inserted between the EcoRI and HindIII sites of pDM1 is shown
 CC in n80049. The hybrid gene was constructed by taking advantage of the
 CC homologies between huIFN alpha-61A & huIFN beta-1 at around AA 40 of both
 CC proteins. The DNA sequence 5'-proximal to the DdeI restriction enzyme
 CC cutting site of the huIFN alpha-61A DNA is ligated to the DNA sequence
 CC 3'-proximal to the site of huIFN beta-1, to create a fusion of the
 CC two genes while preserving the translational reading frame of both.
 CC
 SQ Sequence 12 AA;
 OY 6 DFGFPK 11
 |||||:
 Db 2 dfgfpq 7
 Query Match 28.8%; Score 32; DB 9; Length 12;
 Best Local Similarity 83.3%; Pred. No. 37;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
 Y27814
 ID Y27814 standard; Protein; 14 AA.
 XX
 AC Y27814;
 XX
 DT 30-JUL-1999 (first entry)
 DE Human secreted protein encoded by gene No. 84.
 XX
 DE Human secreted protein encoded by gene No. 84.
 XX
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 KW
 XX
 OS Homo sapiens.
 XX
 XX WO9924836-A1.
 PN
 XX
 PD 20-MAY-1999.
 PD
 PF 04-NOV-1998; 98WO-US23435.
 PF
 PR 17-NOV-1997; 97US-0066100.
 PR
 PR 07-NOV-1997; 97US-0064900.
 PR
 PR 07-NOV-1997; 97US-0064908.
 PR
 PR 07-NOV-1997; 97US-0064911.
 PR
 PR 07-NOV-1997; 97US-0064912.
 PR
 PR 07-NOV-1997; 97US-0064983.
 PR
 PR 07-NOV-1997; 97US-0064984.
 PR
 PR 07-NOV-1997; 97US-0064985.
 PR
 PR 07-NOV-1997; 97US-0064987.
 PR
 PR 07-NOV-1997; 97US-0064988.

CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration); for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target antigen.
 CC Th can replace carrier proteins and pathogen-derived T helper epitopes.
 CC Sequence Y91121 represents a promiscuous T helper epitope from the
 CC measles virus F (WVF) protein and sequences Y91122-Y91142, Y91226 and
 CC Y91245-Y91246 represent synthetic Th epitopes based on the WVF Th
 CC epitope. Sequence Y91143 represents a promiscuous Th epitope from
 CC hepatitis B virus (HBV) surface antigen, and sequences Y91144-Y91155 are
 CC synthetic epitopes derived from this HBV epitope. Y91155-Y91196,
 CC Y91227 and Y91242-Y91244 are antigenic peptides comprising an LHRH
 CC sequence joined to a promiscuous Th epitope. Y91197 is the LHRH target
 CC antigenic peptide used in these LHRH antigenic peptides. Y91200 is
 CC somatostatin, and Y91201-Y91207 are antigenic peptides comprising
 CC somatostatin and a Th epitope. Somatostatin immunogens may be used
 CC to promote growth in livestock. Y91208 is a human CD4 CDR2-like domain
 CC antigenic site, and Y91209-Y90211 are MVA Th epitope/CD4 CDR2
 CC antigenic peptides which may be used to prevent HIV infection of T
 CC cells. Y90212 is a modified version of a human IGE (Immunoglobulin
 CC E) CH3 domain, and Y90213-Y90219 are Th epitope/IGE CH3 antigenic
 CC peptides which may be used in the treatment of allergies. Y91220 is
 CC a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid
 CC protein and Y91221-Y91222 comprise this peptide and a Th epitope. Y91223
 CC is a Plasmodium falciparum circumsporozoite (CS) target antigen, and
 CC Y91224-Y91225 comprise the CS antigen and an MVA Th epitope and may be
 CC used in a malaria vaccine. Y91228-Y91231 represent CERP-derived peptides
 CC and Y91232-Y91241 are immunogens comprising a CERP peptide and a Th
 CC epitope which may be used to prevent or treat arteriosclerosis and
 CC cardiovascular disease. Y91247 and Y91252-Y91257 are HIV-1 neutralising
 CC B-cell epitopes, and Y91248-Y91251 and Y91258-Y91273 are HIV-1 neutralising
 CC peptides comprising MVA Th and HIV-1 B-cell epitope which may be used as
 CC a component in an anti-HIV-1 vaccine. Y91198 and Y91199 are respectively
 CC an immunostimulatory Invasin protein epitope from *Yersinia* species, and
 CC hinge spacer peptide, both of which may optionally be used in the
 CC antigenic peptides of the invention.

SO Sequence 16 AA:

Query Match 71.2%; Score 79; DB 21; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.5e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FGPPKILVDFLOSLS 22
 |||||:|||||
 DB 1 fgiptehllydfllqsls 16

RESULT 6

W24294 ID W24294 standard; peptide: 11 AA.

AC W24294;

DT 17-OCT-1997 (first entry)

DE Human/Rabbit CERP common peptide.

KX Immune response: high density lipoprotein; HDL; cholesterol; human;

KW serum; epitope; cholesterol ester transfer protein; CERP; rabbit.

OS *Oryctolagus cuniculus*.

XX Homo sapiens.

PN W09639168-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 05-JUN-1996; 96MO-US09143.
 XX
 PR 06-JUN-1995; 95US-0482454.
 XX
 PA (IMMU-) IMMUNE RESPONSE CORP.
 XX
 PI Brostoff SW, Carlo DJ, Kwoh DY;
 XX
 DR WPI, 1997-042849/04.
 XX
 PT Stimulating an immune response to increase high density lipoprotein
 PT - avoids repeated administration of toxic drugs to lower cholesterol
 PT ester transfer protein levels
 XX
 PS Claim 5; Page 16; 26pp; English.

CC The sequences given in W24292-94 were used in the method of the
 CC invention to stimulate an immune response to increase high density
 CC lipoprotein (HDL) cholesterol in a mammal exhibiting low levels of
 CC serum HDL. These peptides represent immunogenic epitopes of
 CC cholesterol ester transfer protein (CERP). The method utilizes
 CC the body's own immune system to lower CERP levels, thereby increasing
 CC the level of beneficial HDL cholesterol, preferably in serum. The
 CC method avoids the problems associated with the repeated administration
 CC of drugs which have undesirable side effects. This peptide represents
 CC a region of CERP which is common to both human and rabbit proteins.

SO Sequence 11 AA:

Query Match 47.7%; Score 53; DB 18; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 HLVDLFLOSLS 22
 |||||:|||||
 DB 1 hllydfllqsls 11

RESULT 7

P30225 ID P30225 standard; Protein: 12 AA.

AC P30225;

DT 25-MAY-1992 (first entry)

DE Sequence of interferon (HuIFN) -alpha-61A around amino acid 40.

KX Hybrid interferon; antiviral; therapy; cancer; tumour.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 7 /label= AA No. 40

PN W08302461-A.

PD 21-JUL-1983.

PF 18-JAN-1983; 83MO-0900607.

PR 19-JAN-1982; 82US-0340782.

PR 03-FEB-1983; 83US-0463574.

PR 15-JUL-1985; 85US-0755265.

XX (CERU-) CETUS CORP.

Y91230
 ID Y91230 standard; peptide; 16 AA.
 XX
 AC Y91230:
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Human cholesterol transport protein (CERP) peptide, SEQ ID NO:108.
 XX
 KW Promiscuous T-cell epitope; measles virus F protein; MRF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW luteinizing hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; PMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN WO9966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13975.
 XX
 PR 20-JUN-1998; 98US-0100412.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY:
 XX
 DR WPI: 2000-160564/14.
 XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 XX
 PS Claim 10; Page 62; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th),
 and immunogenic peptides comprising the Th epitopes of the invention
 along with B cell epitopes. The Th epitopes and peptide immunogens
 containing them, are used to induce a T helper cell response,
 specifically against Plasmodium falciparum, cholesterol ester transport
 protein (CERP) or HIV epitopes, but more generally against any pathogen,
 immunoreactive self-antigen or tumour antigen. The Th epitopes and
 peptide immunogens may be used for prevention and/or treatment of
 infections (HIV, foot-and-mouth disease or malaria); for cancer
 immunotherapy; for inhibition of the action of luteinizing hormone
 releasing hormone (LHRH) for contraception, treatment of hormone-
 dependent cancer, prevention of boar taint in meat, and
 immunocastration); for promoting the growth of animals; or for
 treating allergies or arteriosclerosis. Incorporation of a promiscuous
 Th (functional in genetically diverse subjects) into an immunogen
 improves capacity to induce a strong T helper cell-mediated immune
 response, resulting in production of antibodies against a target antigen.
 Th can replace carrier proteins and promiscuous T helper epitopes. From the
 Sequence Y91121 represents a promiscuous T helper epitope from the
 measles virus F (MVF) protein and sequences Y91122-Y91142, Y91226 and
 Y91245-Y91246 represent synthetic Th epitopes based on the MVF Th
 epitope. Sequence Y91143 represents a promiscuous Th epitope from
 hepatitis B virus (HBV) surface antigen, and sequences Y91144-Y91155 are
 synthetic epitopes derived from this HBV epitope. Y91156-Y91196,
 Y91227 and Y91242-Y91244 are antigenic peptides comprising an LHRH
 sequence joined to a promiscuous Th epitope. Y91197 is the LHRH target
 antigenic peptide used in these LHRH antigenic peptides. Y91200 is
 somatostatin, and Y91201-Y91207 are antigenic peptides comprising
 somatostatin and a Th epitope. Somatostatin immunogens may be used
 to promote growth in livestock. Y91208 is a human CD4 CDR2-like domain
 antigenic site, and Y91209-Y90211 are MWN Th epitope/CD4 CDR2
 antigenic peptides which may be used to prevent HIV infection of T
 cells. Y90212 is a modified version of a human IgE (immunoglobulin
 E) CH3 domain, and Y90213-Y90219 are Th epitope/IgE CH3 antigenic

peptides which may be used in the treatment of allergies. Y91220 is
 a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid
 protein and Y91221-Y91222 comprise this peptide and a Th epitope. Y91223
 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and
 Y91224-Y91225 comprise the CS antigen and an MWF Th epitope and may be
 used in a malaria vaccine. Y91228-Y91231 represent CERP-derived peptides
 and Y91232-Y91241 are immunogens comprising a CERP peptide and a Th
 epitope which may be used to prevent or treat arteriosclerosis and
 cardiovascular disease. Y91247 and Y91252-Y91257 are HIV-1 neutralising
 B-cell epitopes, and Y91248-Y91251 and Y91258-Y91273 are antigenic
 peptides comprising MWN Th and HIV-1 B-cell epitope which may be used as
 a component in an anti-HIV-1 vaccine. Y91198 and Y91199 are respectively
 CC an immunostimulatory invasion protein epitope from *Yersinia* species, and
 CC hinge spacer peptide, both of which may optionally be used in the
 CC antigenic peptides of the invention.

Sequence 16 AA:
 S0
 Query Match 74.8%; Score 83; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3,5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 FGEPKHLIVDFLQSTIS 22
 |||||
 Db 1 fgfphllvdfllqstis 16

RESULT 5
 Y91229 Y91229 standard; peptide; 16 AA.
 XX
 AC Y91229:
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Human cholesterol transport protein (CERP) peptide, SEQ ID NO:107.
 XX
 KW Promiscuous T-cell epitope; measles virus F protein; MRF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW luteinizing hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; PMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN WO9966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13975.
 XX
 PR 20-JUN-1998; 98US-0100412.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY:
 XX
 DR WPI: 2000-160564/14.
 XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 XX
 PS Claim 10; Page 50; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th),
 and immunogenic peptides comprising the Th epitopes of the invention
 along with B cell epitopes. The Th epitopes and peptide immunogens
 containing them, are used to induce a T helper cell response,
 specifically against Plasmodium falciparum, cholesterol ester transport

CC	This sequence represents an immunogenic fragment of the rabbit
CC	cholesteryl ester transferase protein (CETP).
CC	The invention relates to recombinant DNA vaccines that contain DNA
CC	encoding CETP, which can be used for producing antibodies to lessen the
CC	transfer of cholesteryl esters from high density lipoprotein (HDL). The
CC	method can provide an autogenous immunological process for lessening the
CC	transfer of cholesteryl esters from HDL particles and for increasing the
CC	HDL cholesterol concentration of a mammal whose blood also contains
CC	CETP. The method may be useful in treating human pro-atherogenic
CC	dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC	method can have an effect that lasts for months as compared to the
CC	short-term effects of the small molecule drugs now available.
SQ	Sequence 22 AA:
Query Match	100.0%; Score 111; DB 20; Length 22;
Best Local Similarity	100.0%; Pred. No. 1.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 LLLDMFGPKHLVDFLOSLS 22 1 ILLqmdfgfPKHLVdflgsls 22
Db	
RESULT 2	
ID	Y13815
XX	Y13815 standard; peptide; 22 AA.
AC	Y13815:
XX	
DT	08-JUL-1999 (first entry)
DE	Rabbit CETP Immunogenic Fragment.
KW	CETP: cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
KM	antibody production; cholesteryl ester transfer; therapy;
KW	high density lipoprotein; HDL cholesterol concentration;
KW	pro-atherogenic dyslipoproteinaemia.
OS	Oryctolagus sp.
PN	MO9915655-A1.
PD	01-APR-1999.
PF	17-SEP-1998; 98WO-US19366.
PR	19-SEP-1997; 97US-0934367.
PA	(MONS) MONSANTO CO.
P1	Glenn K, Needleman P;
DR	WPI; 1999-276984/23.
PT	New recombinant DNA vaccines
PS	Disclosure; Page 75; 99pp; English.
XX	
CC	This sequence represents an immunogenic fragment of the rabbit
CC	cholesteryl ester transferse protein (CETP).
CC	The invention relates to recombinant DNA vaccines that contain DNA
CC	encoding CETP, which can be used for producing antibodies to lessen the
CC	transfer of cholesteryl esters from high density lipoprotein (HDL). The
CC	method can provide an autogenous immunological process for lessening the
CC	transfer of cholesteryl esters from HDL particles and for increasing the
CC	HDL cholesterol concentration of a mammal whose blood also contains
CC	CETP. The method may be useful in treating human pro-atherogenic
CC	dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC	method can have an effect that lasts for months as compared to the
CC	short-term effects of the small molecule drugs now available.

SQ	Sequence	22 AA:
Oy	Query Match	96.4%; Score 107; DB 20; Length 22;
	Best Local Similarity	95.5%; Pred. No. 7.3e-11;
	Matches 21; Conservative 1;	Mismatches 0; Indels 0; Gaps 0;
Dd	1 LLLDMDFGPKHLVDFLOSLS 22 1 ILLqmdfgfpehlvdfllqsIs 22	
RESULT	3	
ID	YI3821 standard; peptide; 22 AA.	
XX	YI3821	
AC	YI3821;	
DT	08-JUL-1999 (first entry)	
DE	Human CERP immunogenic fragment.	
XX	CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;	
KW	antibody production; cholesteryl ester transfer; therapy;	
KM	high density lipoprotein; HDL cholesterol concentration;	
KW	pro-atherogenic dyslipoproteinaemia.	
XX		
OS	Homo sapiens.	
XX		
PM	MO9915655-A1.	
PD	01-APR-1999.	
XX		
PF	17-SEP-1998; 98WO-US19366.	
PR	19-SEP-1997; 97US-0934367.	
XX	(MONS) MONSANTO CO.	
PA		
XX	Glenn K, Needleman P;	
XX	WPt; 1999-276984/23.	
DR		
XX	New recombinant DNA vaccines	
PT		
PS	Disclosure; Page 88; 99p; English.	
XX		
CC	This sequence represents an immunogenic fragment of the human	
CC	cholesteryl ester transferase protein (CERP).	
CC	The invention relates to recombinant DNA vaccines that contain DNA	
CC	encoding CERP, which can be used for producing antibodies to lessen the	
CC	transfer of cholesteryl esters from high density lipoprotein (HDL). The	
CC	method can provide an autogenous immunological process for lessening the	
CC	transfer of cholesteryl esters from HDL particles and for increasing the	
CC	HDL cholesterol concentration of a mammal whose blood also contains	
CC	CERP. The method may be useful in treating human pro-atherogenic	
CC	dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The	
CC	method can have an effect that lasts for months as compared to the	
CC	short-term effects of the small molecule drugs now available.	
XX		
SX	Sequence 22 AA:	
Query Match	96.4%; Score 107; DB 20; Length 22;	
Best Local Similarity	95.5%; Pred. No. 7.3e-11;	
Matches 21; Conservative 1;	Mismatches 0; Indels 0; Gaps 0;	
Oy	1 LLLDMDFGPKHLVDFLOSLS 22 1 ILLqmdfgfpehlvdfllqsIs 22	
Dd		
RESULT	4	

CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,
 CC which forms an amphipathic alpha-helix in presence of lipids. (A),
 CC optionally as a complex with lipids, and host cells that contain (A),
 CC are useful for gene therapy, or prevention, of diseases associated with
 CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
 CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I
 CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat
 CC endotoxemia (septic shock). Host cells containing (A) can also be used
 CC to study the role of apoA-I in lipid metabolism. (B) can be used
 CC diagnostically, e.g. to measure serum HDL (particularly its
 CC subpopulation involved in retrograde cholesterol transport) and for
 CC imaging the circulatory system or HDL accumulations at fatty streaks.
 CC The present sequence represents a peptide from the present invention.
 CC
 XX Sequence 22 AA:
 SO

Query Match 28.8%; Score 32; DB 20; Length 22;
 Best Local Similarity 58.3%; Pred. No. 94;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 11 EHLVDFLOSLS 22
 Db 7 erlledllqaln 18

RESULT 14
 Y19320
 ID Y19320 standard; Peptide: 22 AA.
 XX
 AC Y19320;
 XX
 DT 14-JUL-1999 (first entry)
 XX
 DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #133.
 XX
 KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
 KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
 KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
 KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
 KW septic shock.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN MO9916459-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 28-SEP-1998; 98WO-US20327.
 XX
 PR 29-SEP-1997; 97US-0940095.
 XX
 PA (BUTT/) BUTTNER K.
 PA (CORN/) CORNUT I.
 PA (DASS/) DASSEUX J.
 PA (DUFO/) DUFOURCO J.
 PA (METZ/) METZ G.
 PA (SEKU/) SEKUL R.
 XX
 PI Butner K, Cornut I, Dasseux J, Dufourcq J, Metz G;
 PI Sekul R;
 XX
 DR MPI; 1999-277035/23.
 XX
 PT Peptide agonists of apolipoprotein A-I
 XX
 PS Claim 19; Page 157; 280pp; English.
 XX
 CC The present invention describes an agonist (A) of apolipoprotein A-I
 CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
 CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
 CC complexes, are used to treat or prevent diseases associated with

CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
 CC atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
 CC deficiency; hypertriglyceridemia and metabolic syndrome, also for
 CC treating septic shock. When labeled, (A) can also be used diagnostically
 CC to measure serum levels of HDL, in particular the HDL subpopulation that
 CC is involved in retrograde cholesterol transport, also to image HDL at
 CC e.g. atherosclerotic streaks, and to raise antibodies. Y19188 to Y19441
 CC represent lecithin:cholesterol acyltransferase (LCAT) activity
 CC exhibiting core peptides, which are apoA-I agonists.
 CC
 XX Sequence 22 AA:
 SO

Query Match 28.8%; Score 32; DB 20; Length 22;
 Best Local Similarity 58.3%; Pred. No. 94;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 11 EHLVDFLOSLS 22
 Db 7 erlledllqaln 18

RESULT 15
 Y32796
 ID Y32796 standard; peptide: 12 AA.
 XX
 AC Y32796;
 XX
 DT 09-NOV-1999 (first entry)
 XX
 DE Mammalian prolactin receptor derived polypeptide.
 XX
 KW Signal transduction; proteolytic cleavage; prolactin receptor;
 KW proteosome binding site; muscle wasting; renal tubular defect;
 KW diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin;
 KW growth hormone deficiency; inhibitor.
 XX
 OS Oryzolaus cuniculus.
 OS Rattus sp.
 OS Mus sp.
 XX
 PN EP943624-A1.
 XX
 PD 22-SEP-1999.
 XX
 PF 12-MAR-1998; 98EP-0200799.
 XX
 PR 12-MAR-1998; 98EP-0200799.
 XX
 PA (UYUR-) RIJCSUNIV UTRCHT.
 XX
 DR MPI; 1999-510568/43.
 XX
 PT Controlling the availability and/or signal transduction capability
 PT of a cell surface receptor, useful for treating growth hormone
 PT deficiencies
 XX
 PS Disclosure; Page 9; 36pp; English.
 XX
 CC This sequence is a polypeptide from the mammalian prolactin receptor.
 CC Sequences (Y32794-Y32823) are examples of polypeptide sequences found at
 CC or near the ubiquitin/proteosome complex binding site located on the
 CC intracellular part of a cell surface receptor. These sequences are used
 CC in a method for controlling the availability and signal transduction
 CC capability of a cell surface receptor by administering an inhibitor that
 CC is capable of inhibiting proteolytic cleavage of the receptor. Inhibition
 CC of this proteolytic cleavage results in the receptors being present on
 CC the surface for longer and therefore signalling for longer to the
 CC interior of the cell. This increases the sensitivity of cells to any
 CC hormones which might be present. The inhibitor is either derived from,
 CC competes with or binds to a polypeptide sequence of which sequences
 CC Y32794-Y32823 are examples. The inhibitor may be used to treat muscle
 CC wasting, associated with disorders such as renal tubular defects,

PA	(METZ//) METZ G.
PA	(SEKU//) SEKUL R.
PI	Buttner K, Cornut I, Dasseux J, Metz G, Sekul R;
XX	
DR	WPI; 1999-277034/23.
XX	
PT	Peptide agonists of apolipoprotein A-I
XX	
PS	Example; Page 114; 254pp; English.
XX	
CC	The present invention describes an agonist (A) of apolipoprotein A-I
CC	(apoA-I) which is a 15-29 residue peptide, or analog, that forms an
CC	amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC	complexes, are used to treat or prevent diseases associated with
CC	hyperlipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC	atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
CC	deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC	treating septic shock. When labeled, (A) can also be used diagnostically
CC	to measure serum levels of HDL, in particular the HDL subpopulation that
CC	is involved in retrograde cholesterol transport, also to image HDL at
CC	e.g. atherosclerotic streaks, and to raise antibodies. Y18934 to Y19187
CC	represent lecitin:cholesterol acyltransferase (LCAT) activity
CC	exhibiting core peptides, which are apoA-I agonists.
XX	
S0	Sequence 22 AA:

Query Match	28.8%	Score 32	DB 20	Length 22
Best local Similarity	58.3%	Pred No. 94		
Matches 7; Conservative	2	Mismatches 3	Indels 0	Gaps 0
OY	11	EHLLVDFLOIS	22	
	1	1	1	1
	1	1	1	1
db	7	erlleldlqah	18	

RESULT	12
Y18812	
ID	Y18812 standard; Peptide; 22 AA.

DT	09-JUL-1999 (first entry)
XX	
DE	Lecithin:cholesterol acyltransferase activation exhibiting peptide #133

KM Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
KM human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KM cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KM high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KM septic shock.

OS Synthetic.
OS Homo sapiens.

PN WO9916408-A2.

PD 08-APR-1999.

PF 28-SEP-1998;

PR 29-SEP-1997; 97US-0940093.

PA (BUTT/) BUTTNER K.

PA (DASS/) DASSEUX J.

PA (SEKU/) SEKUL R.

PI Butner K, Cornut I, Dasseux J, Metz G, Sekul R;

DR WPI: 1999-277031/23.

XX Peptide agonists of apolipoprotein A-I
PT
XX
PS Example; Page 111; 152pp; English.

CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 14-22 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
CC deficiency, hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. Y18680 to Y18933
CC represent lecitin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists.

Sequence 22 AA;

Query Match	28.8%;	Score 32;	DB 20;	length 22;
Best Local Similarity	58.3%;	Pred. No. 94;		
Matches 7; Conservative	2;	Mismatches	3;	Indels 0;
				Gaps 0;

```
QY      11 EHLVDFlQSLs 22
          | | | | | :
Db      7 erlleDlqaln 18
```

RESULT	13
Y18549	
ID	Y18549 standard; Peptide; 22 AA.

AC	Y18549;
XX	
DT	09-JUL-1999 (first entry)

DE Lecithin:cholesterol acyltransferase exhibiting peptide #133.

Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder; APOA-I; cardiovascular disease; atherosclerosis; restenosis; LCAT; hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase

05 Synthetic.
05 Homo sapiens.

PN W09916409-A2.

PD 08-APR-1999.

PF 28-SEP-1998; 98WO-US20329.

PR 29-SEP-1997; 97US-0940136.

PA (BUTT/) BUTT

PA (DASS/) DASSEUX J.

PA (METZ/) METZ G.

XX

PI Sekul R;

DR WPI; 1999-254921/21.

PT Nucleic acid encoding apolipoprotein A-I agonist peptides

PS Claim 18; Page 166; 232pp; English.

CC The present invention describes a nucleic acid (A) encoding an

PI Mark DF, Creasey AA;
 XX WPI; 1983-723186/30.
 DR N-PSDB; N30158.
 XX
 PT Multi-class hybrid interferon poly(peptide)s - with restricted
 PT antiviral and cell growth regulatory activities
 XX
 PS Example; Fig 17; 61pp; English.
 XX
 CC The inventors claim a multiclass hybrid interferon polypeptide and a
 CC DNA unit having a nucleotide sequence which encodes it. Pref. the
 CC AA sequence consists of alpha and beta interferons. Pref. IF1 is
 CC (1) the 1-73 AA seq. of HuIFN-alpha-1 (and IF2 is the 1-41 AA seq. of
 CC HuIFN-beta-1) (see N30155, P30222); or (ii) the 1-41 AA seq. of
 CC HuIFN-alpha-61A (and IF2 is the 43-166 AA seq. of HuIFN-beta-1) (see
 CC N30160, P30227). Alternatively IF1 is the amino terminal end of a
 CC beta-IF and IF2 is the carboxy terminal of an alpha-IF (esp. the
 CC 1-73 seq. of HuIFN-beta-1 and the 74-167 seq. of HuIFN-alpha-1
 CC resp.) (see N30156, P30223). In the examples plasmids pGM5 and
 CC pDM101/trp/beta-1 and p-alpha-61A were used (see N30151, N30152,
 CC N30157). HinfI was used to digest the DNA sequences in the region
 CC of significant handicaps (see N30153, N30154, N30158, N30159) and
 CC the restriction fragments were ligated to form hybrid DNA.
 CC
 SQ Sequence 12 AA:
 Query Match 29.7%; Score 33; DB 4; Length 12;
 Best Local Similarity 83.3%; Pred. No. 34;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 6 DFGPE 11
 |||||:
 Db 2 dfgfpq 7
 RESULT 8
 P80053
 ID P80053 standard; protein; 12 AA.
 AC P80053;
 XX
 DT 17-NOV-1990 (first entry)
 DE Sequence of human interferon (huIFN) alpha-61A gene around AA 40.
 XX
 KW Alpha-beta hybrid interferon; multi-class hybrid interferon;
 KW antitumour; antiviral; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 7 /note="Residue 40"
 FT
 PN US4758428-A.
 XX
 PD 19-JUL-1988.
 XX
 PF 15-JUL-1985; 85US-0755265.
 XX
 PR 15-JUL-1985; 85US-0755265.
 PR 19-JAN-1983; 83CA-0419758.
 XX
 PA (CETU) CETUS CORP.
 XX
 PI Mark DF, Creasey AA;
 XX
 DR WPI; 1988-219882/31.
 DR N-PSDB; n80050.
 XX
 PT Multi-class hybrid interferon polypeptide(s) -

PT having sequence from interferon-alpha-1 and sequence from
 PT interferon-beta-1 for restricted activity
 XX
 PS Example; Fig 17; 24pp; English.
 XX
 CC Multi-class hybrid IFN polypeptides having an AA sequence composed
 CC of 2 distinct subsequences are claimed. The plasmids used in the
 CC construction of huIFN-alpha-61A-beta-1 hybrid are plasmids palpha61A and
 CC pDM101/trp/beta-1. Assembly of the palpha61A plasmid involved replacing
 CC the DNA fragment encoding the 23 AA signal polypeptide of preinterferon
 CC with a 120BP EcoRI/Sau3A promoter fragment E.coli trp promoter, operator,
 CC and trp leader ribosome binding site (preoperator, encoding an ATG
 CC initiation codon and using HindIII site that was inserted, 59 nucleotides
 CC 3'-end of the TGA translational stop codon, to insert the gene into the
 CC plasmid pBM11 (a deriv of pBR322 having a deletion between the HindIII
 CC and PvuII sites). The complete DNA sequence of the promoter and gene
 CC fragments inserted between the EcoRI and HindIII sites of pBM11 is shown
 CC in n80049. The hybrid gene was constructed by taking advantage of the
 CC homologues between huIFN alpha-61A & huIFN beta-1 at around AA 40 of both
 CC proteins. The DNA sequence 5'-proximal to the DdeI restriction enzyme
 CC cutting site of the huIFN alpha-61A DNA is ligated to the DNA sequence
 CC 3'-proximal to the site of huIFN beta-1, to create a fusion of the
 CC two genes while preserving the translational reading frame of both.
 CC
 SQ Sequence 12 AA:
 Query Match 29.7%; Score 33; DB 9; Length 12;
 Best Local Similarity 83.3%; Pred. No. 34;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 6 DFGPE 11
 |||||:
 Db 2 dfgfpq 7
 RESULT 9
 Y27814
 ID Y27814 standard; protein; 14 AA.
 AC Y27814;
 XX
 DT 30-JUL-1999 (first entry)
 DE Human secreted protein encoded by gene No. 84.
 XX
 KW Human: secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asplenia; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; osteoclast; thymus;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 XX
 PN WO9924836-A1.
 XX
 PD 20-MAY-1999.
 XX
 PF 04-NOV-1998; 98WO-US23435.
 XX
 PR 17-NOV-1997; 97US-0066100.
 PR 07-NOV-1997; 97US-0064900.
 PR 07-NOV-1997; 97US-0064908.
 PR 07-NOV-1997; 97US-0064911.
 PR 07-NOV-1997; 97US-0064912.
 PR 07-NOV-1997; 97US-0064983.
 PR 07-NOV-1997; 97US-0064984.
 PR 07-NOV-1997; 97US-0064985.
 PR 07-NOV-1997; 97US-0064987.
 PR 07-NOV-1997; 97US-0064988.

CC protein (CETP) or HIV epitopes, but more generally against any pathogen.
 CC Immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of uterine-inhibiting hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration); for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target antigen.
 CC Th can replace carrier proteins and pathogen-derived T helper epitopes.
 CC Sequence Y91121 represents a promiscuous T helper epitope from the
 CC measles virus F (MVF) protein and sequences Y91122-Y91142, Y91226 and
 CC Y91245-Y91246 represent synthetic Th epitopes based on the MVF Th
 CC epitope. Sequence Y91143 represents a promiscuous Th epitope from
 CC hepatitis B virus (HBV) surface antigen, and sequences Y91144-Y91155 are
 CC synthetic epitopes derived from this HBV epitope. Y91156-Y91196,
 CC Y91227 and Y91242-Y91244 are antigenic peptides comprising an LHRH
 CC sequence joined to a promiscuous Th epitope. Y91197 is the LHRH target
 CC antigenic peptide used in these LHRH antigenic peptides. Y91200 is
 CC somatostatin, and Y91201-Y91207 are antigenic peptides comprising
 CC somatostatin and a Th epitope. Somatostatin immunogens may be used
 CC to promote growth in livestock. Y91208 is a human CD4 CD82-like domain
 CC antigenic site, and Y91209-Y90211 are MVF Th epitope/CD4-CD82
 CC antigenic peptides which may be used to prevent HIV infection of T
 CC cells. Y90212 is a modified version of a human IGE (Immunoglobulin
 CC E) CH3 domain, and Y90213-Y90219 are Th epitope/IGE CH3 antigenic
 CC peptides which may be used in the treatment of allergies. Y91220 is
 CC a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid
 CC protein and Y91221-Y91222 comprise this peptide and a Th epitope. Y91223
 CC is a Plasmodium falciparum circumsporozoite (CS) target antigen, and
 CC Y91224-Y91225 comprise the CS antigen and an MVF Th epitope, and may be
 CC used in a malaria vaccine. Y91228-Y91231 represent CETP-derived peptides
 CC and Y91232-Y91241 are immunogens comprising a CETP peptide and a Th
 CC epitope which may be used to prevent or treat arteriosclerosis and
 CC cardiovascular disease. Y91247 and Y91252-Y91257 are HIV-1 neutralising
 CC B-cell epitopes, and Y91248-Y91251 and Y91258-Y91273 are antigenic
 CC peptides comprising MVF Th and HIV-1 B-cell epitope which may be used as
 CC a component in an anti-HIV-1 vaccine. Y91198 and Y91199 are respectively
 CC an immunostimulatory Invasin protein epitope from Yersinia species, and
 CC hinge spacer peptide, both of which may optionally be used in the
 CC antigenic peptides of the invention.

SO Sequence 16 AA:

Query Match 71.2%; Score 79; DB 21; Length 16;
 Best Local Similarity 93.8%; Pred. No. 3.5e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FGPEHLVDFLOSIS 22
 |||||
 Db 1 LGLPKHLVDFLIS 16

RESULT 6
 W24294
 W24294 standard; peptide: 11 AA.

AC W24294:
 XX
 XX 17-OCT-1997 (first entry)
 XX
 DE Human/Rabbit CETP common peptide.

XX Immune response; high density lipoprotein: HDL; cholesterol; human;
 KM serum; epitope; cholesterol ester transfer protein; CETP; rabbit.
 XX
 OS Oryctolagus cuniculus.
 XX Homo sapiens.

OS
 XX

PN WO9639168-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US09143.
 XX
 PR 06-JUN-1995; 95US-0482454.
 XX
 PA (IMMU-) IMMUNE RESPONSE CORP.
 XX
 PI Brostoff SW, Carlo DJ, Kwach DY;
 XX
 DR WPI, 1997-042849/04.
 XX
 PT Stimulating an immune response to increase high density lipoprotein
 PT - avoids repeated administration of toxic drugs to lower cholesterol
 PT ester transfer protein levels
 XX
 PS Claim 5; Page 16; 26pp; English.

CC The sequences given in W24292-94 were used in the method of the
 CC invention to stimulate an immune response to increase high density
 CC lipoprotein (HDL) cholesterol in a mammal exhibiting low levels of
 CC serum HDL. These peptides represent immunogenic epitopes of
 CC cholesterol ester transfer protein (CETP). The method utilizes
 CC the body's own immune system to lower CETP levels, thereby increasing
 CC the level of beneficial HDL cholesterol, preferably in serum. The
 CC method avoids the problems associated with the repeated administration
 CC of drugs which have undesirable side effects. This peptide represents
 CC a region of CETP which is common to both human and rabbit proteins.

SO Sequence 11 AA:

Query Match 47.7%; Score 53; DB 18; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 HLIVDFLOSIS 22
 |||||
 Db 1 hlivdflls 11

RESULT 7
 P30225
 P30225 standard; Protein: 12 AA.

AC P30225:
 XX
 XX 25-MAY-1992 (first entry)
 XX
 DE Sequence of interferon (HuIFN) -alpha-61A around amino acid 40.

XX Hybrid interferon; antiviral; therapy; cancer; tumour.
 XX
 OS Homo sapiens.
 XX

XX Key Location/Qualifiers
 FT Misc-difference 7 /label= AA No. 40
 FT

PN WO8302461-A.

XX 21-JUL-1983.

XX 18-JAN-1983; 83WO-0900607.

XX 19-JAN-1982; 82US-0340782.

XX 03-FEB-1983; 83US-0463574.

XX 15-JUL-1985; 85US-0755265.

XX (CETU-) CETUS CORP.

Y91229
ID Y91229 standard; peptide: 16 AA.
XX
AC Y91229;
XX
DT 22-MAY-2000 (first entry)
DE Human cholesterol transport protein (CEPT) peptide, SEQ ID NO:107.
XX
KM Promiscuous T-cell epitope; measles virus F protein; MVF;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM interleukin releasing hormone; LHRH; contraceptive; anticancer;
KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
KM cholesterol ester transport protein; anti-arteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US13975.
XX
PR 20-JUN-1998; 98US-0100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI: 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus
XX
PS Claim 10; Page 50; 129pp; English.
XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesterol ester transport
CC protein (CEPT) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of interleukin releasing
CC hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunosuppression; for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target antigen.
CC Th can replace carrier proteins and pathogen-derived T helper epitopes.
CC Sequence Y91121 represents a promiscuous T helper epitope from the
CC measles virus F (MVF) protein and sequences Y91122-Y91142, Y91226 and
CC Y91245-Y91246 represent synthetic Th epitopes based on the MVF Th
CC epitope. Sequence Y91143 represents a promiscuous Th epitope from
CC hepatitis B virus (HBV) surface antigen, and sequences Y91144-Y91155 are
CC synthetic epitopes derived from this HBV epitope. Y91156-Y91196,
CC Y91227 and Y91242-Y91244 are antigenic peptides comprising an LHRH
CC sequence joined to a promiscuous Th epitope. Y91197 is the LHRH target
CC antigenic peptide used in these LHRH antigenic peptides. Y91200 is
CC somatostatin, and Y91201-Y91207 are antigenic peptides comprising
CC somatostatin and a Th epitope. Somatostatin immunogens may be used
CC to promote growth in livestock. Y91208 is a human CD4 CD82-like domain
CC antigenic site, and Y91209-Y91211 are MVA Th epitope/CD4 CD82
CC antigenic peptides which may be used to prevent HIV infection of T
CC cells. Y90212 is a modified version of a human IgE (immunoglobulin
CC E) CH3 domain, and Y90213-Y90219 are Th epitope/IgE CH3 antigenic

CC peptides which may be used in the treatment of allergies. Y91220 is
CC a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid
CC protein and Y91221-Y91222 comprise this peptide and a Th epitope. Y91223
CC is a Plasmodium falciparum circumsporozoite (CS) target antigen, and
CC Y91224-Y91225 comprise the CS antigen and an MVA Th epitope and may be
CC used in a malaria vaccine. Y91228-Y91231 represent CEMP-derived peptides
CC and Y91232-Y91241 are immunogens comprising a CEMP peptide and a Th
CC epitope which may be used to prevent or treat arteriosclerosis and
CC cardiovascular disease. Y91247 and Y91252-Y91257 are HIV-1 neutralising
CC B-cell epitopes, and Y91258-Y91273 are antigenic
CC peptides comprising MVA Th and HIV-1 B-cell epitope which may be used as
CC a component in an anti-HIV-1 vaccine. Y91198 and Y91199 are respectively
CC an immunostimulatory invasion protein epitope from Yersinia species, and
CC hinge spacer peptide, both of which may optionally be used in the
CC antigenic peptides of the invention.
XX
SQ Sequence 16 AA;
XX
QY 7 FGPEHLLVDFLQSLIS 22
Db 1 fgfpehllvdfqls 16
Query Match 74.8%; Score 83; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 5
Y91230
ID Y91230 standard; peptide: 16 AA.
XX
AC Y91230;
XX
DT 22-MAY-2000 (first entry)
XX
DE Human cholesterol transport protein (CEPT) peptide, SEQ ID NO:108.
XX
KM Promiscuous T-cell epitope; measles virus F protein; MVF;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM interleukin releasing hormone; LHRH; contraceptive; anticancer;
KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
KM cholesterol ester transport protein; anti-arteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US13975.
XX
PR 20-JUN-1998; 98US-0100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI: 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus
XX
PS Claim 10; Page 62; 129pp; English.
XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesterol ester transport

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:36:13 ; Search time 34.96 Seconds
(without alignments)
21.518 Million cell updates/sec

Title: US-08-934-367-34

Perfect score: 111
Sequence: 1 LLLQMFGRPEHLVDFLOSL 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 134459

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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20: /SIDSI/gcgdata/geneseq/genesqp/AA1999.DAT: *
21: /SIDSI/gcgdata/geneseq/genesqp/AA2000.DAT: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111	100.0	22	20	Y13815
2	111	100.0	22	20	Y13821
3	107	96.4	22	20	Y13809
4	83	74.8	16	21	Y91229
5	79	71.2	16	21	Y91230
6	53	47.7	11	18	W24294
7	33	29.7	12	4	P30225
8	33	29.7	12	9	P80053
9	33	29.7	14	20	Y27814
10	32	28.8	21	19	W65690
11	32	28.8	22	20	Y19066
12	32	28.8	22	20	Y18812

13	32	28.8	22	20	Y18549
14	32	28.8	22	20	Y19320
15	31	27.9	12	20	Y32796
16	31	27.9	21	19	W65666
17	31	27.9	22	19	W65669
18	30	27.0	20	15	R61276
19	30	27.0	20	19	W41190
20	30	27.0	22	17	R95899
21	29	26.1	11	20	W99442
22	29	26.1	11	21	Y82915
23	29	26.1	13	18	W10883
24	29	26.1	19	16	W13199
25	29	26.1	19	19	W57353
26	29	26.1	20	16	R72269
27	29	26.1	20	21	Y59570
28	29	26.1	21	21	Y69793
29	28	25.2	9	19	W72564
30	28	25.2	10	15	Y38102
31	28	25.2	10	20	Y45670
32	28	25.2	13	19	W62713
33	28	25.2	14	13	R21617
34	28	25.2	15	19	W45817
35	28	25.2	15	19	W45612
36	28	25.2	21	18	W38080
37	28	25.2	22	20	Y19067
38	28	25.2	22	20	Y18813
39	28	25.2	22	20	Y18550
40	28	25.2	22	20	Y19321
41	28	25.2	22	20	W96827
42	27.5	24.8	16	17	R98414
43	27	24.3	9	17	R88341
44	27	24.3	12	16	R78515
45	27	24.3	12	18	W28864

ALIGNMENTS

RESULT 1
ID Y13815 standard; peptide; 22 AA.
XX
AC Y13815;
XX
DT 08-JUL-1999 (first entry)
XX
DE Rabbit CERP immunogenic fragment.
XX
KW CERP; cholesterol-ester transfer protein; recombinant DNA vaccine; HDL;
KW antibody production; cholesterol ester transfer; therapy;
KW high density lipoprotein; HDL cholesterol concentration;
KW pro-atherogenic dyslipoproteinaemia.
XX
OS Oryctolagus sp.
XX
PN W09915655-A1.
XX
PD 01-APR-1999.
XX
PE 17-SEP-1998; 98MO-US19366.
XX
PR 19-SEP-1997; 97US-0934367.
XX
PA (MONS) MONSANTO CO.
XX
PI Glenn K. Needleman P;
XX
DR WPI; 1999-276984/23.
XX
PT New recombinant DNA vaccines
XX
PS Disclosure; Page 75; 99pp; English.
XX

KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 OS Homo sapiens.
 XX
 XX
 PN W09924836-A1.
 XX
 PD 20-MAY-1999.
 XX
 PF 04-NOV-1998; 98WO-US23435.
 XX
 PR 17-NOV-1997; 97US-0066100.
 PR 07-NOV-1997; 97US-0064900.
 PR 07-NOV-1997; 97US-0064908.
 PR 07-NOV-1997; 97US-0064911.
 PR 07-NOV-1997; 97US-0064912.
 PR 07-NOV-1997; 97US-0064983.
 PR 07-NOV-1997; 97US-0064984.
 PR 07-NOV-1997; 97US-0064985.
 PR 07-NOV-1997; 97US-0064987.
 PR 07-NOV-1997; 97US-0064988.
 PR 17-NOV-1997; 97US-0066090.
 PR 17-NOV-1997; 97US-0066094.
 PR 17-NOV-1997; 97US-0066095.
 PR 17-NOV-1997; 97US-0066089.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Carter KC, Ebner R, Endress GA, Feng P, Janat F;
 PI Kyaw H, Lafleur DW, Moore PA, Ni J, Olsen HS, Rosen CA;
 PI Ruben SM, Shi Y, Soppet DR, Wei Y;
 XX
 DR WPI: 1999-337740/28.
 DR N-PSDB: X85016.
 XX
 PT New human secreted proteins and coding sequences useful for treating
 PT disorders of the immune system and hyperproliferative disorders
 XX
 PS Disclosure: Page 119; 507pp; English.
 XX
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. X84924) for increasing the stability of the fused protein
 CC as compared to the human protein only.
 CC The invention relates to 125 novel genes and their fragments (nucleic
 CC acid sequences: X84933-X85057; amino acid sequences Y27567-Y27933) which
 CC are useful for preventing, treating or ameliorating medical conditions
 CC e.g. by protein or gene therapy. Also, pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the 125 polynucleotides, based on
 CC which tissues they are most highly expressed in (see X84933 for described
 CC uses).
 CC
 XX
 SQ Sequence 14 AA:

Query Match 24.6%; Score 33; DB 20; Length 14;
 Best Local Similarity 61.5%; Pred. No. 52;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 14 PEHLVDFLOSL 26
 | | | | | | | | | |
 Db 1 phsrsvflqsls 13

Search completed: December 21, 2000, 08:38:46
 Job time: 150 sec

QY 11 FGPEHLVDFLQSL 26
 ID 1 ffgfphlvdfllqsls 16

RESULT 11
 W24294 standard; peptide; 11 AA.

W24294;

17-OCT-1997 (first entry)

Human/Rabbit CERP common peptide.

Immune response; high density lipoprotein; HDL; cholesterol; human; serum; epitope; cholesterol ester transfer protein; CERP; rabbit.

Oryctolagus cuniculus.
 Homo sapiens.

W09639168-A1.

12-DEC-1996.

05-JUN-1996; 96MO-US09143.

06-JUN-1995; 95US-0482454.

(IMMU-) IMMUNE RESPONSE CORP.

Brostoff SW, Carlo DJ, Kwoh DY;

WPI; 1997-042849/04.

Stimulating an immune response to increase high density lipoprotein
 - avoids repeated administration of toxic drugs to lower cholesterol
 ester transfer protein levels

Claim 5; Page 16; 26pp; English.

The sequences given in W24292-94 were used in the method of the
 invention to stimulate an immune response to increase high density
 lipoprotein (HDL) cholesterol in a mammal exhibiting low levels of
 serum HDL. These peptides represent immunogenic epitopes of
 cholesterol ester transfer protein (CERP). The method utilizes
 the body's own immune system to lower CERP levels, thereby increasing
 the level of beneficial HDL cholesterol, preferably in serum. The
 method avoids the problems associated with the repeated administration
 of drugs which have undesirable side effects. This peptide represents
 a region of CERP which is common to both human and rabbit proteins.

Sequence 11 AA;

Query Match 39.6%; Score 53; DB 18; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.035;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLVDLFLQSL 26
 ID 1 hllvdfllqsls 11

RESULT 12
 Y12067 standard; Protein; 25 AA.

Y12067;

18-JUN-1999 (first entry)

XX

Human 5' EST secreted protein SEQ ID NO: 380.

Human; secreted protein; EST; expressed sequence tag; diagnosis;

forensic; gene therapy; chromosome mapping; signal peptide;

upstream regulatory sequence; cytokine activity; cell proliferation;

differentiation; haematopoiesis regulation; tissue growth regulation;

reproductive hormone regulation; chemotactic; haemostatic;

thrombolytic; anti-inflammatory; tumour inhibition.

Homo sapiens.

W09906554-A2.

11-FEB-1999.

31-JUL-1998; 98MO-IB01238.

01-AUG-1997; 97US-0905134.

(GEST) GENSET.

Duclet A, Dumas Milne Edwards J, Lacroix B;

WPI; 1999-153784/13.

N-PSDB; X40900.

New nucleic acids encoding human secreted proteins - obtained from

cDNA libraries prepared from kidney, fetal kidney, dystrophic

muscle, muscle and heart tissue

Claim 34; Page 500-501; 622pp; English.

X40826 to X41093 represent 5' expressed sequence tags (ESTs) for human
 secreted proteins, and encode the proteins given in X01602 and
 X11994 to X12260, respectively. The proteins given represent the signal
 peptide and an N-terminal fragment of a secreted protein. The nucleic
 acid sequences can be used for producing secreted human gene products.
 They can also be used to develop products for diagnosis and therapy.
 The proteins obtained may have cytokine activity, cell
 proliferation/differentiation activity, haematopoiesis regulating
 activity, tissue growth regulating activity, reproductive hormone
 regulating activity, chemotactic/chemokine activity, haemostatic and
 thrombolytic activity, receptor/ligand activity, anti-inflammatory
 activity, tumour inhibition activity or other activities. The products
 can be used in forensic, gene therapy and chromosome mapping procedures.
 The sequences can also be used for obtaining corresponding promoter
 sequences. The nucleic acids encoding the signal peptide can be used
 for directing extracellular secretion of a polypeptide or the insertion
 of a polypeptide into a membrane, or importing a polypeptide into
 a cell.

Sequence 25 AA;

Query Match 25.4%; Score 34; DB 20; Length 25;

Best Local Similarity 50.0%; Pred. No. 69;

Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 9 MDPGPEHLVDFLQSL 26
 ID 1 mggjaesflcnflvsls 18

RESULT 13
 P30225 standard; Protein; 12 AA.

P30225;

25-MAY-1992 (first entry)

Sequence of interferon (HuIFN) -alpha-61A around amino acid 40.

CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell mediated immune
CC response, resulting in production of antibodies against a target antigen.
CC Th can replace carrier proteins and pathogen-derived T helper epitopes.
CC Sequence Y91121 represents a promiscuous T helper epitope from the
CC measles virus F (MVF) protein and sequences Y91122-Y91142, Y91226 and
CC Y91245-Y91246 represent synthetic Th epitopes based on the MVF Th
CC epitope. Sequence Y91143 represents a promiscuous Th epitope from
CC hepatitis B virus (HBV) surface antigen, and sequences Y91144-Y91155 are
CC synthetic epitopes derived from this HBV epitope. Y91156-Y91196,
CC Y91227 and Y91242-Y91244 are antigenic peptides comprising an LHRH
CC sequence joined to a promiscuous Th epitope. Y91197 is the LHRH target
CC antigenic peptide used in these LHRH antigenic peptides. Y91200 is
CC somatostatin, and Y91201-Y91207 are antigenic peptides comprising
CC somatostatin and a Th epitope. Somatostatin immunogens may be used
CC to promote growth in livestock. Y91208 is a human CD4 CDR2-like domain
CC antigenic site, and Y91209-Y90211 are MVF Th epitope/CD4 CDR2
CC antigenic peptides which may be used to prevent HIV infection of T
CC cells. Y90212 is a modified version of a human IGE (immunoglobulin
CC E) CH3 domain, and Y90213-Y90219 are Th epitope/IGE CH3 antigenic
CC peptides which may be used in the treatment of allergies. Y91220 is
CC a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid
CC protein and Y91221-Y91222 comprise this peptide and a Th epitope. Y91223
CC is a Plasmodium falciparum circumsporozoite (CS) target antigen, and
CC Y91224-Y91225 comprise the CS antigen and an MVF Th epitope and may be
CC used in a malaria vaccine. Y91228-Y91231 represent CERP-derived peptides
CC and Y91232-Y91241 are immunogens comprising a CERP peptide and a Th
CC epitope which may be used to prevent or treat arteriosclerosis and
CC cardiovascular disease. Y91247 and Y91252-Y91257 are HIV-1 neutralising
CC B-cell epitopes, and Y91248-Y91251 and Y91258-Y91273 are antigenic
CC peptides comprising MVF Th and HIV-1 B-cell epitope which may be used as
CC a component in an anti-HIV-1 vaccine. Y91198 and Y91199 are respectively
CC an immunostimulatory Invasin protein epitope from Yersinia species, and
CC hinge spacer peptide, both of which may optionally be used in the
CC antigenic peptides of the invention.

Sequence 16 AA:

Query Match 61.9%; Score 83; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FGFPEHLVDFLOSLSS 26
| | | | | | | | | | | | | | | | | |
Db 1 fgtpehlvdfloslss 16

RESULT 10
Y91230
ID Y91230 standard; peptide: 16 AA.

XX Y91230;

22-MAY-2000 (first entry)

Human cholesterol transport protein (CETP) peptide, SEQ ID NO:108.

CC Promiscuous T-cell epitope: measles virus F protein; MVF;
CC hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
CC luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
CC somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
CC foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;
CC Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
CC cholesterol ester transport protein; anti-arteriosclerotic.

OS Homo sapiens.

PN WO9666957-A2.

XX 29-DEC-1999.

PF 21-JUN-1999; 99NO-US13975.
XX
PR 20-JUN-1998; 9805-0100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX

PI Wang CY;

DR WPI: 2000-160564/14.

PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus

PS Claim 10; Page 62; 129p; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesterol ester transport
CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria) for cancer
CC immunotherapy, for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration; for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell mediated immune
CC response, resulting in production of antibodies against a target antigen.
CC Th can replace carrier proteins and pathogen-derived T helper epitopes.
CC Sequence Y91121 represents a promiscuous T helper epitope from the
CC measles virus F (MVF) protein and sequences Y91122-Y91142, Y91226 and
CC Y91245-Y91246 represent synthetic Th epitopes based on the MVF Th
CC epitope. Sequence Y91143 represents a promiscuous Th epitope from
CC hepatitis B virus (HBV) surface antigen, and sequences Y91144-Y91155 are
CC synthetic epitopes derived from this HBV epitope. Y91156-Y91196,
CC Y91227 and Y91242-Y91244 are antigenic peptides comprising an LHRH
CC sequence joined to a promiscuous Th epitope. Y91197 is the LHRH target
CC antigenic peptide used in these LHRH antigenic peptides. Y91200 is
CC somatostatin, and Y91201-Y91207 are antigenic peptides comprising
CC somatostatin and a Th epitope. Somatostatin immunogens may be used
CC to promote growth in livestock. Y91208 is a human CD4 CDR2-like domain
CC antigenic site, and Y91209-Y90211 are MVF Th epitope/CD4 CDR2
CC antigenic peptides which may be used to prevent HIV infection of T
CC cells. Y90212 is a modified version of a human IGE (immunoglobulin
CC E) CH3 domain, and Y90213-Y90219 are Th epitope/IGE CH3 antigenic
CC peptides which may be used in the treatment of allergies. Y91220 is
CC a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid
CC protein and Y91221-Y91222 comprise this peptide and a Th epitope. Y91223
CC is a Plasmodium falciparum circumsporozoite (CS) target antigen, and
CC Y91224-Y91225 comprise the CS antigen and an MVF Th epitope and may be
CC used in a malaria vaccine. Y91228-Y91231 represent CERP-derived peptides
CC and Y91232-Y91241 are immunogens comprising a CERP peptide and a Th
CC epitope which may be used to prevent or treat arteriosclerosis and
CC cardiovascular disease. Y91247 and Y91252-Y91257 are HIV-1 neutralising
CC B-cell epitopes, and Y91248-Y91251 and Y91258-Y91273 are antigenic
CC peptides comprising MVF Th and HIV-1 B-cell epitope which may be used as
CC a component in an anti-HIV-1 vaccine. Y91198 and Y91199 are respectively
CC an immunostimulatory Invasin protein epitope from Yersinia species, and
CC hinge spacer peptide, both of which may optionally be used in the
CC antigenic peptides of the invention.

Sequence 16 AA:

Query Match 59.0%; Score 79; DB 21; Length 16;
Best Local Similarity 93.8%; Pred. No. 5.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

PI Glenn K, Needleman P;
XX
DR WPI; 1999-276984/23.
XX
PT New recombinant DNA vaccines
XX
PS Disclosure: Page 88; 99pp; English.
XX
CC This sequence represents an immunogenic fragment of the human
CC cholesteryl ester transferase protein (CETP).
CC The invention relates to recombinant DNA vaccines that contain DNA
CC encoding CETP, which can be used for producing antibodies to lessen the
CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
CC method can provide an autogenous immunological process for lessening the
CC transfer of cholesteryl esters from HDL particles and for increasing the
CC HDL cholesterol concentration of a mammal whose blood also contains
CC CETP. The method may be useful in treating human pro-atherogenic
CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC method can have an effect that lasts for months as compared to the
CC short-term effects of the small molecule drugs now available.
XX
SQ Sequence 22 AA;

Query Match 82.8%; Score 111; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLQMDFGPEHLVDFLOSLS 26
Db 1 LLLQMDGfphkllvdfllqsls 22
|||||

RESULT 8
Y13809
ID Y13809 standard; peptide: 22 AA.
XX
AC Y13809;
XX
DT 08-JUL-1999 (first entry)
XX
DE Rabbit CETP immunogenic fragment.
XX
KM CETP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
KM antibody production; cholesteryl ester transfer; therapy;
KW high density lipoprotein; HDL cholesterol concentration;
KW pro-atherogenic dyslipoproteinaemia.
XX
OS Oryctolagus sp.
XX
PN WO9915655-A1.
XX
PD 01-APR-1999.
XX
PF 17-SEP-1998; 98WO-US19366.
XX
PR 19-SEP-1997; 97US-0934367.
XX
PA (MONS) MONSANTO CO.
XX
PI Glenn K, Needleman P;
XX
DR WPI; 1999-276984/23.
XX
PT New recombinant DNA vaccines
XX
PS Example 1; Page 73; 99pp; English.
XX
CC This sequence represents an immunogenic fragment of the rabbit
CC cholesteryl ester transferase protein (CETP).
CC The invention relates to recombinant DNA vaccines that contain DNA
CC encoding CETP, which can be used for producing antibodies to lessen the
CC transfer of cholesteryl esters from high density lipoprotein (HDL). The

CC method can provide an autogenous immunological process for lessening the
CC transfer of cholesteryl esters from HDL particles and for increasing the
CC HDL cholesterol concentration of a mammal whose blood also contains
CC CETP. The method may be useful in treating human pro-atherogenic
CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC method can have an effect that lasts for months as compared to the
CC short-term effects of the small molecule drugs now available.
XX
SQ Sequence 22 AA;

Query Match 79.9%; Score 107; DB 20; Length 22;
Best Local Similarity 95.5%; Pred. No. 4.3e-10;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLQMDFGPEHLVDFLOSLS 26
Db 1 LLLQMDGfphkllvdfllqsls 22
|||||

RESULT 9
Y91229
ID Y91229 standard; peptide: 16 AA.
XX
AC Y91229;
XX
DT 22-MAY-2000 (first entry)
XX
DE Human cholesteryl transport protein (CETP) peptide, SEQ ID NO:107.
XX
KM Promiscuous T-cell epitope; measles virus F protein; MVF;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KM cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO9966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US13975.
XX
PR 20-JUN-1998; 98US-0100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus
XX
PS Claim 10; Page 50; 129pp; English.
XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration); for promoting the growth of animals; or for

CC epitope. Sequence Y91143 represents a promiscuous Th epitope from
 CC hepatitis B virus (HBV) surface antigen, and sequences Y91144-Y91155 are
 CC synthetic epitopes derived from this HBV epitope. Y91156-Y91196.
 CC Y91227 and Y91242-Y91244 are antigenic peptides comprising an LHRH
 CC sequence joined to a promiscuous Th epitope. Y91197 is the LHRH target
 CC antigenic peptide used in these LHRH antigenic peptides. Y91200 is
 CC somatostatin, and Y91201-Y91207 are antigenic peptides comprising
 CC somatostatin and a Th epitope. Somatostatin immunogens may be used
 CC to promote growth in livestock. Y91208 is a human CD4 CDR2-like domain
 CC antigenic site, and Y91209-Y90211 are MVA Th epitope/CD4 CDR2
 CC antigenic peptides which may be used to prevent HIV infection of T
 CC cells. Y90212 is a modified version of a human IgE (immunoglobulin
 CC E) CH3 domain, and Y90213-Y90219 are Th epitope/IgE CH3 antigenic
 CC peptides which may be used in the treatment of allergies. Y91220 is
 CC a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid
 CC protein and Y91221-Y91222 comprise this peptide and a Th epitope. Y91223
 CC is a Plasmodium falciparum circumsporozoite (CS) target antigen, and
 CC Y91224-Y91225 comprise the CS antigen and an MVA Th epitope and may be
 CC used in a malaria vaccine. Y91228-Y91231 represent CERP-derived peptides
 CC and Y91232-Y91241 are immunogens comprising a CERP peptide and a Th
 CC epitope which may be used to prevent or treat arteriosclerosis and
 CC cardiovascular disease. Y91247 and Y91252-Y91257 are HIV-1 neutralising
 CC B-cell epitopes, and Y91248-Y91251 and Y91258-Y91273 are antigenic
 CC peptides comprising MVA Th and HIV-1 B-cell epitope which may be used as
 CC a component in an anti-HIV-1 vaccine. Y91198 and Y91199 are respectively
 CC an immunostimulatory invasive protein epitope from *Yersinia* species, and
 CC hinge spacer peptide, both of which may optionally be used in the
 CC antigenic peptides of the invention.
 CC Note: Sequence Y91227 is also designated SEQ ID NO:106 in the
 CC specification.

XX SQ Sequence 26 AA:

Query Match 100.0%; Score 134; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.9e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLQLQMDFGPEHLVDFLOSL 26
 ||||||||||||||||||||
 Db 1 rdgflqlqmdfgpehlvdflosls 26

RESULT 4
 ID Y13802 standard; peptide: 26 AA.
 XX
 AC Y13802;

DT 08-JUL-1999 (first entry)

DE Rabbit CERP immunogenic fragment.

XX CERP: cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 KM antibody production; cholesteryl ester transfer; therapy;
 KW high density lipoprotein; HDL cholesterol concentration;
 XX pro-atherogenic dyslipoproteinaemia.

OS *Oryctolagus* sp.

PN WO915655-A1.

PD 01-APR-1999.

PF 17-SEP-1998; 98WO-US19366.

PR 19-SEP-1997; 97US-0934367.

PA (MONS) MONSANTO CO.

PI Glenn K, Needleman P;

DR WPI; 1999-276984/23.

XX New recombinant DNA vaccines
 PT
 XX
 PS Claim 15; Page 94; 99pp; English.

CC This sequence represents an immunogenic fragment of the rabbit
 CC cholesteryl ester transferase protein (CERP).
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CERP, which can be used for producing antibodies to lessen the
 CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
 CC transfer of cholesteryl esters from HDL particles and for lessening the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CERP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.

XX SQ Sequence 26 AA:

Query Match 87.3%; Score 117; DB 20; Length 26;
 Best Local Similarity 92.0%; Pred. No. 1.5e-11;
 Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 DGFLLQMDFGPEHLVDFLOSL 26
 ||||||||||||||||||||
 Db 2 dgclllqmdfgpehlvdflosls 26

RESULT 5
 ID Y91231 standard; peptide: 26 AA.
 XX
 AC Y91231;

DT 22-MAY-2000 (first entry)

DE Human cholesteryl transport protein (CERP) peptide, SEQ ID NO:109.

XX Promiscuous T-cell epitope; measles virus F protein; MVA;
 KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KM interleukin hormone releasing hormone; LHRH; contraceptive; anticancer;
 KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; PMDV;
 KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KM Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
 KM cholesteryl ester transport protein; anti-arteriosclerotic.

OS *Homo sapiens*.

PN WO966957-A2.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US13975.

PR 20-JUN-1998; 98US-0100412.

PA (UNBT-) UNITED BIOMEDICAL INC.

PI Wang CY;

PD WPI; 2000-160564/14.

PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus

PS Claim 10; Page 62; 129pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:36:16 ; Search time 26.24 Seconds
(without alignments)
33.881 Million cell updates/sec

Title: US-08-934-367-29

Perfect score: 134
Sequence: 1 RDGFLLLQMDFGFPEHLLVDFLOSLIS 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 143201

Minimum DB seq length: 0

Maximum DB seq length: 26

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36.*
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3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT.*
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21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134	100.0	26	17	W06128 Human cholesteryl
2	134	100.0	26	20	Rabbit CETP immuno
3	134	100.0	26	21	Human cholesteryl
4	117	87.3	26	20	Human cholesteryl
5	117	87.3	26	21	Human cholesteryl
6	111	82.8	22	20	Human CETP immuno
7	111	82.8	22	20	Human CETP immuno
8	107	79.9	22	20	Human CETP immuno
9	83	59.0	16	21	Human cholesteryl
10	79	59.0	16	21	Human cholesteryl
11	53	39.6	11	18	Human/Rabbit CETP
12	34	25.4	25	20	Human 5' EST seque

13	33	24.6	12	4	P30225	Sequence of Interf
14	33	24.6	12	9	P80053	Sequence of human
15	33	24.6	14	20	V27814	Human secreted pro
16	33	24.6	21	18	M38080	PPPI motif contai
17	33	24.6	24	18	M22196	Endogenous TCR alp
18	32	23.9	21	19	M65690	Fibronectin bindin
19	32	23.9	22	20	V19066	lecithin:cholester
20	32	23.9	22	20	V18812	lecithin:cholester
21	32	23.9	22	20	V18549	lecithin:cholester
22	32	23.9	22	20	V19320	lecithin:cholester
23	31	23.1	12	20	V32796	Mammalian prolacti
24	31	23.1	21	19	M65666	Fibronectin bindin
25	31	23.1	22	19	M65669	Peptide #13. Synt
26	30	22.4	17	21	V68335	Amyotrophic latera
27	30	22.4	20	15	R61276	Transactivating pr
28	30	22.4	20	19	RA1190	Tax protein fragme
29	30	22.4	22	17	R95899	Fragment #4 of 7-a
30	29	21.6	10	19	W78506	SH2 domain binding
31	29	21.6	11	20	W99442	Interleukin-2 rece
32	29	21.6	11	21	V82915	Peptide exhibiting
33	29	21.6	13	18	M10883	Mab anti-HBsAg bin
34	29	21.6	19	16	M13199	Fragment of p53 bl
35	29	21.6	19	19	W57353	Human MBP immuno
36	29	21.6	20	16	R72269	Glutamic acid deca
37	29	21.6	20	20	W73610	Human myelin basic
38	29	21.6	20	21	V85547	Human MBP peptide
39	29	21.6	20	21	V59570	GAD65 fragment, pe
40	29	21.6	21	21	V69793	Human Interleukin-
41	29	21.6	23	20	V27486	E. coli beta-subun
42	29	21.6	24	20	V13053	Human secreted pro
43	29	21.6	25	20	V42791	Human sulphonamide
44	29	21.6	25	20	W90234	Human sulphonamide
45	28.5	21.3	20	20	V10894	Amino acid sequenc

ALIGNMENTS

RESULT 1
W06128
ID W06128 standard; Peptide; 26 AA.
XX
AC W06128;
XX
DT 07-FEB-1997 (first entry)
XX
DE Human cholesteryl ester transfer protein C-terminal B-cell epitope.
XX
KW Cholesteryl ester transfer protein; CETP; antigen; vaccine;
KW cardiovascular disease; atherosclerosis; B-cell epitope.
XX
OS Homo sapiens.
XX
PN W09634888-AA.
XX
PD 07-NOV-1996.
XX
PF 01-MAY-1996; 96WO-US06147.
XX
PR 01-MAY-1995; 95US-0432483.
XX
PA (TCEL-) T CELL SCI INC.
XX
PI Rittershaus CW, Thomas LJ;
XX
DR WPI; 1996-506103/50.
XX
PT Cholesteryl ester transfer protein B cell epitope linked to T cell
PT epitope used to generate vaccine to regulate CETP activity for
PT decreasing the risk of developing a cardiovascular disease e.g.
PT atherosclerosis
XX
PS Claim 5; Page 41; 72pp; English.

not used as antigen
they applied for patent

Db 1 IVGVKQA 9

RESULT 7
ID 004817 PRELIMINARY; PRT; 19 AA.
AC 004817;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE HYPOTHETICAL 2.3 KDA PROTEIN (FRAGMENT).
OS Sporobolus stipitanus.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
RN Magnoliophyta; Liliopsida; Poales; Poaceae; Sporobolus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RA Blomstedt C.K., Gianello R.D., Neale A.D., Hamill J.D., Gaff D.F.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y10781; CAA71753.1; .
KM Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 19 AA: 2270 MW: 4C644625813F244E CRC64;

Query Match 25.5%; Score 26; DB 10; Length 19;
Best Local Similarity 27.3%; Pred. No. 7.8e+02;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 QEIFQEVVGGF 11
|:::|:|
Db 1 OKLYDDLTSGF 11

RESULT 8
ID 09R424 PRELIMINARY; PRT; 20 AA.
AC 09R424;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE AMBIENT-TEMPERATURE FIMBRITA; ATF.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
RN [1]
RP SEQUENCE.
RX MEDLINE: 94222573.
RA Messad G., Bahrani F.K., Mobley H.L.;
RT "Proteus mirabilis fimbriae: identification, isolation, and
characterization of a new ambient-temperature fimbriae";
RL Infect. Immun. 62:1989-1994(1994).
SQ SEQUENCE 20 AA: 2017 MW: B2FC481003883AE2 CRC64;

Query Match 25.5%; Score 26; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 8.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFPSQAQVTV 19
|:|:|:|
Db 4 GTPAPTEVTV 13

RESULT 9
ID 09UCA3 PRELIMINARY; PRT; 20 AA.
AC 09UCA3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE PROSTASIN (FRAGMENT).
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE: 94308140.
RA Yu J.X., Chao L., Chao J.;
RT "Prostasin is a novel human serine proteinase from seminal fluid.
purification, tissue distribution, and localization in prostate
gland.";
RL J. Biol. Chem. 269:18843-18848(1994).
DR INTERPRO: IPR001254; .
DR PFAM: PF00089; trypsin.1.
SQ SEQUENCE 20 AA: 2108 MW: EDF142A1F9F880FE CRC64;

Query Match 25.5%; Score 26; DB 4; Length 20;
Best Local Similarity 41.7%; Pred. No. 8.3e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VVGFPSSQAQVTV 18
|:|:|:|
Db 8 VAGQMPQVQVSI 19

RESULT 10
ID 09S8T0 PRELIMINARY; PRT; 20 AA.
AC 09S8T0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE JACALIN BETA-SUBUNIT.
OS Artocarpus champeden.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Rosales; Moraceae;
OC Artocarpus.
RN [1]
RP SEQUENCE.
RX MEDLINE: 93152601.
RA Ngoc L.D., Brillard M., Hoebeke J.;
RT "The alpha- and beta-subunits of the jacalins are cleavage products
from a 17-kDa precursor.";
RL Biochim. Biophys. Acta 1156:219-222(1993).
SQ SEQUENCE 20 AA: 2071 MW: 8D5AE975F4D0E212 CRC64;

Query Match 25.0%; Score 25.5; DB 10; Length 20;
Best Local Similarity 56.2%; Pred. No. 1e+03;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 3 IFQEVVGGFPSSQAQVTV 18
|:|:|:|
Db 6 ISQTVIVG-PWGAQVTV 20

RESULT 11
ID 09TWL4 PRELIMINARY; PRT; 18 AA.
AC 09TWL4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE 25 KDA CHYMOTRYPSIN-LIKE ENZYME (FRAGMENT).
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Calliphoridae; Lucilia.
RN [1]
RP SEQUENCE.
RX MEDLINE: 95219141.
RA Casu R.E., Pearson R.D., Jarney J.M., Cadogan L.C., Ridding G.A.,
Teillac R.L.;
RT "Excretory/secretory chymotrypsin from Lucilia cuprina: purification,

RT enzymatic specificity and amino acid sequence deduced from mRNA."
 RL Insect Mol. Biol. 3:201-211(1994).
 SQ SEQUENCE 18 AA; 1922 MW; 352EB0729B126B11 CRC64;

Query Match 24.5%; Score 25; DB 5; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 5 QEVVGGFPQ 14
 DB 6 EATVGGFPQ 15

RESULT 12
 006140 PRELIMINARY; PRT; 19 AA.
 AC 006140;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MAJOR OUTER MEMBRANE PROTEIN PL.16 (PORIN)(FRAGMENT).
 GN FORA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93116032.
 RA Wedge E., Daisey R., Gaugant D.A., Poolman J.T., Froholm L.O.;
 RT "Expression of an Inaccessible PL.7 subtype epitope on meningococcal
 RT class 1 proteins."
 RL J. Med. Microbiol. 38:23-28(1993).
 CC -I- SUBUNIT: MONOMER.
 DR EMBL: S51901; AAB24741.1; -
 KM Outer membrane; Antigen.
 FT NON_TER 1
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 1773 MW; AFAC572B037E0484 CRC64;

Query Match 24.5%; Score 25; DB 2; Length 19;
 Best Local Similarity 42.9%; Pred. No. 1.2e+03;
 Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 5 QEVVGGFPQAVT 18
 DB 2 QAANGAGSGVAVT 15

RESULT 13
 09R511 PRELIMINARY; PRT; 19 AA.
 AC 09R511;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE NITRILE HYDROLASE ALPHA SUBUNIT (FRAGMENT).
 OS Brevibacterium.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Micrococciaceae; Brevibacteriaceae.
 RN [1]
 RP SEQUENCE: 92407758.
 RX Duran R., Chion C.K., Bigey F., Arnaud A., Galzy P.;
 RT "The N-terminal amino acid sequences of Brevibacterium sp. R312
 RT nitrile hydratase."
 RL J. Basic Microbiol. 32:13-19(1992).
 SQ SEQUENCE 19 AA; 1923 MW; 84726D1A1282FB63 CRC64;

Query Match 24.5%; Score 25; DB 2; Length 19;
 Best Local Similarity 71.4%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 PSQAQVT 18
 DB 13 PAQAPVT 19

RESULT 14
 0908F7 PRELIMINARY; PRT; 18 AA.
 AC 0908F7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE PAIRED DOMAIN TRANSCRIPTIONAL FACTOR EX (FRAGMENT).
 GN EYELESS.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xu P.-X., Yoon A., Heaney S., Zhang X., Michelson A., Maas R.L.;
 RT "The regulation of Pax6 is conserved between mice and flies."
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF089733; AAD54001.1; -
 FT NON_TER 1
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1680 MW; 642A9C256071D610 CRC64;

Query Match 23.5%; Score 24; DB 5; Length 18;
 Best Local Similarity 66.7%; Pred. No. 1.6e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 VGGFPS 13
 DB 12 VGGIPA 17

RESULT 15
 062637 PRELIMINARY; PRT; 19 AA.
 AC 062637;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE XANTHINE DEHYDROGENASE (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN: SPRAGUE DAWLEY;
 RX MEDLINE: 94268906.
 RA Chow C.W., Clark M., Rinaldo J., Chalkley R.;
 RT "Identification of the rat xanthine dehydrogenase/oxidase promoter."
 RL Nucleic Acids Res. 22:1846-1854(1994).
 DR EMBL: U08123; AAB60444.1; -
 FT NON_TER 1
 FT NON_TER 19
 FT VARIANT 19
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 2128 MW; A02841D686F50139 CRC64;

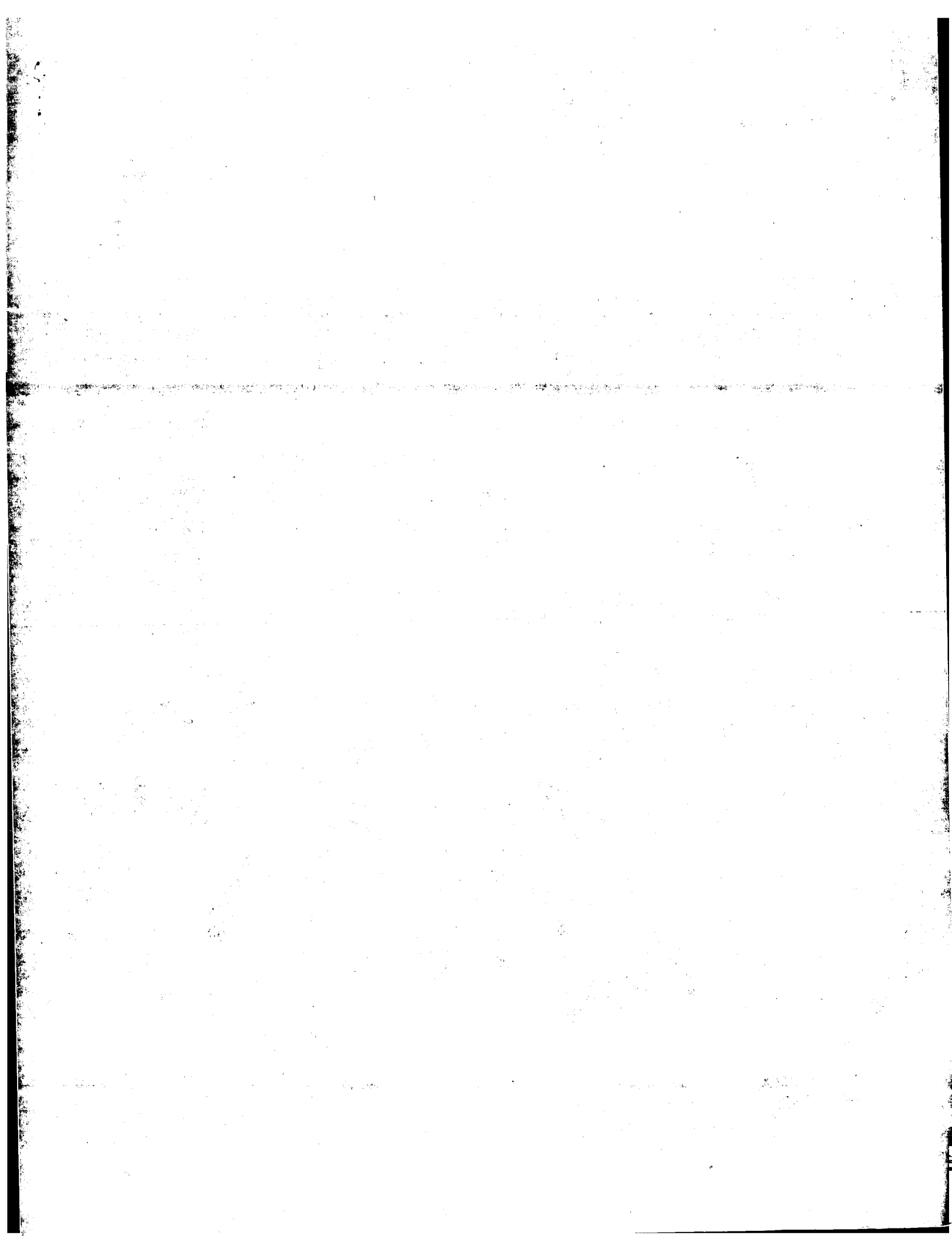
Query Match 23.5%; Score 24; DB 11; Length 19;
 Best Local Similarity 28.6%; Pred. No. 1.7e+03;
 Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 QETFGVGGFPQ 14
 DB 4 EELQSVGAGLAE 17

Thu Dec 21 08:51:23 2000

Search completed: December 21, 2000, 08:35:40
Job time: 603 sec

us-08-934-367-32.rspt



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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:31:50 ; Search time 59.91 Seconds
(Without alignments)
3.355 Million cell updates/sec

Title: US-08-934-367-33
Perfect score: 107
Sequence: 1 VVWFLFPDPDQHSVATYF 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761166 residues

Total number of hits satisfying chosen parameters: 87906

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/Backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	31.8	10	3	US-08-159-339A-935 Sequence 935, App
2	31	29.0	20	1	US-08-440-861-11 Sequence 11, Appl
3	30	28.0	10	3	US-08-159-339A-1076 Sequence 1076, Ap
4	30	28.0	14	1	US-08-483-021-3 Sequence 3, Appl
5	30	28.0	20	2	US-08-468-540B-1 Sequence 1, Appl
6	30	28.0	20	2	US-08-606-639A-5 Sequence 5, Appl
7	30	28.0	20	3	US-08-297-395-14 Sequence 14, Appl
8	29	27.1	13	3	US-08-974-775-12 Sequence 12, Appl
9	29	27.1	14	3	US-08-974-775-11 Sequence 11, Appl
10	28	26.2	10	3	US-08-974-775-39 Sequence 39, Appl
11	27	25.2	13	3	US-08-159-339A-558 Sequence 558, App
12	27	25.2	13	4	US-08-221-580-7 Sequence 7, Appl
13	27	25.2	15	2	PCT-US95-04018-69 Sequence 69, Appl
14	27	25.2	15	2	US-08-432-871C-73 Sequence 73, Appl
15	26.5	24.8	20	1	US-07-678-974D-8 Sequence 8, Appl
16	26.5	24.8	20	2	US-08-945-168-13 Sequence 13, Appl
17	26	24.3	8	3	US-08-159-339A-1049 Sequence 1049, Ap
18	26	24.3	8	3	US-08-925-002-49 Sequence 49, Appl
19	26	24.3	11	2	US-08-540-388-1 Sequence 1, Appl
20	26	24.3	12	1	US-07-778-233B-23 Sequence 23, Appl
21	26	24.3	12	1	US-07-963-321-23 Sequence 23, Appl
22	26	24.3	12	1	US-08-290-641-23 Sequence 23, Appl
23	26	24.3	12	1	US-08-548-540-23 Sequence 23, Appl
24	26	24.3	12	4	PCT-US96-09809-23 Sequence 23, Appl
25	26	24.3	13	1	US-08-469-005A-13 Sequence 13, Appl
26	26	24.3	13	1	US-08-188-426-7 Sequence 7, Appl
27	26	24.3	13	1	US-08-469-009-7 Sequence 7, Appl
28	26	24.3	13	2	US-08-469-007-7 Sequence 7, Appl

ALIGNMENTS

29	26	24.3	13	3	US-08-974-775-16	Sequence 16, Appl
30	26	24.3	13	3	US-08-462-331-8	Sequence 8, Appl
31	26	24.3	13	5	5194425-9	Patent No. 5194425
32	26	24.3	14	3	US-08-974-775-15	Sequence 15, Appl
33	26	24.3	18	2	US-08-951-871-10	Sequence 10, Appl
34	26	24.3	19	2	US-08-482-142-80	Sequence 80, Appl
35	26	24.3	19	2	US-08-613-225-6	Sequence 6, Appl
36	26	24.3	19	2	US-08-478-572-80	Sequence 80, Appl
37	25.5	23.8	20	2	US-08-107-676-21	Sequence 21, Appl
38	25	23.4	4	5	5425936-4	Patent No. 5425936
39	25	23.4	4	5	5433940-1	Patent No. 5433940
40	25	23.4	5	1	US-08-022-381A-12	Sequence 12, Appl
41	25	23.4	5	1	US-08-475-827A-12	Sequence 12, Appl
42	25	23.4	5	5	5196404-17	Patent No. 5196404
43	25	23.4	5	5	5433940-22	Patent No. 5433940
44	25	23.4	7	1	US-08-482-880-32	Sequence 32, Appl
45	25	23.4	7	2	US-08-273-274-32	Sequence 32, Appl

RESULT 1
US-08-159-339A-935
Sequence 935, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Cells, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159, 339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926, 666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027, 746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103, 396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 935:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-935

Query Match 31.8%; Score 34; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 4;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 9 RPDQSHSVAY 18
1111111111
DB 1 QPKQYDVSY 10

RESULT 2

US-08-440-861-11
; Sequence 11, Application US/08440861
; Patent No. 5710126
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.
; APPLICANT: Kuo, Mei-Chang
; APPLICANT: Luqman, Mohammad
; TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
; TITLE OF INVENTION: ALLEGEN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,861
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,016
; FILING DATE: 31-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-075 (IMI-040cp)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; US-08-440-861-11

Query Match 29.0%; Score 31; DB 1; Length 20;
Best Local Similarity 46.2%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 6 LPPRPDOHSHVAY 18
1111111111
DB 3 LIPKLDPTAYDVAY 15

RESULT 3

US-08-159-339A-1076
; Sequence 1076, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA

COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/159,339A

FILING DATE: 29-NOV-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/926,666

FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/027,746

FILING DATE: 05-MAR-1993

APPLICATION NUMBER: US 08/103,396

FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-005030US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 1076:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-159-339A-1076

Query Match 28.0%; Score 30; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 RPDQSHSVAY 18
1111111111
DB 1 RPSQRHSGSKY 10

RESULT 4

US-08-483-021-3
; Sequence 3, Application US/08483021
; Patent No. 5734023
; GENERAL INFORMATION:
; APPLICANT: Nag, Bishwajit
; APPLICANT: Clark, Brian R.
; APPLICANT: Sharma, Suresh
; APPLICANT: McConnell, Harden
; TITLE OF INVENTION: MHC Subunit Conjugates Useful in
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California

COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,021
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/210,594
FILING DATE: 23-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/367,751
FILING DATE: 21-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,840
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/690,840
FILING DATE: 23-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,938
FILING DATE: 19-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,946
FILING DATE: 18-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,072
FILING DATE: 03-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,533
FILING DATE: 02-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14058-16-1-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "Xaa = N-acetyl alanine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..14
OTHER INFORMATION: /note= "rat myelin basic protein"
OTHER INFORMATION: peptide analog of MBP(1-14)4-A"
US-08-483-021-3

Query Match 28.0%; Score 30; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 RPDQHSVAY 18
|||:|
DB 5 RPSQRHGSKY 14

RESULT 5
US-08-468-540B-1
; Sequence 1, Application US/08468540B

Patent No. 5858980
GENERAL INFORMATION:
APPLICANT: Weiner, Howard
APPLICANT: Haffler, David
APPLICANT: Miller, Ariel
APPLICANT: Al-Sabbagh, Ahmad
TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P.C.
STREET: 805 Third Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,540B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H
REGISTRATION NUMBER: 32,140
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5858980e
US-08-468-540B-1

Query Match 28.0%; Score 30; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 RPDQHSVAY 18
|||:|
DB 5 RPSQRHGSKY 14

RESULT 6
US-08-606-639A-5
; Sequence 5, Application US/08606639A
; Patent No. 5939400
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Waisman, Ari
; TITLE OF INVENTION: DNA VACCINATION FOR INDUCTION OF
; TITLE OF INVENTION: SUPPRESSIVE T CELL RESPONSE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,639A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A-63005/PJS STAN-187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-606-639A-5

Query Match 28.0%; Score 30; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 RPDOQHSVAY 18
| | | | |
DB 5 RPSORHGSKY 14

RESULT 7
US-08-297-395-14
Sequence 14, Application US/08297395A
Patent No. 6039947
GENERAL INFORMATION:
APPLICANT: Howard L. Weiner
APPLICANT: David A. Hafler
TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
FILE REFERENCE: 1010/057230S3
CURRENT APPLICATION NUMBER: US/08/297,395A
EARLIER FILING DATE: 1994-08-11
EARLIER APPLICATION NUMBER: 08/059,189
EARLIER FILING DATE: 1993-05-06
EARLIER APPLICATION NUMBER: 07/502,559
EARLIER FILING DATE: 1990-03-30
EARLIER APPLICATION NUMBER: PCT/US88/02139
EARLIER FILING DATE: 1988-06-24
EARLIER APPLICATION NUMBER: 07/065,734
EARLIER FILING DATE: 1987-06-24
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 14
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-08-297-395-14

Query Match 28.0%; Score 30; DB 3; Length 20;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 RPDOQHSVAY 18
| | | | |
DB 5 RPSORHGSKY 14

RESULT 8
US-08-974-775-12
Sequence 12, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
APPLICANT: Walsh-Reitz, Margaret
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Plaza Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-12

Query Match 27.1%; Score 29; DB 3; Length 13;
Best Local Similarity 45.5%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 8 RPDOQHSVAY 18
| | | | |
DB 3 PYPQGNHEAY 13

RESULT 9
US-08-974-775-11
Sequence 11, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
APPLICANT: Walsh-Reitz, Margaret
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Plaza Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/974,775
: FILING DATE: 20-NOV-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Martin, Alice O.
: REGISTRATION NUMBER: 35,601
: REFERENCE/DOCKET NUMBER: 7814/27
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-321-4200
: TELEFAX: 312-321-4299
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 14 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-974-775-11

```

Query Match	27.18;	Score 29;	DB 3;	Length 14
Best Local Similarity	45.58;	Pred. No. 44;		
Matches	5;	Conservative	0;	Mismatches 6;
				Index

QY	8	PRPDQHSVAY	18
Db	3	PRPGNHEAY	13

```

RESULT 10
US-08-974-775-39
Sequence 39, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
APPLICANT: Walsh-Reltz, Margaret
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIGONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Plaza Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35, 601
REFERENCE/DOCKET NUMBER: 7914/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

```

MOLECULE TYPE: peptide
US-08-974-775-39

Query Match	26.28;	Score 28;	DB 3;	Length 14;
Best Local Similarity	36.48;	Pred. No. 66;		
Matches	4;	Conservative	2;	Mismatches 5;
				Indels 0;
				Gaps 0;

```
QY      8 PRPDQQHSVAY 18
        | | : | : |
Db      3 PYEGNHSEASY 13
```

```

: RESULT 11
: US-08-159-339A-558
: Sequence 558, Application US/08159339A
: Patent No. 6037135
: GENERAL INFORMATION:
: APPLICANT: Kubo, Ralph T.
: APPLICANT: Grey, Howard M.
: APPLICANT: Sette, Alessandro
: APPLICANT: Celis, Esteban
: TITLE OF INVENTION: HLA Binding peptides and Their
: TITLE OF INVENTION: Uses
: NUMBER OF SEQUENCES: 1254
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/159, 339A
: FILING DATE: 29-NOV-1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/926,666
: FILING DATE: 07-AUG-1992
: APPLICATION NUMBER: US 08/027,746
: FILING DATE: 05-MAR-1993
: APPLICATION NUMBER: US 08/103,396
: FILING DATE: 06-AUG-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Weber, Ellen Lauver
: REGISTRATION NUMBER: 32,762
: REFERENCE/DOCKET NUMBER: 018623-005030US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: TELEX:
: INFORMATION FOR SEQ ID NO: 558:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-159-339A-558

```

Query Match	25.28;	Score 27;	DB 3;	Length 10;
Best Local Similarity	50.08;	Pred. NO. 67;		
Matches	4;	Conservative	2;	Mismatches 2;
				Indels 0;
				Gaps 0;

QY	7	FPRDQH	14
		:	1
Db	1	FYTPDKH	8

RESULT 12
US-08-221-580-7
; Sequence 7, Application US/08221580
; Patent No. 5519000
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszyński, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5519000r1s
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: United States of America
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,580
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; US-08-221-580-7

Query Match 25.28; Score 27; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 QOHSVAYTF 20
| | | : | |
Db 5 QSHSWPTTF 13

RESULT 13
PCT-US95-04018-69
; Sequence 69, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszyński, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESS: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; PCT-US95-04018-69

Query Match 25.28; Score 27; DB 4; Length 13;
Best Local Similarity 55.6%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 QOHSVAYTF 20
| | | : | |
Db 5 QSHSWPTTF 13

RESULT 14
US-08-432-871C-73
; Sequence 73, Application US/08432871C
; Patent No. 5877010
; GENERAL INFORMATION:
; APPLICANT: Loeb, Lawrence A.
; APPLICANT: Black, Margaret E.
; TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,871C
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMaisters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 240052.409C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900

Page 7

Page 7

Page 7

Page 7

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:30:07 ; Search time 112.59 Seconds
(without alignments)
11.273 Million cell updates/sec

Title: US-08-934-367-33

Perfect score: 107
Sequence: 1 VVWKLFRPPDOHSVAATF 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_65:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	25.2	12	2 S10059	tachykinin - Affric
2	27	25.2	12	2 JP0053	ribosomal protein
3	26	24.3	20	2 A54083	p190/210 fatty ac
4	25	23.4	14	2 A60770	cell surface alioa
5	25	23.4	15	2 PS0221	gastrin-releasing
6	25	23.4	15	2 A41436	alpha-macroglobuli
7	24	22.4	11	2 JN0023	substance P - chic
8	24	22.4	11	2 S23306	substance P - Atla
9	24	22.4	12	2 S47395	T-cell antigen rec
10	24	22.4	15	2 S29207	avenin gamma-4 - O
11	24	22.4	15	2 A28965	ribulose-bisphosph
12	24	22.4	17	2 B25348	UDPglucose-glycoq
13	24	22.4	19	2 S19613	globin - polychaet
14	24	22.4	19	2 S69166	ferredoxin b - Jap
15	24	22.4	20	2 JP0055	ribosomal protein
16	24	22.4	20	2 A34859	halothamine - Mex
17	23	21.5	9	2 A60108	exotoxin A - Strep
18	23	21.5	10	2 S19286	lek protein - poul
19	23	21.5	11	2 S78026	ribosomal protein
20	23	21.5	11	2 S33300	probable substance
21	23	21.5	11	2 S23308	substance P - rain
22	23	21.5	16	2 A60551	leukocyte elastase
23	23	21.5	20	2 A47105	hydroglycan - chi
24	22	20.6	7	4 I56685	hypothetical L2 pr
25	22	20.6	11	2 B60409	kassinin-like pept
26	22	20.6	11	2 C60409	kassinin-like pept
27	22	20.6	11	2 E60409	substance P-like p
28	22	20.6	14	2 S60353	amylopululanase -
29	22	20.6	18	2 A35704	cytochrome P450 O1

30	22	20.6	18	2 A42016	mammary-derived gr
31	22	20.6	19	2 JP0054	ribosomal protein
32	21	19.6	9	4 S15594	orf 1 rara 5'-regl
33	21	19.6	11	1 SPHO	substance P - hors
34	21	19.6	11	1 A60654	substance P - guin
35	21	19.6	12	2 S47391	T-cell antigen rec
36	21	19.6	15	2 S26515	T-cell receptor al
37	21	19.6	16	2 S57517	T cell receptor be
38	21	19.6	17	2 JH0785	DNA-directed RNA p
39	21	19.6	17	2 S05033	photosystem II pro
40	21	19.6	18	2 S55002	protein 1 - Legion
41	21	19.6	20	2 S18582	hypothetical prote
42	21	19.6	20	2 A56046	urinary tract ston
43	20	18.7	8	2 S66646	cardioacceleratory
44	20	18.7	10	1 XAV16B	angiotensin-conver
45	20	18.7	10	2 A61007	hementin (EC 3.4.-

ALIGNMENTS

RESULT 1
S10059
tachykinin - African tree frog (Kassina maculata)
N:Alternate names: hylambates-Kassinin
C:Species: Kassina maculata
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999
C:Accession: S10059
R:Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.
Biomed. Res. 2, 613-617, 1981
A:Title: New tachykinins, Gu2, Pro5-kassinin (hylambates-kassinin) and hylambactin, 1
A:Reference number: S07436
A:Accession: S10059
A:Molecule type: protein
A:Residues: 1-12 <YAS>
A:Experimental source: skin
A:Note: the source is designated as Hylambates maculatus
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 25.2%; Score 27; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PRPD 12
DB 3 PKPD 7

RESULT 2
JP0053
ribosomal protein L30 - Bacillus macerans (fragment)
C:Species: Bacillus macerans
C>Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
C:Accession: JP0053
R:Ochi, K.
Submitted to JRPD, February 1994
A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal
A:Reference number: JP0042
A:Accession: JP0053
A:Molecule type: protein
A:Residues: 1-20 <OCH>
C:Keywords: protein biosynthesis; ribosome

Query Match 25.2%; Score 27; DB 2; Length 20;
Best Local Similarity 35.7%; Pred. No. 2.5e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 VVWKLFRPPDOHS 15
DB 7 LVRSIDGRPEXORT 20

RESULT 3
A54083
p190/210, fatty acid synthase, p140ex02 strand exchange protein activator - fission yeast
C:Species: Schizosaccharomyces pombe
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
C:Accession: A54083
R:Kaslan, E.; Heyer, W.D.
J. Biol. Chem. 269, 14103-14110, 1994
A:Title: Schizosaccharomyces pombe fatty acid synthase mediates DNA strand exchange in vivo
A:Reference number: A54083; MUID:94245730
A:Accession: A54083
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <KAS>
A:Note: sequence extracted from NCBI backbone (NCBIRP:148744)
C:superfamily: yeast fatty-acid synthase

Query Match 24.4%; Score 26; DB 2; Length 20;
Best Local Similarity 36.4%; Pred. No. 3.7e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 9 RPDQHSVAT 19
||| : ||| :
Db 2 RPEVEQLAHT 12

RESULT 4
A60770
cell surface alloantigen gp60 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-Feb-1997
C:Accession: A60770
R:Schendendorf, D.; Yamaguchi, H.; Old, L.J.; Srivastava, P.K.
J. Immunol. 142, 1621-1625, 1989
A:Title: A novel heteromorphic human cell surface alloantigen, gp60, defined by a human
A:Reference number: A60770; MUID:89140352
A:Accession: A60770
A:Molecule type: protein
A:Residues: 1-14 <SCH>
C:Comment: This protein is an alloantigen in human populations but is not found on cells
C:Keywords: glycoprotein; polymorphism; surface antigen

Query Match 23.4%; Score 25; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 14 HSVAYT 19
||| : ||| :
Db 3 HSVSYT 8

RESULT 5
PS0221
gastrin-releasing peptide - laughing frog (fragment)
C:Species: Rana ridibunda (laughing frog)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 03-Mar-1995
C:Accession: PS0221
R:Conlon, J.M.; O'Harte, F.; Vaudry, H.
Biochem. Biophys. Res. Commun. 178, 526-530, 1991
A:Title: Primary structures of the bombesin-like neuropeptides in frog brain show that t
A:Reference number: PQ0177; MUID:91315477
A:Accession: PS0221
A:Molecule type: protein
A:Residues: 1-15 <CON>
A:Experimental source: brain
C:Keywords: neuropeptide

Query Match 23.4%; Score 25; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 PDQOH 14
||| : ||| :
Db 2 PSQOH 6

RESULT 6
A41436
alpha-macroglobulin - green sea turtle (fragment)
C:Species: Chelonia mydas (green sea turtle)
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 18-Jun-1993
C:Accession: A41436
R:Osada, T.; Sasaki, T.; Irai, A.
J. Biochem. 103, 212-217, 1988
A:Title: Purification and characterization of alpha-macroglobulin and ovomacroglobulin
A:Reference number: A41436; MUID:88227890
A:Accession: A41436
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <OSA>

Query Match 23.4%; Score 25; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VMVKELF 7
||| : ||| :
Db 8 VLVEFLF 14

RESULT 7
JN0023
substance P - chicken
C:Species: Gallus gallus (chicken)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997
C:Accession: JN0023
R:Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thin, L.
Regul. Pept. 20, 171-180, 1988
A:Title: [Arg3]substance P and neurokinin A from chicken small intestine.
A:Reference number: JN0023; MUID:88204263
A:Accession: JN0023
A:Molecule type: protein
A:Residues: 1-11 <CON>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; tachykinin
F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 22.4%; Score 24; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PRPDQ 12
||| : ||| :
Db 2 PRPDQ 6

RESULT 8
S23306
substance P - Atlantic cod
C:Species: Gadus morhua (Atlantic cod)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Feb-1999
C:Accession: S23306
R:Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A:Title: Substance-P-related and neurokinin-A-related peptides from the brain of the
A:Reference number: S23186; MUID:92289992
A:Accession: S23306
A:Molecule type: protein

A:Residues: 1-11 <JEN>
A:Experimental source: brain

C:Function:
A:Description: may play a physiological role in the regulation of cardiovascular and gas
A:Note: substance P is derived by post-translational processing of preprotachykinin A
C:Keywords: neuropeptide; amidated carboxyl end; tachykinin
F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match

Best Local Similarity 22.4%; Score 24; DB 2; Length 11;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 PRPDQ 12
1 1 1 1

Db 2 PRPDQ 6

RESULT 9

S47395
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47395
R:Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47395
A:Status: preliminary
A:Alternate names: CIP-1; coeliac immunoreactive protein 1
A:Molecule type: mRNA
A:Residues: 1-12 <LEH>
A:Cross-references: EMBL:Z55715; NID:9527525; PIDN:CAA84784.1; PID:9527526
C:Keywords: T-cell receptor

Query Match

Best Local Similarity 22.4%; Score 24; DB 2; Length 12;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 13 QHSVATPF 20
1 1 1 1 1 1 1 1

Db 5 QGSGYVTF 12

RESULT 10

S29207
Aventin gamma-4 - oat (fragment)
N:Alternate names: CIP-1; coeliac immunoreactive protein 1
C:Species: Avena sativa (oat)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
R:Roche, A.; Collia, F.; Ortiz, M.L.; Mendez, E.
FEBS Lett. 310, 37-40, 1992
A:Title: Identification of the three major coeliac immunoreactive proteins and one alpha
A:Reference number: S29207; MUID:92405739
A:Accession: S29207
A:Molecule type: protein
A:Residues: 1-15 <ROC>
A:Experimental source: endosperm
C:Superfamily: gliadin
C:Keywords: prolamin; seed

Query Match

Best Local Similarity 22.4%; Score 24; DB 2; Length 15;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 PRPDQ 13
1 1 1 1 1 1 1 1

Db 7 PYPDQ 12

RESULT 11

A28965
ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - spinach (fragments)
C:Species: Spinacia oleracea (spinach)
C:Date: 22-Dec-1988 #sequence_revision 22-Dec-1988 #text_change 23-Feb-1997
C:Accession: A28965
R: Mulligan, R.M.; Houtz, R.L.; Tolbert, N.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 1513-1517, 1988
A:Title: Reaction-Intermediate analogue binding by ribulose biphosphate carboxylase/
cetylated proline.
A:Reference number: A28965; MUID:88144466
A:Accession: A28965
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <MUL>
C:Keywords: carbon-carbon lyase; carboxy-lyase; chloroplast

Query Match

Best Local Similarity 22.4%; Score 24; DB 2; Length 15;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 KFLPPRPD 11
1 1 1 1 1

Db 6 KFEFPAMD 13

RESULT 12

B25348
UDPglucose--glycogen glucosyltransferase (EC 2.4.1.11) P-2 peptide - rabbit (fragment)
N:Alternate names: UDPglucose-glycogen glucosyltransferase
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 06-Dec-1996
C:Accession: B25348
R:Wang, Y.; Bell, A.W.; Hermodson, M.A.; Roach, P.J.
J. Biol. Chem. 261, 16909-16915, 1986
A:Title: Liver isozyme of rabbit glycogen synthase. Amino acid sequences surrounding
A:Reference number: A92570; MUID:87057401
A:Accession: B25348
A:Molecule type: protein
A:Residues: 1-17 <WAN>
C:Function:
A:Description: catalyzes the alpha-1,4-glucosylation of glycogen by UDPglucose produc
C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match

Best Local Similarity 22.4%; Score 24; DB 2; Length 17;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 LPPRP 10
1 1 1 1 1 1

Db 1 MPPRP 5

RESULT 13

S19613
globin - polychaete (Eudistylia vancouveri) (fragment)
C:Species: Eudistylia vancouveri
C:Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998
C:Accession: S19613
R:Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Timkovich, R.; Wall, J.S.; Kapp, J.
Mol. Biol. 222, 1109-1129, 1991
A:Title: Hierarchy of globin complexes. The quaternary structure of the extracellular
A:Reference number: S19532; MUID:92106333
A:Accession: S19613
A:Molecule type: protein
A:Residues: 1-19 <QAB>
A:Experimental source: plume
C:Complex: dodecamers, each consisting of a trimer of tetramers of globin chains; dode
C:Keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier

Query Match 22.4%; Score 24; DB 2; Length 19;
 Best Local Similarity 71.4%; Pred. No. 7.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 QOHSVAY 18
 |||
 Db 12 QOWSMAY 18

RESULT 14

S69166
 ferredoxin b - Japanese radish (fragments)
 C:Species: Kaikware daikon (Japanese radish)
 C>Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
 C:Accession: S69166
 R:Odata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shln, M.
 Arch. Biochem. Biophys. 316, 797-802, 1995
 A:Title: Four ferredoxins from Japanese radish leaves.
 A:Reference number: S69164; MUID:95168867
 A:Accession: S69166
 A:Molecule type: protein
 A:Residues: 1-19 <OBA>
 C:Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match 22.4%; Score 24; DB 2; Length 19;
 Best Local Similarity 28.6%; Pred. No. 7.6e+02;
 Matches 4; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 3 VKFLFPPDOQHSV 16
 |||
 Db 5 VKFIRPTHEEDM 18

RESULT 15

JP0055
 ribosomal protein L30 - Bacillus polymyxa (fragment)
 C:Species: Bacillus polymyxa
 C>Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
 C:Accession: JP0055
 R:Ochl, K.
 submitted to JIPID, February 1994
 A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pr
 A:Reference number: JP0042
 A:Accession: JP0055
 A:Molecule type: protein
 A:Residues: 1-20 <OCH>
 C:Keywords: protein biosynthesis; ribosome

Query Match 22.4%; Score 24; DB 2; Length 20;
 Best Local Similarity 35.7%; Pred. No. 8.1e+02;
 Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 2 MVKFLFPPDOQHS 15
 :|:|
 Db 7 LVRSIGRPGTORT 20

Search completed: December 21, 2000, 08:30:08
 Job time: 272 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:32:59 ; Search time 62.7 Seconds
(without alignments)
10.191 Million cell updates/sec

Title: US-08-934-367-33
Perfect score: 107
Sequence: 1 VMWKLFPKPPDOHSAVYTF 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues
Total number of hits satisfying chosen parameters: 1086

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	27	25.2	1	TKN1_KASMA
2	25	23.4	15	ALB2_TRASC
3	24	22.4	11	TKNA_CHICK
4	24	22.4	11	TKNA_GADMO
5	24	22.4	18	GALS_SALTY
6	24	22.4	20	HELT_HELHO
7	23	21.5	11	TKNA_ONCMY
8	23	21.5	11	TKNA_SCYCA
9	22	20.6	11	TKN1_PSEGU
10	22	20.6	11	TKN2_PSEGU
11	22	20.6	11	CPAX_BOVIN
12	22	20.6	18	UPA3_HUMAN
13	21	19.6	9	TKNA_HORSE
14	21	19.6	11	TKNA_HORSE
15	21	19.6	13	ECDE_LYMDI
16	21	19.6	15	MK2A_PALPR
17	21	19.6	17	PSBL_SYNVU
18	21	19.6	16	PAR9_ASCSU
19	20	18.7	9	BP22_BOVJA
20	20	18.7	10	BP22_BOVJA
21	20	18.7	11	TKNA_RANCA
22	20	18.7	13	BP1_BOVJA
23	20	18.7	13	GER1_HORVU
24	20	18.7	17	SRY_URSAR
25	20	18.7	19	OXLA_OPHHA
26	20	18.7	20	ACPH_BOVIN
27	20	18.7	20	LEC3_ARTIN
28	19	17.8	5	PAP2_PAPMA
29	19	17.8	10	PAP3_PAPMA
30	19	17.8	11	BP3_BOVIN
31	19	17.8	11	BP4_BOVIN
32	19	17.8	11	BPB_AGRHA
33	19	17.8	12	TKN2_KASMA

34	19	17.8	12	1	TKN_KASSSE	P08611 kassina sen
35	19	17.8	13	1	GER2_HORVU	P28526 hordeum vul
36	19	17.8	13	1	YC1A_SALTY	P25944 salmoneia
37	19	17.8	15	1	MK1_PALPR	P80408 palomona pr
38	19	17.8	16	1	MK2B_PALPR	P80410 palomona pr
39	19	17.8	17	1	APID_BOMPA	P81464 bombus pasc
40	19	17.8	17	1	VALA_TRYB	P17961 trypanosoma
41	19	17.8	20	1	ALAT_PIG	P13191 sus scrofa
42	19	17.8	20	1	PYRAT_PYRAP	P37362 pyrrhocoris
43	18.5	17.3	18	1	HEM4_THETS	P80155 thermozon
44	18	16.8	10	1	UPA2_HUMAN	P30088 homo sapien
45	18	16.8	13	1	CRBL_ICASP	P17237 icarla sp.

ALIGNMENTS

RESULT 1
TKN1_KASMA STANDARD: PRT: 12 AA.

AC P08613.
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HYLAMABATES KASSININ (GLU(2)-PRO(5) KASSININ).
OS KASSINA maculata (African rhacophorid frog) (Hylambates maculatus).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Hyperoliidae;
OC KASSINA.
RN [1]
RP SEQUENCE.
RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.:
RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
RT hylambatin, in the skin of the African rhacophorid frog Hylambates
RT maculatus.";
RL Blomed. Res. 2:613-617(1981).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS.
CC EVOKE BEHAVIORAL RESPONSES. ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC DR PIR: S10059; S10059.
CC DR INTERPRO: IPR002040; -1-
CC DR PROSITE: PS00267; TACHYKININ: 1.
CC KW Tachykinin; Neuropeptide; Amidation; Amphibian skin.
CC FT MOD_RS 12
CC SO SEQUENCE 12 AA; 1376 MM; 3E756D279DD6DAB7 CRC64;

Query Match 25.2% Score 27; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 69;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PRPDQ 12
I:|I|I|
Db 3 PKPDQ 7

RESULT 2
ALB2_TRASC STANDARD: PRT: 15 AA.
AC P81189;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 68 KDA SERUM ALBUMIN (ALB-2) (FRAGMENT).
OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
RN [1]
RP SEQUENCE.
RA MEDLINE: 98103404.
RA Brown M.A., Chambers G.K., Licht P.;

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RT "Purification and partial amino acid sequences of two distinct
  albumins from turtle plasma."
RL Comp. Biochem. Physiol. 118B:367-374(1997).
CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
  BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
  BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
  COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC COLLOIDAL LOCATION: EXTRACELLULAR.
CC -1- SUBCELLULAR LOCATION: PLASMA.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC MISCELLANEOUS: IN THE RED-EARED SLIDER TURTLE, THERE ARE TWO FORMS
  OF ALBUMIN, ALB-1 AND ALB-2.
CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
DR INTERPRO: IPR000264;
CC PROSITE: PS00212; ALBUMIN, PARTIAL.
KW Plasma; Metal-binding; Lipid-binding; Albumin.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1733 MW; 487422B89FF73223 CRC64;

Query Match 23.4%; Score 25; DB 1; Length 15;
Best Local Similarity 30.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 11 DOOHVAATF 20
DB 3 DETHTGHXF 12

RESULT 3
TKNA.CHICK STANDARD; PRT; 11 AA.
AC P19850;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN (1)
RP SEQUENCE.
RC TISSUE=INTESTINE;
RX MEDLINE: 88204263.
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT "[Arg3]substance P and neurokinin A from chicken small intestine.";
RL Regl. Pept. 20:171-180(1988).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
  EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
  SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
  MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC PIR: JN0023; JN0023.
DR INTERPRO: IPR002040;
CC PROSITE: PS00267; TACHYKININ: 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11
RL MOL. Gen. Genet. 214:579-587(1988).
SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 22.4%; Score 24; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PRPDQ 12
DB 2 PRPDQ 6

RESULT 4
TKNA.GADMO STANDARD; PRT; 11 AA.
AC P28498;

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DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidae; Gadidae;
OC Gadus.
RN (1)
RP SEQUENCE.
RC TISSUE=BRAIN;
RX MEDLINE: 92298992.
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
  of the cod and trout.";
RL Eur. J. Biochem. 206:559-664(1992).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
  EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
  SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
  MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR INTERPRO: IPR002040;
CC PROSITE: PS00267; TACHYKININ: 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

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Query Match 22.4%; Score 24; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PRPDQ 12
DB 2 PRPDQ 6

RESULT 5
GALS.SALTY STANDARD; PRT; 18 AA.
AC P41030;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE MGL REPRESSOR AND GALACTOSE ULTRAINDUCTION FACTOR (FRAGMENT).
GN GALS.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
RN (1)
RP SEQUENCE FROM N.A..
RC STRAIN=LT2;
RX MEDLINE: 89112167.
RA Benner-Luger D., Boos W.;
RT "The mglB sequence of Salmonella typhimurium LT2; promoter analysis
  by gene fusions and evidence for a divergently oriented gene coding
  for the mgl repressor.";
RL Mol. Gen. Genet. 214:579-587(1988).
CC -1- FUNCTION: REPRESSOR OF THE MGL OPERON. BINDS GALACTOSE AND
  D-FUCOSE AS INDUCERS. GALS BINDS TO AN OPERATOR DNA SEQUENCE
  WITHIN ITS OWN CODING SEQUENCE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LACI FAMILY OF TRANSCRIPTIONAL
  REGULATORS.
CC STYGENE: SG10521; GALS.
DR INTERPRO: IPR00043;
CC PROSITE: PS00356; HTH_LACI_FAMILY; PARTIAL.
KW Transcription regulation; DNA-binding; Repressor.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2133 MW; 7AA77150FA49FB8B CRC64;

Query Match 22.4%; Score 24; DB 1; Length 18;

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Best Local Similarity 57.1%; Pred. No. 3.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 12 QOHSVAV 18
Db 3 RHISVAV 9

RESULT 6

HELT_HELHO STANDARD; PRT; 20 AA.
AC P4693;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE HELTHERMINE (FRAGMENT).
OS Heloderma horridum horridum (Mexican beaded lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
OC Heloderma.
RN [1]
RP SEQUENCE.
RC TISSUE-VENOM.
RA MEDLINE: 90260878.
RX Mochiz-Morales J., Martin B.M., Possani L.D.;
RT "Isolation and characterization of helothermine, a novel toxin from
RT Heloderma horridum horridum (Mexican beaded lizard) venom."
RL Toxicon 28:299-309(1990).
CC -1- FUNCTION: TOXIC TO MICE; INDUCES LETHARGY, PARTIAL PARALYSIS OF
CC REAR LIMBS AND LOWERING OF BODY TEMPERATURE, SUGGESTING THAT IT
CC MIGHT BE A HYPOTHERMIC TOXIN.
CC -1- MISCELLANEOUS: THE COMPLETE PROTEIN HAS AN APPARENT MW OF 25 KDA
CC AND A PI OF 6.8.
DR PIR: A34859; A34859.
KM TOXIN
FT NON_TER 20
SQ SEQUENCE 20 AA; 2156 MW; 91D62B36F7B4F940 CRC64;

Query Match 22.4%; Score 24; DB 1; Length 30;
Best Local Similarity 57.1%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 10 PDQHSV 16
Db 14 PDQTEI 20

RESULT 7

TKNA_ONCMY STANDARD; PRT; 11 AA.
AC P28499;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
RN [1]
RP SEQUENCE.
RC TISSUE-BRAIN.
RX MEDLINE: 92298992.
RJ Jensen J., Conlon J.M.;
RT "Substance P-related and neurokinin-A-related peptides from the brain
RT of the cod and trout."
RL Eur. J. Biochem. 206:659-664(1992).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR PIR: S23307; S23307.
DR PIR: S23308; S23308.
DR INTERPRO: IPR002040; -.
DR PROSITE: PS00267; TACHYKININ; 1.
RW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1358 MW; 214860DEC96D1F7 CRC64;

Query Match 21.5%; Score 23; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 8 PRPDQ 12
Db 2 PRPDQ 6

RESULT 8

TKNA_SCYCA STANDARD; PRT; 11 AA.
AC P41333;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE-BRAIN.
RX MEDLINE: 93292508.
RA Waugh D., Wang Y., Hazen N., Balmert R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance P-related
RT peptides from the brain of the dogfish, Scyliorhinus canicula."
RL Eur. J. Biochem. 214:469-474(1993).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC INTERPRO: IPR002040; -.
DR PIR: S33300; S33300.
DR PROSITE: PS00267; TACHYKININ; 1.
RW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1278 MW; 214860DEC96D867 CRC64;

Query Match 21.5%; Score 23; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 8 PRPDQ 12
Db 2 PRPDQ 6

RESULT 9

TKN1_PSEGU STANDARD; PRT; 11 AA.
AC P42986;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE KASSININ-LIKE PEPTIDE K-I (PG-KI).
OS Pseudophryne guentheri (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
RN [1]
RP SEQUENCE.

RP SEQUENCE.
RC TISSUE-SKIN.
RX MEDLINE: 90287814.
RA Sirmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RT Roberts J.D., Melchiorri P., Ersamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RL the Australian frog *Pseudophryne guntheri*.";
RL Peptides 11:299-304(1990).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: B60409; B60409.
DR INTERPRO: IPR002040; -.
DR PROSITE: PS00267; TACHYKININ.1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 1 11 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 11 AMIDATION.
SQ SEQUENCE 11 AA: 1269 MW: 3DBA7C37C9CB1AB7 CRC64;

Query Match 20.6%; Score 22; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 PRPDQ 12
1 11:
Db 2 PNPDE 6

RESULT 10
TKN2_PSEGU STANDARD; PRT; 11 AA.
AC P42987;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE KASSININ-LIKE PEPTIDE K-II (PG-KII).
OS Pseudophryne guntheri (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Pseudophryne.
RN [1]
RP SEQUENCE.
RC TISSUE-SKIN.
RX MEDLINE: 90287814.
RA Sirmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RT Roberts J.D., Melchiorri P., Ersamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RL the Australian frog *Pseudophryne guntheri*.";
RL Peptides 11:299-304(1990).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: C60409; C60409.
DR INTERPRO: IPR002040; -.
DR PROSITE: PS00267; TACHYKININ.1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 1 11 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 11 AMIDATION.
SQ SEQUENCE 11 AA: 1246 MW: 3A247C37C9CB1AB7 CRC64;

Query Match 20.6%; Score 22; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 PRPDQ 12
1 11:
Db 2 PNPDE 6

RESULT 11
TKN4_PSEGU STANDARD; PRT; 11 AA.
AC P42989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P-LIKE PEPTIDE I (PG-SP1).
OS Pseudophryne guntheri (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Pseudophryne.
RN [1]
RP SEQUENCE.
RC TISSUE-SKIN.
RX MEDLINE: 90287814.
RA Sirmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RT Roberts J.D., Melchiorri P., Ersamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RL the Australian frog *Pseudophryne guntheri*.";
RL Peptides 11:299-304(1990).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: E60409; E60409.
DR INTERPRO: IPR002040; -.
DR PROSITE: PS00267; TACHYKININ.1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 1 11 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 11 AMIDATION.
SQ SEQUENCE 11 AA: 1294 MW: 3A247C2CC9CB1AB7 CRC64;

Query Match 20.6%; Score 22; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 PRPDQ 12
1 11:
Db 2 PNPDE 6

RESULT 12
CPAX_BOVIN STANDARD; PRT; 18 AA.
AC P22779;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450 2A (OLF2) (OLFACTIVE) (P52) (EC 1.14.14.1) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RX MEDLINE: 91027757.
RA Lazard D., Tal N., Rubinstein M., Khen M., Lancel D., Zupko K.;
RT "Identification and biochemical analysis of novel olfactory-specific
RT cytochrome P-450IIA and UDP-glucuronosyl transferase.";
RL Biochemistry 29:7433-7440(1990).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR PIR: A35704; A35704.
 DR INTERPRO: IPR001128; -
 DR PROSITE: PS00086; CYTOCHROME_P450; PARTIAL.
 KW Microdredcylase; Monooxygenase; Electron transport; Membrane; Heme;
 RN Microsome; Endoplasmic reticulum; Olfaction.
 FT NON_TER 1 1
 FT VARIANT 6 6 G -> D.
 FT VARIANT 11 11 A -> E.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2058 MW; F80746F76CCD77FF CRC64;

Query Match 20.6%; Score 22; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 7.8e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 8 PRPDQ 13
 DB 5 PGPOQ 10

RESULT 13
 ID UPA3_HUMAN STANDARD; PRT; 9 AA.
 AC P30089;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 11) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RP SEQUENCE.
 RC TISSUE=PLASMA;
 RX MEDLINE: 93092937.
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquall C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjelqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing."
 RL Electrophoresis 13:707-714(1992).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.6, ITS MW IS: 46 KDA.
 DR SWISS-2DPAGE: P30089; HUMAN.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 19.6%; Score 21; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 8.8e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 LPRPD 11
 DB 3 LFPXTD 8

RESULT 14
 ID TKNA_HORSE STANDARD; PRT; 11 AA.
 AC P01290;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 GN TAC1 OR NKKA OR TAC2 OR NKA.
 OS Equus caballus (Horse), and Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 RP SEQUENCE.

RC SPECIES=HORSE;
 RA Studer R.O., Trececlak A., Lergier W.;
 RT "Isolation and amino acid sequence of substance P from horse
 RT intestine."
 RL Helv. Chim. Acta 56:860-866(1973).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C.PORCELLUS;
 RX MEDLINE: 90044685.
 RA Murphy R.;
 RT "Primary amino acid sequence of guinea-pig substance P."
 RL Neuropeptides 14:105-110(1989).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: A01558; SPPO.
 DR PIR: A60654; A60654.
 DR INTERPRO: IPR002040; -
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11
 SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 19.6%; Score 21; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 6.8e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 PRPDQ 12
 DB 2 PKPOQ 6

RESULT 15
 ID ECDE_LYMDI STANDARD; PRT; 13 AA.
 AC P80941;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE TESTIS ECDYSTROPHIN PEPTIDE E (TE).
 OS Lymantria dispar (Gypsy moth).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuidae; Lymantriidae; Lymantria.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=BRAIN;
 RX MEDLINE: 97387807.
 RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
 RA Bell R.A.;
 RT "Naturally occurring analogs of Lymantria testis ecdystrophin, a
 RT gonadotropin isolated from brains of Lymantria dispar pupae."
 RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
 CC -1- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
 CC OF LARVAE AND PUPAE.
 SQ SEQUENCE 13 AA; 1357 MW; 1841B4CA3275B764 CRC64;

Query Match 19.6%; Score 21; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 8.1e+02;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 8 PRPDQHS 15
 DB 5 PNPDPPDS 12

Search completed: December 21, 2000, 08:33:00
 Job time: 443 sec

Thu Dec 21 08:51:24 2000

us-08-934-367-33.rsp

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:35:40 ; Search time 157.2 Seconds
(without alignments)
11.880 Million cell updates/sec

Title: US-08-934-367-33

Perfect score: 107
Sequence: 1 VMVKFLFRPRDQHSVAYTF 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_14:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_undefined:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	31.8	17	3	006800
2	32	29.9	18	12	073487
3	30	28.0	19	12	09W9U1
4	30	28.0	20	12	09W1D2
5	29	27.1	18	12	073461
6	29	27.1	18	12	073463
7	29	27.1	18	12	073465
8	29	27.1	18	12	073467
9	29	27.1	18	12	073469
10	29	27.1	18	12	073471
11	29	27.1	18	12	073473
12	29	27.1	18	12	073475
13	29	27.1	18	12	073477
14	29	27.1	18	12	073479
15	29	27.1	18	12	073481
16	29	27.1	18	12	073483
17	29	27.1	18	12	073485
18	29	27.1	18	12	073489
19	29	27.1	18	12	073491

20	29	27.1	18	12	073493
21	29	27.1	18	12	073495
22	29	27.1	18	12	073497
23	29	27.1	18	12	073499
24	29	27.1	18	12	073501
25	29	27.1	18	12	073503
26	29	27.1	18	12	073505
27	29	27.1	18	12	073507
28	29	27.1	18	12	073509
29	29	27.1	18	12	073511
30	29	27.1	18	12	073513
31	29	27.1	18	12	073515
32	29	27.1	18	12	073519
33	29	27.1	18	12	073521
34	29	27.1	18	12	073525
35	29	27.1	18	12	073527
36	29	27.1	18	12	073529
37	28	26.2	14	12	089818
38	28	26.2	16	12	079458
39	28	26.2	19	12	090625
40	27	25.2	17	12	073531
41	27	25.2	17	12	073533
42	27	25.2	17	12	073535
43	27	25.2	17	12	073537
44	27	25.2	17	12	073539
45	27	25.2	17	12	073541

ALIGNMENTS

```

RESULT 1
ID 006800 PRELIMINARY; PRT; 17 AA.
AC 006800;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE N1780.
GN N1780.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96287653.
RA Nasr F., Becam A.M., Herbert C.J.;
RT "The sequence of 36.8 kb from the left arm of chromosome XIV reveals
RT 24 complete open reading frames: 18 correspond to new genes, one of
RT which encodes a protein similar to the human myotonic dystrophy
RT kinase."
RL Yeast 12:169-175(1996).
DR EMBL; X92517; CAA63292.1; -.
SQ SEQUENCE 17 AA; 2139 MW; BD7E9AFADF754AF CRC64;

Query Match 31.8%; Score 34; DB 3; Length 17;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 QOHSVAYT 19
DB 3 QOHSVCF 10

RESULT 2
ID 073487 PRELIMINARY; PRT; 18 AA.
AC 073487;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).

```

GN POL.
OC Human immunodeficiency virus type 1.
OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RA MEDLINE: 96242958.
RX Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovir. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RA Leigh Brown A.J.;
RX Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U45053; AAB04204.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
FT SEQUENCE 18 AA; 2191 MW; B36910F4583BA0C3 CRC64;

Query Match 29.9%; Score 32; DB 12; Length 18;
Best Local Similarity 38.5%; Pred. No. 63;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 MVKLFPPDOOH 14
DB 2 LTKWGFTTPDKH 14

RESULT 3
O9W901 ID 09W901 PRELIMINARY; PRT; 19 AA.
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GLYCOPROTEIN G (FRAGMENT).
GN USA.
OS Simian herpes B virus (Cercopithecoid herpesvirus 1) (Shbv).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-20620, 9400371, 7709642, 7709609;
RA Eberle R., Smith A., Black D.;
RT "Molecular evidence for distinct genotypes of monkey B virus
(Herpesvirus simiae) which are related to the Macaque host species."
RL J. Virol. 0:0-0(1998).
RU EMBL: AF082804; AAC34447.1; -.
DR EMBL: AF082812; AAC34111.1; -.
DR EMBL: AF082813; AAC34114.1; -.
DR EMBL: AF082814; AAC34117.1; -.
FT NON_TER 1 1
FT SEQUENCE 19 AA; 2220 MW; E585178F064B278B CRC64;

Query Match 28.0%; Score 30; DB 12; Length 19;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 9 RPDQHSVAVT 19
DB 2 RSPQSHRVRT 12

RESULT 4
O9WLD2 ID 09WLD2 PRELIMINARY; PRT; 20 AA.
AC 09WLD2;
DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GLYCOPROTEIN G (FRAGMENT).
GN USA.
OS Simian herpes B virus (Cercopithecoid herpesvirus 1) (Shbv).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-12930;
RA Eberle R., Smith A., Black D.;
RT "Molecular evidence for distinct genotypes of monkey B virus
(Herpesvirus simiae) which are related to the Macaque host species."
RL J. Virol. 0:0-0(1998).
DR EMBL: AF082808; AAC34459.1; -.
FT NON_TER 1 1
FT SEQUENCE 20 AA; 2377 MW; E58517E7DBAB278B CRC64;

Query Match 28.0%; Score 30; DB 12; Length 20;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 9 RPDQHSVAVT 19
DB 3 RSPQSHRVRT 13

RESULT 5
O73461 ID 073461 PRELIMINARY; PRT; 18 AA.
AC 073461;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE: 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovir. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RA Leigh Brown A.J.;
RX Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U45027; AAB04178.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
FT SEQUENCE 18 AA; 2219 MW; B36918D4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MVKLFPPDOOH 14
DB 2 LTKWGFTTPDKH 14

RESULT 6
O73463 ID 073463 PRELIMINARY; PRT; 18 AA.
AC 073463;
DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45029; AAB04180.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 18
SQ SEQUENCE 18 AA; 2219 MW; B36138D4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. NO. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MVKFLFPPDOOH 14
Db 2 LTRMGFTTPDKKH 14

RESULT 7
O73465 PRELIMINARY; PRT; 18 AA.
ID O73465;
AC O73465;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45031; AAB04182.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 18
SQ SEQUENCE 18 AA; 2219 MW; B36138D4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. NO. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MVKFLFPPDOOH 14
Db 2 LTRMGFTTPDKKH 14

RESULT 8
O73467 PRELIMINARY; PRT; 18 AA.
ID O73467;
AC O73467;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45033; AAB04184.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 18
SQ SEQUENCE 18 AA; 2219 MW; B36138D4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. NO. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MVKFLFPPDOOH 14
Db 2 LTRMGFTTPDKKH 14

RESULT 9
O73469 PRELIMINARY; PRT; 18 AA.
ID O73469;
AC O73469;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45035; AAB04186.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 18
SQ SEQUENCE 18 AA; 2219 MW; B36138D4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MKFLFPPDOOH 14
: : : : | | : : |
Db 2 LIRWGFTTPDKKH 14

RESULT 10

OY 073471 PRELIMINARY; PRT; 18 AA.
AC 073471;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients.";
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Leigh Brown A.J.;
RT Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45037; AAB04188.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2219 MW; B36138D4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MKFLFPPDOOH 14
: : : : | | : : |
Db 2 LIRWGFTTPDKKH 14

RESULT 11

OY 073473 PRELIMINARY; PRT; 18 AA.
AC 073473;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients.";
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Leigh Brown A.J.;
RT Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U45039; AAB04190.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2219 MW; B36138D4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MKFLFPPDOOH 14
: : : : | | : : |
Db 2 LIRWGFTTPDKKH 14

RESULT 12

OY 073475 PRELIMINARY; PRT; 18 AA.
AC 073475;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
immunodeficiency virus type 1-infected patients.";
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Leigh Brown A.J.;
RT Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45041; AAB04192.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2219 MW; B36138D4583BBFFE CRC64;

Query Match 27.1%; Score 29; DB 12; Length 18;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MKFLFPPDOOH 14
: : : : | | : : |
Db 2 LIRWGFTTPDKKH 14

RESULT 13

OY 073477 PRELIMINARY; PRT; 18 AA.
AC 073477;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human

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RT Immunodeficiency virus type 1-infected patients."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45043; AAB04194.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 18
FT SEQUENCE 18 AA; 2219 MW; B36910F4583BBFFE CRC64;
SQ

Query Match
Best Local Similarity 27.1%; Score 29; DB 12; Length 18;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MVKFLFPPDOOH 14
DB 2 LLRWGFTTPDKH 14

RESULT 14
O73479 PRELIMINARY; PRT; 18 AA.
ID O73479
AC O73479
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RL Immunodeficiency virus type 1-infected patients."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45043; AAB04196.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 18
FT SEQUENCE 18 AA; 2219 MW; B36910F4583BBFFE CRC64;
SQ

Query Match
Best Local Similarity 27.1%; Score 29; DB 12; Length 18;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MVKFLFPPDOOH 14
DB 2 LLRWGFTTPDKH 14

RESULT 15
O73481 PRELIMINARY; PRT; 18 AA.
ID O73481
AC O73481
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.

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OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RX MEDLINE; 96242958.
RA Cleland A., Watson H.G., Robertson P., Ludlam C.A., Brown A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RL Immunodeficiency virus type 1-infected patients."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74;
RA Leigh Brown A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45047; AAB04198.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1 18
FT SEQUENCE 18 AA; 2219 MW; B36910F4583BBFFE CRC64;
SQ

Query Match
Best Local Similarity 27.1%; Score 29; DB 12; Length 18;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 MVKFLFPPDOOH 14
DB 2 LLRWGFTTPDKH 14

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Search completed: December 21, 2000, 08:35:40
 Job time: 603 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:36:43 ; Search time 25.87 seconds
(without alignments)
14.254 Million cell updates/sec

Title: US-08-934-367-34

Perfect score: 111
Sequence: 1 LLLQMDGFPFHLVDFLQSL 22

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 92835

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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2: /cgn2_6/ptodata/2/laa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/2/laa/PCITUS.COMB.pep:*
5: /cgn2_6/ptodata/2/laa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	32	28.8	22 3 US-08-940-095-133	Sequence 133, App
2	32	28.8	22 3 US-08-940-093-133	Sequence 133, App
3	32	28.8	22 3 US-08-940-096-133	Sequence 133, App
4	30	27.0	20 1 US-08-199-508-2	Sequence 2, Appl
5	29	26.1	19 1 US-08-399-696-85	Sequence 85, Appl
6	29	26.1	20 2 US-08-484-530-22	Sequence 22, Appl
7	29	26.1	20 2 US-08-827-618A-22	Sequence 22, Appl
8	29	26.1	20 3 US-08-483-952A-22	Sequence 22, Appl
9	28	25.2	10 3 US-08-159-339A-401	Sequence 401, App
10	28	25.2	22 3 US-08-940-095-134	Sequence 134, App
11	28	25.2	22 3 US-08-940-093-134	Sequence 134, App
12	28	25.2	22 3 US-08-940-096-134	Sequence 134, App
13	27	24.3	9 2 US-08-765-783A-83	Sequence 83, Appl
14	27	24.3	15 3 US-08-596-257A-10	Sequence 10, Appl
15	27	24.3	15 3 US-08-860-339-10	Sequence 10, Appl
16	27	24.3	20 1 US-07-678-974D-8	Sequence 8, Appl
17	27	24.3	20 2 US-08-162-149-10	Sequence 10, Appl
18	27	24.3	20 2 US-08-945-168-13	Sequence 13, Appl
19	27	24.3	22 2 US-08-559-524A-12	Sequence 12, Appl
20	27	24.3	22 2 US-08-749-707-12	Sequence 12, Appl
21	26	23.4	7 1 US-07-923-724-47	Sequence 47, Appl
22	26	23.4	7 2 US-08-609-426A-47	Sequence 47, Appl
23	26	23.4	7 2 US-08-374-652C-37	Sequence 37, Appl
24	26	23.4	11 1 US-08-039-778B-6	Sequence 6, Appl
25	26	23.4	12 1 US-08-555-394-13	Sequence 13, Appl
26	26	23.4	12 1 US-08-745-892-13	Sequence 13, Appl
27	26	23.4	13 1 US-08-620-213-3	Sequence 3, Appl
28	26	23.4	16 1 US-08-346-455B-52	Sequence 52, Appl

29	26	23.4	16 3 US-08-977-221-52	Sequence 52, Appl
30	26	23.4	16 4 PCT-US95-06613-52	Sequence 52, Appl
31	26	23.4	17 1 US-08-620-213-1	Sequence 1, Appl
32	26	23.4	19 1 US-08-238-163-20	Sequence 20, Appl
33	26	23.4	19 1 US-07-977-696C-36	Sequence 36, Appl
34	26	23.4	19 1 US-08-129-930B-36	Sequence 36, Appl
35	26	23.4	22 1 US-08-039-778B-5	Sequence 5, Appl
36	25	22.5	6 1 US-08-487-006-76	Sequence 76, Appl
37	25	22.5	6 2 US-08-488-659A-76	Sequence 76, Appl
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39	25	22.5	8 3 US-08-434-831B-29	Sequence 29, Appl
40	25	22.5	10 2 US-08-318-157B-25	Sequence 25, Appl
41	25	22.5	11 1 US-08-039-778B-3	Sequence 3, Appl
42	25	22.5	13 3 US-09-140-149-21	Sequence 21, Appl
43	25	22.5	15 1 US-07-918-181A-17	Sequence 17, Appl
44	25	22.5	15 1 US-07-918-181A-21	Sequence 21, Appl
45	25	22.5	15 1 US-08-080-073-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-940-095-133
Sequence 133, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penie & Edmonds LLP
SREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6004925e
US-08-940-095-133

GENERAL INFORMATION:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage

COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,508
FILING DATE: February 18, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,536
FILING DATE: February 23, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5717058ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 121 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3322
TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
TOPOLOGY: unknown to applicant
MOLECULE TYPE: peptide
HYPOTHETICAL: yes
US-08-199-508-2

Query Match 27.0%; Score 30; DB 1; Length 20;
Best Local Similarity 38.5%; Pred. No. 63;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 7 EGFPEHLVDFLQ 19
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DB 1 EGFVYVFGDCVQ 13

RESULT 5
US-08-399-696-85
Sequence 85, Application US/08399696
Patent No. 5756569
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: P53-BINDING POLYPEPTIDES AND
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME
NUMBER OF SEQUENCES: 126
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,696
FILING DATE: 02-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/156,671
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15522-000710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-399-696-85

Query Match 26.1%; Score 29; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 87;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 11 EHLVDFL 18
||:|:|:|:
DB 12 EHLIDGL 19

RESULT 6
US-08-484-530-22
Sequence 22, Application US/08484530
Patent No. 5846740
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J.
APPLICANT: Kaufman, Mark G.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,530
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-8/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-530-22

Query Match 26.1%; Score 29; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 MDGPEHL 14
||:|:|:|:
DB 9 IDHYHNELL 18

RESULT 7
US-08-827-618A-22
Sequence 22, Application US/08827618A
Patent No. 5998366
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J.
APPLICANT: Kaufman, Mark G.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,618A
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,725
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-12/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-618A-22

Query Match 26.1%; Score 29; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 MDGFPPEHL 14
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Db 9 IDHYPNELL 18

RESULT 8
US-08-483-952A-22
; Sequence 22, Application US/08483952A
; Patent No. 6011139
; GENERAL INFORMATION:
; APPLICANT: Tobin, Allan J
; APPLICANT: Erlander, Mark G
; APPLICANT: Kautman, Daniel L
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,952A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,859
FILING DATE: 17-SEP-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-7/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-952A-22

Query Match 26.1%; Score 29; DB 3; Length 20;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 MDGFPPEHL 14
:|:|:|
Db 9 IDHYPNELL 18

RESULT 9
US-08-159-339A-401
; Sequence 401, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cells, Estepan
; TITLE OF INVENTION: H1A Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746

FILING DATE: 05-MAR-1993
 APPLICATION NUMBER: US 08/103,396
 FILING DATE: 06-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen Lauver
 REGISTRATION NUMBER: 32,762
 REFERENCE/DOCKET NUMBER: 018623-005030US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 TELEX:
 INFORMATION FOR SEQ ID NO: 401:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-159-339A-401

Query Match 25.2%; Score 28; DB 3; Length 10;
 Best Local Similarity 66.7%; Pred. No. 61;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPEHL 14
 :||||:
 Db 2 YPEHLV 7

RESULT 10
 US-08-940-095-134
 Sequence 134, Application US/08940095
 Patent No. 6004925
 GENERAL INFORMATION:
 APPLICANT: Dasseux, Jean-Louis
 APPLICANT: Sekul, Renate
 APPLICANT: Butner, Klaus
 APPLICANT: Cornut, Isabelle
 APPLICANT: Metz, Gunther
 APPLICANT: Dufourcq, Jean
 TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
 TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
 NUMBER OF SEQUENCES: 258
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036-2811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/940,095
 FILING DATE: 29-SEP-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 009196-0004-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-493-4935
 TELEFAX: 650-493-5556
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 134:
 SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 6004925e
 US-08-940-095-134

Query Match 25.2%; Score 28; DB 3; Length 22;
 Best Local Similarity 50.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 EHLVDPLQSLUS 22
 :|||||:
 Db 7 ERLLEDLKLALN 18

RESULT 11
 US-08-940-093-134
 Sequence 134, Application US/08940093
 Patent No. 6037323
 GENERAL INFORMATION:
 APPLICANT: Dasseux, Jean-Louis
 APPLICANT: Sekul, Renate
 APPLICANT: Butner, Klaus
 APPLICANT: Cornut, Isabelle
 APPLICANT: Metz, Gunther
 TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
 TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
 NUMBER OF SEQUENCES: 258
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036-2811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/940,093
 FILING DATE: 29-SEP-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 009196-0006-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-493-4935
 TELEFAX: 650-493-5556
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 134:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 6037323e
 US-08-940-093-134

Query Match 25.2%; Score 28; DB 3; Length 22;
 Best Local Similarity 50.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 EHLVDPLQSLUS 22
 :|||||:
 Db 7 ERLLEDLKLALN 18


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: APPLICATION NUMBER: US/08/596,257A
: FILING DATE: 08-FEB-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 4327165.0
: FILING DATE: 09-AUG-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Meilman, Edward A.
: REGISTRATION NUMBER: 24,735
: REFERENCE/DOCKET NUMBER: P/951-118
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 382-0700
: TELEFAX: (212) 382-0888
: TELEX: 236925
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: solanum tuberosum
: US-08-596-257A-10
    
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Query Match          24.3%  Score 27;  DB 3;  Length 15;
Best Local Similarity 30.8%  Pred. No. 1.4e+02;
Matches 4;  Conservative 5;  Mismatches 4;  Indels 0;  Gaps 0;
    
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Qy      2 LLOMDFGFPEHL 14
| | : | | : |
Db      1 LEQTNVGLPQQVI 13
    
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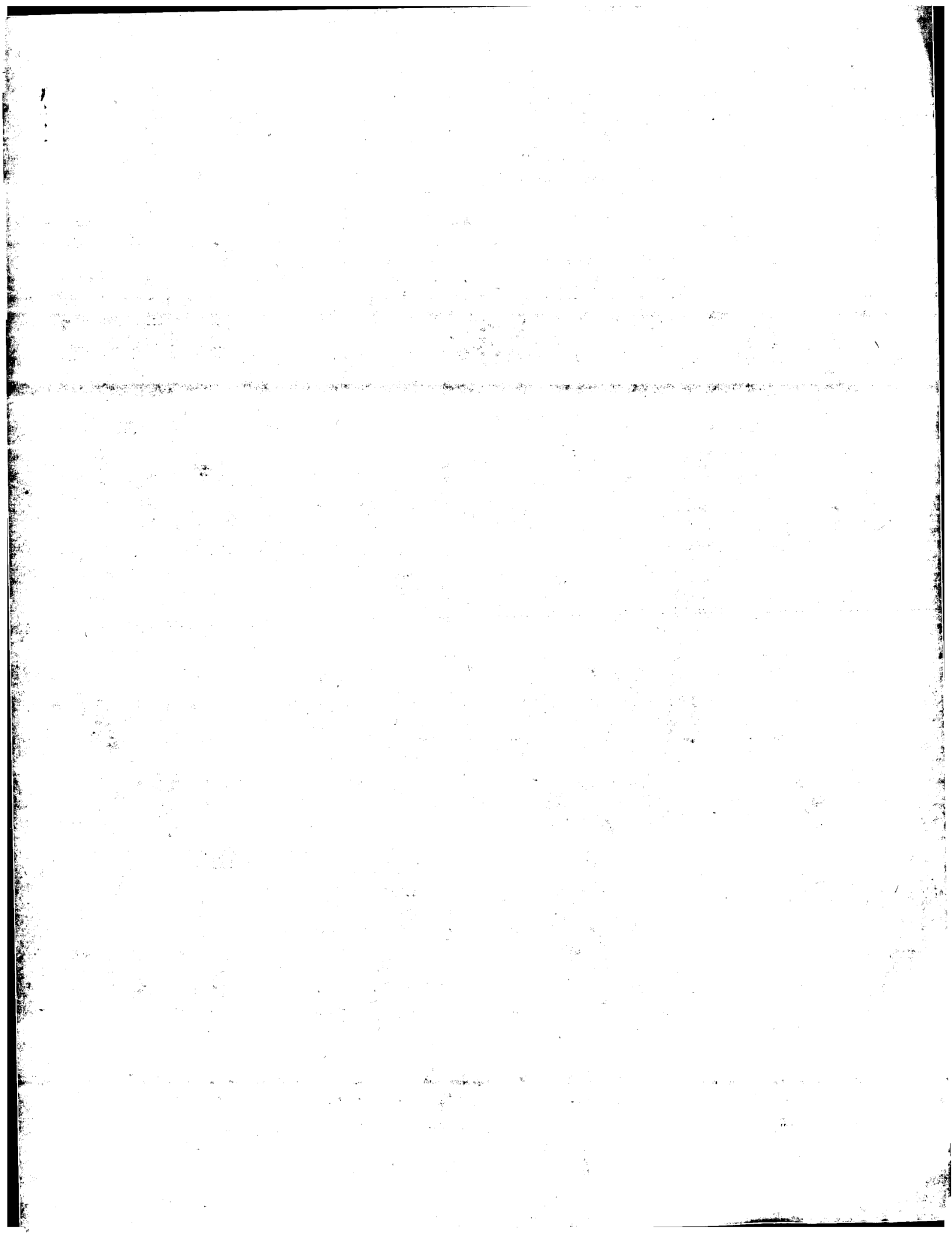
RESULT 15
US-08-860-339-10
: Sequence 10, Application US/08860339
: Patent No. 6117665
: GENERAL INFORMATION:
: APPLICANT: Kossmann, Jens
: APPLICANT: Emmertmann, Michael
: APPLICANT: Virgin, Ivar
: APPLICANT: Renz, Andreas
: TITLE OF INVENTION: DNA MOLECULES CODING FOR DEBRANCHING ENZYMES DERIVED
: FILE REFERENCE: AGREVO-6
: CURRENT APPLICATION NUMBER: US/08/860,339
: CURRENT FILING DATE: 1997-11-25
: EARLIER APPLICATION NUMBER: DE P4447387.7
: EARLIER FILING DATE: 1994-12-22
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 10
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Solanum tuberosum
: US-08-860-339-10
    
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Query Match          24.3%  Score 27;  DB 3;  Length 15;
Best Local Similarity 30.8%  Pred. No. 1.4e+02;
Matches 4;  Conservative 5;  Mismatches 4;  Indels 0;  Gaps 0;
    
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```

Qy      2 LLOMDFGFPEHL 14
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Db      1 LEQTNVGLPQQVI 13
    
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:37:13 ; Search time 26.84 Seconds
(without alignments)
52.017 Million cell updates/sec

Title: US-08-934-367-34

Perfect score: 111
Sequence: 1 LLLQMDFGFPEHLLVDFLOSL 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 4315

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.65:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	25.2	19	2 A39504	octamer-binding pr
2	27	24.3	21	2 A32521	hexokinase (EC 2.7
3	26	23.4	15	2 S59492	formate dehydrogen
4	25	22.5	15	2 S71306	heat shock protein
5	25	22.5	16	2 T44936	calmodulin kinase
6	24.5	22.1	14	2 B61597	cytochrome P450 AL
7	24	21.6	13	2 S03879	6-phosphofructokin
8	24	21.6	14	2 A01250	angiotensin precur
9	24	21.6	15	2 A60834	angiotensin I prec
10	24	21.6	17	2 B31769	cell receptor de
11	24	21.6	18	2 PN0175	glutathione transf
12	24	21.6	18	2 H75063	hypothetical prote
13	24	21.6	20	2 A37984	ADP,ATP carrier pr
14	23	20.7	7	2 S36662	demorphin (lys-7)
15	23	20.7	14	2 PA0015	seed storage prote
16	23	20.7	19	2 I46654	cell receptor de
17	23	20.7	21	2 T07683	proteinase inhibit
18	22	19.8	7	1 A61324	demorphin - Rohde
19	22	19.8	11	2 PT0250	ig heavy chain CRD
20	22	19.8	12	2 C36201	1-aminocyclopropan
21	22	19.8	14	2 A61002	photosystem II oxy
22	22	19.8	20	2 S72501	protein kinase C 1
23	22	19.8	20	2 A31049	calsequestrin, fas
24	22	19.8	20	2 S77989	cytochrome-c oxida
25	22	19.8	20	2 A47105	dystroglycan - chi
26	22	19.8	20	2 S50203	zona pellucida gly
27	22	19.8	21	2 PX0078	alanine dehydrogen
28	21	18.9	9	2 B45796	dihydroallopoamide S
29	21	18.9	2	2 B20569	serum amyloid P-co

30	21	18.9	14	2 PA0104	protein QP200070 -
31	21	18.9	15	2 PH1788	T cell receptor al
32	21	18.9	15	2 S72432	epoxypropan isomer
33	21	18.9	17	2 A60743	ornithine carbamoy
34	21	18.9	18	2 I49408	cytochrome-c oxida
35	21	18.9	19	2 B60822	cytochrome P450 UP
36	21	18.9	19	2 D32071	T-cell receptor de
37	21	18.9	20	2 A60822	cytochrome P450 PB
38	21	18.9	20	2 S07232	ribulose-bisphosph
39	21	18.9	20	2 H49034	nuclear antigen EB
40	21	18.9	20	2 S35921	T-cell receptor ga
41	21	18.9	20	2 A54077	cytochrome b558 -
42	21	18.9	22	2 B54397	ubiquitin-carrier
43	21	18.9	22	2 D56978	collagen alpha 1(I
44	20	18.0	9	2 I46023	growth hormone rec
45	20	18.0	12	2 S56122	type I DNA methylt

ALIGNMENTS

RESULT 1
A39504
octamer-binding protein, Ku-like, 72K chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: A39504
R:May, G.; Sutton, C.; Gould, H.
J. Biol. Chem. 266, 3052-3059, 1991
A:Title: Purification and characterization of Ku-2, an octamer-binding protein relate
A:Reference number: A39504; MUID:91131605
A:Accession: A39504
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <MAY>

Query Match 25.2% Score 28; DB 2; Length 19;
Best Local Similarity 71.4% Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LQMDFGF 9
DB 11 LEMDVGF 17

RESULT 2
A32521
hexokinase (EC 2.7.1.1) I peptide III - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 12-Apr-1995
C:Accession: A32521
R:Schlirch, D.M.; Wilson, J.E.
Arch. Biochem. Biophys. 257, 1-12, 1987
A:Title: Rat brain hexokinase: amino acid sequence at the substrate hexose binding si
A:Reference number: A30080; MUID:87324917
A:Accession: A32521
A:Molecule type: protein
A:Residues: 1-21 <SCH>
C:Superfamily: human hexokinase I; hexokinase homology
C:Keywords: ATP; glycolysis; phosphotransferase

Query Match 24.3% Score 27; DB 2; Length 21;
Best Local Similarity 50.0% Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 LQMDFGFPEH 12
DB 3 LGFTSFPEH 12

RESULT 3

S59492
Formate dehydrogenase alpha chain - Alcaligenes eutrophus (fragment)
C:Species: Alcaligenes eutrophus
C>Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C:Accession: S59492
R:Riedelbold, J.; Mayer, F.; Bill, E.; Trautwein, A.X.; Bowien, B.
Biol. Chem. Hoppe-Seyler 376, 561-568, 1995
A>Title: Structural and immunological studies on the soluble formate dehydrogenase from
A:Reference number: S59492; MUID:96145736
A:Accession: S59492
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <PRL>

Query Match 23.4%; Score 26; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 3.5e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 QMDGFP 10
:|||||
Db 6 EIDGTP 12

RESULT 4
S71306
heat shock protein 90 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C:Accession: S71306
R:Conconi, M.; Szewda, L.I.; Levine, R.L.; Stadtman, E.R.; Frignet, B.
Arch. Biochem. Biophys. 331, 232-240, 1996
A>Title: Age-related decline of rat liver multicatalytic proteinase activity and protect
A:Reference number: S71306; MUID:96299287
A:Accession: S71306
A:Molecule type: protein
A:Residues: 1-15 <CON>
A:Experimental source: liver
C:Keywords: heat shock; phosphoprotein; stress-induced protein

Query Match 22.5%; Score 25; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 10 PEHLVDFLQ 19
|:|:|:|:
Db 6 PDHPIVETLR 15

RESULT 5
T44936
calmodulin kinase 2 - fission yeast (Schizosaccharomyces pombe) (fragment)
C:Species: Schizosaccharomyces pombe
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T44936
R:Allemamy, V.; Allique, R.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z22873
A:Accession: T44936
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-16 <ALE>
A:Cross-references: EMBL:U57982; PIDN:AMD09466.1

Query Match 22.5%; Score 25; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FGFP 10
|||||
Db 5 FGFP 8

RESULT 6
B61597
cytochrome P450 AL-2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: B61597
R:Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.
Drug Metab. Dispos. 19, 291-297, 1991
A>Title: Purification and aminopyrine monooxygenase activity of liver microsomal cyto
A:Reference number: A61597; MUID:91292910
A:Accession: B61597
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SHR>

Query Match 22.1%; Score 24.5; DB 2; Length 14;
Best Local Similarity 47.1%; Pred. No. 5.7e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 5; Gaps 1;

QY 1 LLLQMDGFPPEHLVDF 17
|||:|:|:
Db 3 LLLSLSF-----LLVGF 14

RESULT 7
S03879
6-phosphofructokinase (EC 2.7.1.11) B - rabbit (fragment)
N:Alternate names: phosphofructo-1-kinase B
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 28-Apr-1993
C:Accession: S03879
R:Valaitis, A.P.; Foe, L.G.; Kwiatkowska, D.; Latshaw, S.P.; Kemp, R.G.
Biochim. Biophys. Acta 995, 187-194, 1989
A>Title: The sites of phosphorylation of rabbit brain phosphofructo-1-kinase by cycl
A:Reference number: S03878; MUID:89194250
A:Accession: S03879
A:Molecule type: protein
A:Residues: 1-13 <VAL>
A>Note: the sequence from the summary is inconsistent with that from table I and Fig.
C:Keywords: glycolysis; phosphotransferase

Query Match 21.6%; Score 24; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LQMDGFP 9
|:|:|:
Db 7 LSMDKGF 13

RESULT 8
A01250
angiotensin precursor - horse (fragment)
C:Species: Equus caballus (domestic horse)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 20-Mar-1998
C:Accession: A92775; A01250
R:Skeggis Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.
J. Exp. Med. 106, 439-453, 1957
A:Reference number: A92775
A:Accession: A92775
A:Molecule type: protein
A:Residues: 1-14 <SKE>
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; hormone; vasoconstrictor
F:1-10/Product: angiotensin I #status experimental <ANI>
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 21.6%; Score 24; DB 2; Length 14;

Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 PEHLV 15
1 ||||
Db 7 PEHLV 12

RESULT 9

A60834
angiotensin I precursor - dog (fragment)
N:Alternate names: angiotensinogen I
M:Contains: angiotensin I
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1998
C:Accession: A60834
R:Oliver, J.A.
Hypertension 11, 21-27, 1988
A:Title: Purification and partial characterization of canine angiotensinogen.
A:Reference number: A60834; MUID:88113996
A:Accession: A60834
A:Molecule type: protein
A:Residues: 1-15
C:Superfamily: antithrombin III
C:Keywords: glycoprotein; plasma
F:1-10/Product: angiotensin I status predicted <MAT>

Query Match 21.6%; Score 24; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 PEHLV 15
1 ||||
Db 7 PEHLV 12

RESULT 10

B31769
T-cell receptor delta-2 chain J region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 05-Nov-1999
C:Accession: B31769
R:Loth, E.Y.; Cwirla, S.; Serafini, A.T.; Phillips, J.H.; Lanier, L.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 9714-9718, 1988
A:Title: Human T-cell-receptor delta chain: genomic organization, diversity, and expression
A:Reference number: A94221; MUID:85071766
A:Accession: B31769
A:Molecule type: DNA
A:Residues: 1-17 <LOH>
A:Cross-references: GB:L36386; NID:g540455; PIDN:AAA61108.1; PID:g540456
C:Keywords: T-cell receptor

Query Match 21.6%; Score 24; DB 2; Length 17;
Best Local Similarity 37.5%; Pred. No. 8.6e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 LLLQDFGPEHLVD 16
1 : || : || : ||
Db 1 LTAOLFEGKGTOLIVE 16

RESULT 11

PN0175
glutathione transferase (EC 2.5.1.18) 1 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 22-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 15-Jun-1996
C:Accession: PN0175
R:Tsuigita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
submitted to JIPID, December 1995
A:Description: Two dimensional electrophoresis of plant proteins and standardization of
A:Reference number: PN0173

A:Accession: PN0175
A:Molecule type: protein
A:Residues: 1-18 <TSU>
A:Experimental source: leaf
C:Keywords: transferase

Query Match 21.6%; Score 24; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 DRGFP 10
1 ||||
Db 5 DRGFP 9

RESULT 12

H75063
hypothetical protein PAB7382 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: H75063
R:Anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: Insights into archaeal chromosome s
A:Reference number: A75001
A:Accession: H75063
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18 <RAM>
A:Cross-references: GB:A1248287; GB:AL096836; NID:g5458657; PIDN:CAB50405.1; PID:e151
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB7382

Query Match 21.6%; Score 24; DB 2; Length 18;
Best Local Similarity 35.7%; Pred. No. 9.2e+02;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 3 LQMDFGPEHLVD 16
1 : : : ||||
Db 3 LRVETGCDRLVLD 16

RESULT 13

A37984
ADP/ATP carrier protein - yeast (Candida parapsilosis) (fragment)
C:Species: Candida parapsilosis
C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 07-Jun-1996
C:Accession: A37984
R:Guerin, B.; Bukusoglu, C.; Rakotomanana, F.; Wohlrab, H.
J. Biol. Chem. 265, 19736-19741, 1990
A:Title: Mitochondrial phosphate transport. N-ethylmaleimide insensitivity correlates
A:Reference number: A37984; MUID:91060585
A:Accession: A37984
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <GUE>

Query Match 21.6%; Score 24; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 12 HLVDLFL 18
1 : ||||
Db 5 NLDLFL 11

RESULT 14

S3662
dermorphin (Lys-7) [validated] - two-colored leaf frog

C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 31-Mar-2000
C:Accession: S36662
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of th
A:Reference number: S21152; MUID:92339502
A:Accession: S36662
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIG>

Query Match 20.7%; Score 23; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 7 FGPE 11
1111:
Db 3 FGPK 7

RESULT 15

PA0015
seed storage protein 12S 2 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 11-Jul-1997
C:Accession: PA0015
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPED, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensions
A:Reference number: PA0001
A:Accession: PA0015
A:Molecule type: protein
A:Residues: 1-14 <KAM>
A:Experimental source: seed
C:Keywords: pyroglutamic acid; seed; storage protein
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.7%; Score 23; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 4 QMDGFPEHL 13
1111:
Db 1 QOYLGVEPOL 10

Search completed: December 21, 2000, 08:37:13
Job time: 317 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:38:16 ; Search time 18.39 Seconds

(without alignments)
38.219 Million cell updates/sec

Title: US-08-934-367-34

Perfect score: 111

Sequence: 1 LILQMDGFPPEHLVDFLQSLIS 22

Scoring table: BLOSUM62

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 1213

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	21.6	14	1	ANGT_HORSE
2	22	19.8	20	1	CAOS_RAT
3	22	19.8	20	1	COXN_THUOB
4	21	18.9	9	1	SAMP_MUSCA
5	20	18.0	11	1	CH60_DROME
6	20	18.0	11	1	TEML_RANTE
7	20	18.0	14	1	DCMM_PSECF
8	20	18.0	16	1	MDH_SYNY4
9	20	18.0	21	1	ATPB_PHTPA
10	19.5	17.6	20	1	DEP4_BOVIN
11	19	17.1	19	1	OXLA_OPHHA
12	19	17.1	19	1	UP21_UPEIN
13	19	17.1	19	1	UP25_UPEIN
14	19	17.1	20	1	SUCB_CANFA
15	19	17.1	21	1	DCMS_PSRCA
16	19	17.1	21	1	YD90_HAEIN
17	18	16.2	8	1	ALL7_CYPDPO
18	18	16.2	8	1	ALL5_CALVO
19	18	16.2	12	1	ALLS_CYPDPO
20	18	16.2	12	1	GRAR_RANRU
21	18	16.2	13	1	ORCK_ORCLI
22	18	16.2	13	1	PSBP_PINPS
23	18	16.2	15	1	LM42_LOCMI
24	18	16.2	17	1	FLA2_BARBA
25	18	16.2	18	1	RS4_PSEAE
26	18	16.2	19	1	HB82_UROHA
27	18	16.2	19	1	NUO6_SOUTU
28	18	16.2	20	1	THIO_CANPA
29	18	16.2	20	1	UN05_PINPS
30	18	16.2	21	1	CSPS_STRTR
31	18	16.2	21	1	OMP4_PASHA
32	17	15.3	8	1	CCKN_MACEU
33	17	15.3	9	1	P4RL_CALVO

ALIGNMENTS

RESULT	1	ALIGNMENT
ANGT_HORSE	1	
ID	ANGT_HORSE	STANDARD: PRT: 14 AA.
AC	P01016	
DT	21-JUL-1986 (Rel. 01, Created)	
DT	21-JUL-1986 (Rel. 01, Last sequence update)	
DT	01-FEB-1996 (Rel. 33, Last annotation update)	
DE	ANGIOTENSINOGEN (FRAGMENT).	
CN	AGT.	
OS	Equus caballus (Horse).	
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.	
RN	[1]	
RP	SEQUENCE.	
RA	Skeggs L.T., Kahn J.R., Lentz K., Shumway N.P.;	
RT	"The preparation, purification, and amino acid sequence of a	
RL	polypeptide renin substrate."	
J.	J. Exp. Med. 106:439-453(1957).	
CC	-1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN	
CC	CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN	
CC	CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE	
CC	PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II. THE MOST POTENT	
CC	PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL	
CC	BALANCE OF BODY FLUIDS.	
CC	-1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.	
CC	-1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.	
DR	PIR: A01250; A01250.	
DR	INTERPRO: IPR000215; -	
DR	PROSITE: PS00284; SERPIN; PARTIAL.	
KM	Vasocosticticor; Plasma; Serpin.	
FT	PEPTIDE	
FT	PEPTIDE	
FT	NON_TER	
SO	SEQUENCE	
	14 AA; 1759 MW; 2E9921F8EEFBD07 CRC64;	
Query Match	21.6%; Score 24; DB 1; Length 14;	
Best Local Similarity	83.3%; Pred. NO. 4.6e+02;	
Matches	5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Oy	10 PPHLYV 15	
Db	7 PPHLYV 12	
RESULT	2	
CAOS_RAT	1	
ID	CAOS_RAT	STANDARD: PRT: 20 AA.
AC	P19633	
DT	01-FEB-1991 (Rel. 17, Created)	
DT	01-FEB-1991 (Rel. 17, Last sequence update)	
DT	01-OCT-1996 (Rel. 34, Last annotation update)	
DE	CALSEQUESTRIN, SKELETAL MUSCLE ISOFORM (ASPARTACTIN) (LAMININ-BINDING	
DE	PROTEIN) (FRAGMENT).	
CN	CASQ1.	
OS	Rattus norvegicus (Rat).	

P56264 Iltoria xan
P17645 drosophila
P80662 physcomitre
P54712 canis famli
Q10583 megathura c
P03057 escherichia
P20404 locusta mig
P33714 macaca mula
P12666 cavia porce
P82030 uperoleia 1
P80055 papio sp. (

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 88331073.
 RA Hall D.E., Frazer K.A., Hann B.C., Reichardt L.F.;
 RT "Isolation and characterization of a laminin-binding protein from rat
 and chick muscle.";
 J. Cell Biol. 107:687-697(1988).
 CC -1- FUNCTION: CALSQUESTRIN IS A HIGH-CAPACITY, MODERATE AFFINITY,
 CALCIUM-BINDING PROTEIN AND THUS ACTS AS AN INTERNAL CALCIUM STORE
 IN MUSCLE. THE RELEASE OF CALCIUM BOUND TO CALSQUESTRIN THROUGH
 A CALCIUM RELEASE CHANNEL TRIGGERS MUSCLE CONTRACTION. BINDS 40
 TO 50 MOLES OF CALCIUM. ALSO BINDS LAMININ.
 CC -1- SUBCELLULAR LOCATION: THIS ISOFORM OF CALSQUESTRIN OCCURS IN THE
 SARCOPLASMIC RETICULUM'S TERMINAL CISTERNAE. LUMINAL SPACES OF
 FAST SKELETAL MUSCLE CELLS. ASPARACTIN IS FOUND IN THE BASAL
 LAMINA SURROUNDING INDIVIDUAL MUSCLE FIBERS.
 CC -1- TISSUE SPECIFICITY: SKELETAL AND HEART MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE CALSQUESTRIN FAMILY.
 DR INTERPRO: IPR001393; -;
 DR PIR: A31049; A31049.
 DR PROSITE: PS00864; CALSQUESTRIN_2; PARTIAL.
 DR PROSITE: PS00863; CALSQUESTRIN_1; 1.
 KM Muscle; Glycoprotein; Calcium-binding.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2238 MW; 92ADE04FC2A69280 CRC64;

Query Match 19.8%; Score 22; DB 1; Length 20;
 Best Local Similarity 62.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 9 GFPEHLVD 16
 ||| |
 DB 6 GFPEYDGD 13

RESULT 3
 COXN_THUOB STANDARD; PRT; 20 AA.
 AC P80960;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE VIIB-HEART (EC 1.9.3.1) (FRAGMENT).
 OS Thunnus obesus (Bigeye tuna).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=HEART;
 RX MEDLINE: 97454291.
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lotispeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 liver.";
 Eur. J. Biochem. 248:99-103(1997).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
 4 FERRICYTOCHROME C.
 KM Oxidoreductase; Mitochondrion.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2303 MW; 0A33BD34006E5AA6 CRC64;

Query Match 19.8%; Score 22; DB 1; Length 20;
 Best Local Similarity 57.1%; Pred. No. 1.4e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 DFGPEH 12
 ||| |
 DB 14 DNGMPVH 20

RESULT 4
 SAMP_MUSCA STANDARD; PRT; 9 AA.
 AC P19095;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SERUM AMYLOID P-COMPONENT (SAP) (FRAGMENT).
 OS Mustelus canis (Smooth dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes; Triakidae;
 OC Mustelus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 83160932.
 RA Robey F.A., Tanaka T., Liu T.-Y.;
 RT "Isolation and characterization of two major serum proteins from the
 dogfish, Mustelus canis, C-reactive protein and amyloid P
 component.";
 J. Biol. Chem. 258:3889-3894(1983).
 CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
 ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
 IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
 CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
 DR PIR: B20569; B20569.
 DR INTERPRO: IPR001759; -;
 DR PROSITE: PS00289; PENTAXIN; PARTIAL.
 KM Amyloid; Glycoprotein; Plasma; Pentaxin.
 FT DOMAIN 1
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 965 MW; D05B5735B386769 CRC64;

Query Match 18.9%; Score 21; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 8.8e+04;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 8 GFPEHLIV 15
 ||| |
 DB 1 GFPEKSLI 8

RESULT 5
 CH60_DROME STANDARD; PRT; 11 AA.
 AC P35380;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MITOCHONDRIAL MATRIX PROTEIN P1 (60 KDa CHAPERONIN) (HEAT SHOCK
 PROTEIN 60) (HSP-60) (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).
 GN MMP-P1 OR HSP60.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=VALLECAS; TISSUE=WING IMAGINAL DISK;
 RX MEDLINE: 93272852.
 RA Santaren J.F., van Damme J., Puype M., Vandekerckhove J.,
 RA Garcia-Bellido A.;
 RT "Identification of Drosophila wing imaginal disc proteins by two-
 dimensional gel analysis and microsequencing.";
 Exp. Cell Res. 206:220-226(1993).
 CC -1- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND

MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL MATRIX (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

DR FLVBASE; FBgn0010375; Mmp-P1.

DR INTERPRO; IPR001844; -.

DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.

KW Chaperone; ATP-binding; Mitochondrion.

FT NON_TER 1 1

FT NON_TER 11 11

SQ SEQUENCE 11 AA: 1243 MW: 78501A36365A6DB CRC64;

Query Match 18.0%; Score 20; DB 1; Length 11;
Best Local Similarity 18.2%; Pred. No. 1.5e+03;
Matches 2; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 1 LLLQMDFGFPE 11
DB 1 VIIQSWGSPK 11

RESULT 6
TEML_RANFE
ID ID_TEMPL_RANFE STANDARD: PRT; 11 AA.
AC P36923;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE TEMPORIN L.
OS Rana temporaria (European common frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
RN [1]
RP SEQUENCE.
RC TISSUE-SKIN;
RX MEDLINE; 97175050.
RA Slimaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L., Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAESURIN/RUGOSIN FAMILY.
KW Amphibian skin; Antibiotic; Amidation; Multigene family.
FT MOD_RES 11 11
FT MOD_RES 1194 MW: 1E990549B372724 CRC64;
SQ SEQUENCE 11 AA: 1194 MW: 1E990549B372724 CRC64;

Query Match 18.0%; Score 20; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 13 LLLVFLQSL 21
DB 1 LLPNLKSL 9

RESULT 7
DCMM_PSECF
ID ID_DCMM_PSECF STANDARD: PRT; 14 AA.
AC P19914;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARBON MONOXIDE DEHYDROGENASE MEDIUM CHAIN (EC 1.2.99.2) (FRAGMENT).
OS Pseudomonas carboxydoflava.

Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
OC Hydrogenophaga.
RN [1]
RP SEQUENCE.
RX MEDLINE; 90055678.
RA Krut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in carboxydotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED ACCEPTOR.
CC -1- COFACTOR: MOLYBDENUM.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND SMALL.
DR PIR; PL0142; PL0142.
KW Oxidoreductase; Molybdenum.
FT NON_TER 14 14
FT NON_TER 14 14
SQ SEQUENCE 14 AA: 1756 MW: 65583C6D1FB7C25B CRC64;

Query Match 18.0%; Score 20; DB 1; Length 14;
Best Local Similarity 15.4%; Pred. No. 2e+03;
Matches 2; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

OY 1 LLLQMDFGFPEHL 13
DB 2 MIPREYHAKHV 14

RESULT 8
MDH_SYNY4
ID ID_MDH_SYNY4 STANDARD: PRT; 16 AA.
AC P80460;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MALATE DEHYDROGENASE (EC 1.1.1.37) (FRAGMENT).
GN MDH.
OS Synechocystis sp. (strain PCC 6714).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
RN [1]
RP SEQUENCE.
RA Naterstad K., Synstad B., Sirevag R.;
RL Submitted (SEP-1996) to the SWISS-PROT data bank.
CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE + NADH.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
DR INTERPRO; IPR001252; -.
DR PROSITE; PS00068; MDH; PARTIAL.
KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT NON_TER 16 16
FT NON_TER 16 16
SQ SEQUENCE 16 AA: 1780 MW: 61D1896F14E81964 CRC64;

Query Match 18.0%; Score 20; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LQMDFG 8
DB 9 LTTDFG 14

RESULT 9
ATPB_PHYPA
ID ID_ATPB_PHYPA STANDARD: PRT; 21 AA.
AC P80658;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) (FRAGMENT).
GN ATPB.
OS Physcomitrella patens (Moss).

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OC Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
OC Funariidae; Funariales; Funariaceae; Physcomitrella.
RN [1]
RP SEQUENCE.
RC TISSUE=PROTONEMA;
RA MEDLINE: 97275459.
RA Kasten B., Buck F., Nuske J., Reski R.;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
RT plastid enzymes."
RL Planta 201;261-272(1997).
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
CC SUBUNIT.
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
DR MENDEL: 13023; PHYPA:atpb.1.
DR INTERPRO: IPR000194; -.
DR PROSITE: PS00152; ATPASE_ALPHA_BETA_PARTIAL.
KM ATP synthetase; Chloroplast; Thylakoid membrane; CF(1);
KW Hydrolase; ATP-binding; Hydrogen ion transport.
FT NON_TER 21
SQ SEQUENCE 21 AA; 2298 MW; 9558E4F5AC8D81A CRC64;

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Query Match 18.0%; Score 20; DB 1; Length 21;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 5 MDGFEP 10
   : 1 1
Db 16 LDIXEP 21

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RESULT 10
DPP4_BOVIN STANDARD; PRT; 20 AA.
AC P81425;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (ADENOSINE DEAMINASE
DE COMPLEXING PROTEIN) (ADCP-I) (FRAGMENTS).
GN DPP4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RC TISSUE=KIDNEY;
RA MEDLINE: 98293306.
RA Ben-Shoshan I., Parola A.H.;
RT "The CP-I subunit of adenosine deaminase complexing protein from calf
RT kidney is identical to human, mouse, and rat dipeptidyl peptidase
RT IV."
RL Comp. Biochem. Physiol. 119B:289-292(1998).
CC -1- FUNCTION: REMOVES N-TERMINAL DIPEPTIDES SEQUENTIALLY FROM
CC POLYPEPTIDES HAVING UNSUBSTITUTED N-TERMINI PROVIDED THAT THE
CC PENULTIMATE RESIDUE IS PROLINE. BINDS AND REGULATES THE ACTIVITY
CC OF ADA.
CC -1- CATALYTIC ACTIVITY: DIPEPTIDYL-POLYPEPTIDE + H(2)O = DIPEPTIDE +
CC POLYPEPTIDE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS IN
CC A SOLUBLE FORM (BY SIMILARITY).
CC -1- PTM: THE SOLUBLE FORM (SDPP) DERIVES FROM THE MEMBRANE FORM (MDPP)
CC BY PROTEOLYTIC PROCESSING.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE

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CC PROLYL OLIGOPEPTIDASE FAMILY.
DR INTERPRO: IPR002471; -.
DR PROSITE: PS00708; PRO_ENDOPEP_SER; PARTIAL.
KM Hydrolase; Dipeptidase; Serine protease; Transmembrane; Glycoprotein;
KW Signal-anchor.
FT NON_TER 1
FT NON_TER 1
FT NON_CONS 10 11
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2356 MW; 28B78E62639F7276 CRC64;

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Query Match 17.6%; Score 19.5; DB 1; Length 20;
Best Local Similarity 33.3%; Pred. No. 3.4e+03;
Matches 5; Conservative 6; Mismatches 1; Indels 3; Gaps 1;

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QY 1 LLLMDFGFPEHLV 15
   |||:: : ||::|
Db 5 LLLEV---YTENIIV 16

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RESULT 11
OXLA_OPNHA STANDARD; PRT; 19 AA.
ID OXLA_OPNHA
AC P81383;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE L-AMINO ACID OXIDASE (EC 1.4.3.2) (LAO) (LAO) (FRAGMENT).
OS Ophiophagus hannah (king cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylidae; Squamata; Scleroglossae; Serpentes; Colubroidae;
OC Elapidae; Elapinae; Ophiophagus.
RN [1]
RP SEQUENCE.
RC TISSUE=VENOM;
RX MEDLINE: 94361525.
RX Pennudurai G., Chung M.C.M., Tan N.-H.;
RT "Purification and properties of the L-amino acid oxidase from Malayan
RT pit viper (Calloselasma rhodostoma) venom."
RL Arch. Biochem. Biophys. 313:373-378(1994).
RN [2]
RP SEQUENCE OF 1-15.
RC TISSUE=VENOM;
RX MEDLINE: 97449790.
RA Ahn M.Y., Lee B.M., Kim Y.S.;
RT "Characterization and cytotoxicity of L-amino acid oxidase from the
RT venom of king cobra (Ophiophagus hannah)."
RL Int. J. Biochem. Cell Biol. 29:911-919(1997).
CC -1- FUNCTION: HAS CYTOTOXIC ACTIVITY (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: A L-AMINO ACID + H(2)O + O(2) = A 2-OXO ACID +
CC NH(3) + H(2)O(2).
CC -1- COFACTOR: FAD.
CC -1- SUBUNIT: HOMODIMER (PROBABLE).
CC -1- PTM: GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
CC -1- STRONG, TO MOUSE FIG-1.
KM Oxidoreductase; Flavoprotein; FAD; Glycoprotein; Venom.
FT CONFLICT 1
FT NON_TER 19 19
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2298 MW; DD911A5B414F1427 CRC64;

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Query Match 17.1%; Score 19; DB 1; Length 19;
Best Local Similarity 40.0%; Pred. No. 3.9e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY 3 LQMDGFEPFH 12
   ||: | ||:
Db 5 LEESEFGPEFY 14

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RESULT 12
UP21_UPEIN

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ID UP21_UPEIN STANDARD; PRT; 19 AA.
 AC P82027;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE UPERIN 2.1.
 OS Uperoleia Innudata (Flooplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 OC Uperoleia.
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-SKIN SECRETION;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 Adams G.W., Severini C.;
 RT "Novel upeirin peptides from the dorsal glands of the Australian
 Flooplain toadlet Uperoleia Innudata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -1- FUNCTION: SHOWS A MEDIUM ANTIBACTERIAL ACTIVITY AGAINST
 L. MESAENTERIOIDES, M. LUTEUS AND S. UBERIS.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=1926; METHOD=FA-B.
 KW Amphibian skin; Antibiotic.
 SQ SEQUENCE 19 AA; 1927 MW; 328834D77BA353D2 CRC64;

Query Match 17.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 37.5%; Pred. No. 3.9e+03;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 14 LVDFLOSL 21
 : : : : :
 Db 2 IVDFAKKV 9

RESULT 13
 UP25_UPEIN STANDARD; PRT; 19 AA.
 AC P82031;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE UPERIN 2.5.
 OS Uperoleia Innudata (Flooplain toadlet).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 OC Uperoleia.
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-SKIN SECRETION;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 Adams G.W., Severini C.;
 RT "Novel upeirin peptides from the dorsal glands of the Australian
 Flooplain toadlet Uperoleia Innudata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -1- FUNCTION: SHOWS A MEDIUM ANTIBACTERIAL ACTIVITY AGAINST M. LUTEUS,
 L. MESAENTERIOIDES AND S. UBERIS.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=1940; METHOD=FA-B.
 KW Amphibian skin; Antibiotic.
 SQ SEQUENCE 19 AA; 1941 MW; 5E94C6C757B463D9 CRC64;

Query Match 17.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 37.5%; Pred. No. 3.9e+03;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 14 LVDFLOSL 21
 : : : : :
 Db 2 IVDFAKKV 9

RESULT 14

SUCB_CANPA STANDARD; PRT; 20 AA.
 ID SUCB_CANPA
 AC P99507;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE PURATIVE SUCCINYL-COA LIGASE (GDP-FORMING) BETA-CHAIN (EC 6.2.1.4)
 OS (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA) (FRAGMENT).
 CC Canis familiaris (Dog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-HEART;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -1- CATALYTIC ACTIVITY: SUCCINATE + COA + GTP = SUCCINYL-COA + GDP +
 ORTHOPHOSPHATE.
 CC -1- PATHWAY: SUBSTRATE LEVEL PHOSPHORYLATION STEP OF THE TRICARBOXYLIC
 ACID CYCLE.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
 CC -1- SIMILARITY: TO OTHER BETA SUBUNITS OF SUCCINYL-COA SYNTHETASE,
 OF MALATE-COA LIGASE AND TO ATP CITRATE-LYASE.
 DR HSC-2DPAGE: P99507; DOG.
 DR INTERPRO: IPR000303; -
 DR PROSITE: PS01217; SUCCINYL-COA LIG_3; PARTIAL.
 KW Ligase; Glycolysis; Tricarboxylic acid cycle; Mitochondrion.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2248 MW; BE8AEFD54BDAC2E CRC64;

Query Match 17.1%; Score 19; DB 1; Length 20;
 Best Local Similarity 33.3%; Pred. No. 4.1e+03;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 11 EHLVDFLO 19
 : : : : :
 Db 5 EYMSWELLQ 13

RESULT 15
 DCMS_PSECA STANDARD; PRT; 21 AA.
 ID DCMS_PSECA
 AC P19921;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE CARBON MONOXIDE OXYGENASE [CYTOCHROME B-561] SMALL CHAIN (EC 1.2.2.4)
 OS Pseudomonas carboxydovorans.
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Bradyrhizobium group; Oligotropa.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=OM5;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 carboxydophilic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- CATALYTIC ACTIVITY: CO + H(2O) + FERROCYTOCHROME B-561 = CO(2) +
 2 H(+) + FERRICCYTOCHROME B-561.
 CC -1- COFACTOR: MOLYBDENUM.
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 SMALL.
 DR PIR: P10144; P10144.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 21
 SQ SEQUENCE 21 AA; 2270 MW; 68D4380629401B9C CRC64;

Query Match 17.18; Score 19; DB 1; Length 21;
 Best Local Similarity 44.48; Pred. No. 4.3e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 GPEPRLVD 16
 | | | | |
 Db 12 CHEVEALVE 20

Search completed: December 21, 2000, 08:38:16
 Job time: 149 sec

RESULT	2		
P70861			
AC	P70861	PRELIMINARY;	PRT; 21 AA.
DT	01-FEB-1997	(TREMBLrel. 02, Created)	
DT	01-FEB-1997	(TREMBLrel. 02, Last sequence update)	
DT	01-NOV-1998	(TREMBLrel. 08, Last annotation update)	
DE	TIME (FRAGMENT).		
OS	<i>Borrelia burgdorferi</i> (Lyme disease spirochete).		
NC	Bacteria; Spirochaetales; Spirochaetaceae; <i>Borrelia</i>		
CC	[1]		

RP SEQUENCE FROM N.A.
RC STRAIN=212;
RX MEDLINE: 97312006.
RA Ge Y., Old I.G., Girons I.S., Charon N.W.;
RT "The flag motility operon of *Borrelia burgdorferi* is initiated by a
DR sigma 70-like promoter.";
RL Microbiology 143:1681-1690(1997).
EMBL: U62901; AAB62742.1; -.
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2432 MW; F33E1EC548BD5B33 CRC64;

Query Match 27.0%; Score 30; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 5 MDGPFPHLL 14
Db 7 IEDFPEGIL 16

RESULT 3
O9TWH5 PRELIMINARY; PRT; 20 AA.
AC O9TWH5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 40 KDA GAP JUNCTION PROTEIN (FRAGMENT).
OS Heliothis virescens (Noctuid moth) (Owllet moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Heliothinae; Heliothis.
RN [1]
RX MEDLINE: 95347000.
RA Ryerse J.S.;
RT "Immunocytochemical, electrophoresis, and immunoblot analysis of
RT Heliothis virescens gap junctions isolated in the presence and absence
RT of protease inhibitors.";
RL Cell Tissue Res. 281:179-186(1995).
SQ SEQUENCE 20 AA; 2304 MW; A298D3EB3E89586B CRC64;

Query Match 26.1%; Score 29; DB 5; Length 20;
Best Local Similarity 35.3%; Pred. No. 3.5e+02;
Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 LLIQMDFGPEHLLVDF 17
Db 3 VIFNIDGYLFLTRDF 19

RESULT 4
O9UGS1 PRELIMINARY; PRT; 12 AA.
AC O9UGS1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE DJ796117.4 (NOVEL PROTEIN SIMILAR TO GS2) (FRAGMENT).
GN DJ796117.4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RX SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AL035398; CAB63074.1; -.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1430 MW; AF7740ABECB69AA6 CRC64;

Query Match 24.3%; Score 27; DB 4; Length 12;
Best Local Similarity 44.4%; Pred. No. 4.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LLIQMDFGF 9
Db 1 MILEMDSF 9

RESULT 5
O9TR07 PRELIMINARY; PRT; 14 AA.
AC O9TR07;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CALCYCLIN-ASSOCIATED PROTEIN PEPTIDE L-8, CAP-50-ANNEXIN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RX SEQUENCE.
RA MEDLINE: 92317074.
RA Mizutani A., Usuda N., Tokumitsu H., Minami H., Yasui K.,
RA Kobayashi R., Hidaka H.;
RT "CAP-50, a newly identified annexin, localizes in nuclei of cultured
RT fibroblast 3Y1 cells.";
RL J. Biol. Chem. 267:13498-13504(1992).
SQ SEQUENCE 14 AA; 1446 MW; C8322EB96DD9C6C6 CRC64;

Query Match 24.3%; Score 27; DB 6; Length 14;
Best Local Similarity 41.7%; Pred. No. 4.9e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 7 FGPEHLLVDFL 18
Db 2 FGDEQALIDL 13

RESULT 6
O9S8E1 PRELIMINARY; PRT; 22 AA.
AC O9S8E1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE ANNEXIN (FRAGMENT).
OS Capsicum annuum (Bell pepper).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Asteridae; eusterids I; Solanales;
OC Solanaceae; Capsicum.
RN [1]
RX SEQUENCE.
RA MEDLINE: 95353219.
RA Hoshino T., Mizutani A., Chida M., Hidaka H., Mizutani J.;
RT "Plant annexin form homodimer during Ca(2+)-dependent liposome
RT aggregation.";
RL Biochem. Mol. Biol. Int. 35:749-755(1995).
SQ SEQUENCE 22 AA; 2465 MW; A36D1A1FE311F0F CRC64;

Query Match 24.3%; Score 27; DB 10; Length 22;
Best Local Similarity 41.7%; Pred. No. 8e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 7 FGPEHLLVDFL 18
Db 3 WGTDEKLIDL 14

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RESULT 7
09ZG55 PRELIMINARY: PRT: 21 AA.
AC 09ZG55:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE ATP-BINDING PROTEIN (FRAGMENT).
OC Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L2 434B;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RT "Gene Identification of Chlamydia trachomatis by random DNA
sequencing."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF087306; AAD04082.1; -.
KW ATP-binding.
FT NON_TER 1 1
SO SEQUENCE 21 AA; 2336 MW; 0185D9AC428276D9 CRC64;

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Query Match 23.9%; Score 26.5; DB 2; Length 21;
Best Local Similarity 41.7%; Pred. No. 9.2e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

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OY 2 LIQMDFGPEHL 13
:|: |::
DB 8 ILQL-ISPKHL 18

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RESULT 8
ID 002830 PRELIMINARY: PRT: 22 AA.
AC 002830:
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE PRO ALPHA1 TYPE II COLLAGEN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96377339.
RA Mesaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
RA Vuorio E.;
RT "Evidence for Insufficient chondrocytic differentiation during repair
of full-thickness defects of articular cartilage."
RL Matrix Biol. 15:39-47(1996).
DR EMBL: S83370; AAB50773.1; -.
DR INTERPRO: IPR000885; -.
DR PFM: PF01410; COLF1.1.
FT NON_TER 1 1
SO SEQUENCE 22 AA; 2292 MW; 2E05FE169844236D CRC64;

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Query Match 23.4%; Score 26; DB 6; Length 22;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 5 MDGPEPE 11
| | | | |
DB 3 MDGPEPE 9

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RESULT 9
094554 PRELIMINARY: PRT: 16 AA.
ID 094554
AC 094554;

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DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE CALMODULIN KINASE 2 (FRAGMENT).
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RA Alemany V., Alligue R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U57982; AAD09466.1; -.
KW kinase.
FT NON_TER 1 1
SO SEQUENCE 16 AA; 1846 MW; 4A673B1F4C328BD9 CRC64;

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Query Match 22.5%; Score 25; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 7 FGFP 10
| | | |
DB 5 FGFP 8

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```

RESULT 10
09PS70 PRELIMINARY: PRT: 19 AA.
ID 09PS70:
AC 09PS70:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE.
RX MEDLINE: 92011685.
RA Stifani S., Barber D.L., Aebersold R., Steyrer E., Shen X., Nimpf J.,
RA Schneider W.J.;
RT "The laying hen expresses two different low density lipoprotein
receptor-related proteins."
RL J. Biol. Chem. 266:19079-19087(1991).
SO SEQUENCE 19 AA; 1861 MW; 4EEC931205620608 CRC64;

```

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Query Match 22.5%; Score 25; DB 13; Length 19;
Best Local Similarity 40.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

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OY 2 LIQMDFGPEHLVD 16
| | | | |
DB 1 LLAQGLGKPTALALD 15

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RESULT 11
09S878 PRELIMINARY: PRT: 20 AA.
ID 09S878
AC 09S878:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE NADPH-CYTOCHROME P450 REDUCTASE (Pecunia).
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
OC Solanaceae; Petunia.
RN [1]
RP SEQUENCE.
RX MEDLINE: 95083756.

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RA Menting J.G., Cornish E., Scopes R.K.;
 RT "Purification and partial characterization of MDPH-cytochrome c
 RT reductase from Petunia hybrida flowers.";
 RL Plant Physiol. 106:643-650(1994).
 SQ SEQUENCE 20 AA; 2390 MW; 8BCDA6F8CF7EEDDE CRC64;

Query Match 22.5%; Score 25; DB 10; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 QMDFPEHL 13
 Db 1 QMDFPEHL 10

RESULT 12

Q9PS42. PRELIMINARY; PRT; 22 AA.
 AC Q9PS42;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE PHENOBARBITAL-INDUCED 48 KDA CYTOCHROME P-450 (FRAGMENT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 RN Gallus.
 RP SEQUENCE.
 RX MEDLINE; 92406903.
 RA Nakai K., Ward A.M., Gannon M., Rifkind A.B.;
 RT "Beta-naphthoflavone induction of a cytochrome P-450 arachidonic acid
 RT epoxide hydrolase in chick embryo liver from the aryl hydrocarbon
 RT hydroxylase and from phenobarbital-induced arachidonate epoxide hydrolase.";
 RL J. Biol. Chem. 267:19503-19512(1992).
 SQ SEQUENCE 22 AA; 2377 MW; 6BA9C990EB3E9C1 CRC64;

Query Match 22.1%; Score 24.5; DB 13; Length 22;
 Best Local Similarity 58.3%; Pred. No. 2e+03;
 Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 5 MDF-GEPEHLV 15
 Db 1 MDF-GEPEHLV 12

RESULT 13
 Q03364. PRELIMINARY; PRT; 13 AA.
 AC Q03364;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DE GUAA (FRAGMENT).
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 RN Borrelia garinii.
 RP SEQUENCE FROM N.A.
 RX STRAIN=625;
 RX MEDLINE; 97426044.
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
 RA Rosa P.;
 RT "The Borrelia burgdorferi circular plasmid cp26: conservation of
 RT plasmid structure and targeted inactivation of the ospC gene.";
 RL Mol. Microbiol. 25:361-374(1997).
 RT EMBL; U93700; AAC45534.1; -.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1449 MW; 08FAB9B0E0BC720 CRC64;

Query Match 21.6%; Score 24; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 1.4e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLOMDPG 8
 Db 6 LLOMDPG 12

RESULT 14

Q031365. PRELIMINARY; PRT; 13 AA.
 AC Q031365;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DE GUAA (FRAGMENT).
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 RN Borrelia garinii.
 RP SEQUENCE FROM N.A.
 RX STRAIN=IP90.
 RX MEDLINE; 97426044.
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
 RA Rosa P.;
 RT "The Borrelia burgdorferi circular plasmid cp26: conservation of
 RT plasmid structure and targeted inactivation of the ospC gene.";
 RL Mol. Microbiol. 25:361-374(1997).
 RT EMBL; U93701; AAC45536.1; -.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1382 MW; 08FBA180E0BC720 CRC64;

Query Match 21.6%; Score 24; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 1.4e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLOMDPG 8
 Db 6 LLOMDPG 12

RESULT 15
 Q034622. PRELIMINARY; PRT; 13 AA.
 AC Q034622;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DE GUAA (FRAGMENT).
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 RN Borrelia burgdorferi (Lyme disease spirochete).
 RP SEQUENCE FROM N.A.
 RX STRAIN=CT39 (IL-1), DN127CL9-2, AND 25015;
 RX MEDLINE; 97426044.
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
 RA Rosa P.;
 RT "The Borrelia burgdorferi circular plasmid cp26: conservation of
 RT plasmid structure and targeted inactivation of the ospC gene.";
 RL Mol. Microbiol. 25:361-374(1997).
 RT EMBL; U93694; AAC45522.1; -.
 FT NON_TER 12 12
 SQ SEQUENCE FROM N.A.
 RX STRAIN=DN127CL9-2, AND 25015;
 RX MEDLINE; 95154673.
 RA Stevenson B., Barthold S.W.;
 RT "Expression and sequence of outer surface protein C among North
 RT American isolates of Borrelia burgdorferi.";
 RL FEMS Microbiol. Lett. 124:367-372(1994).
 RT EMBL; U93694; AAC45522.1; -.
 DR EMBL; U04280; AAC45543.1; -.

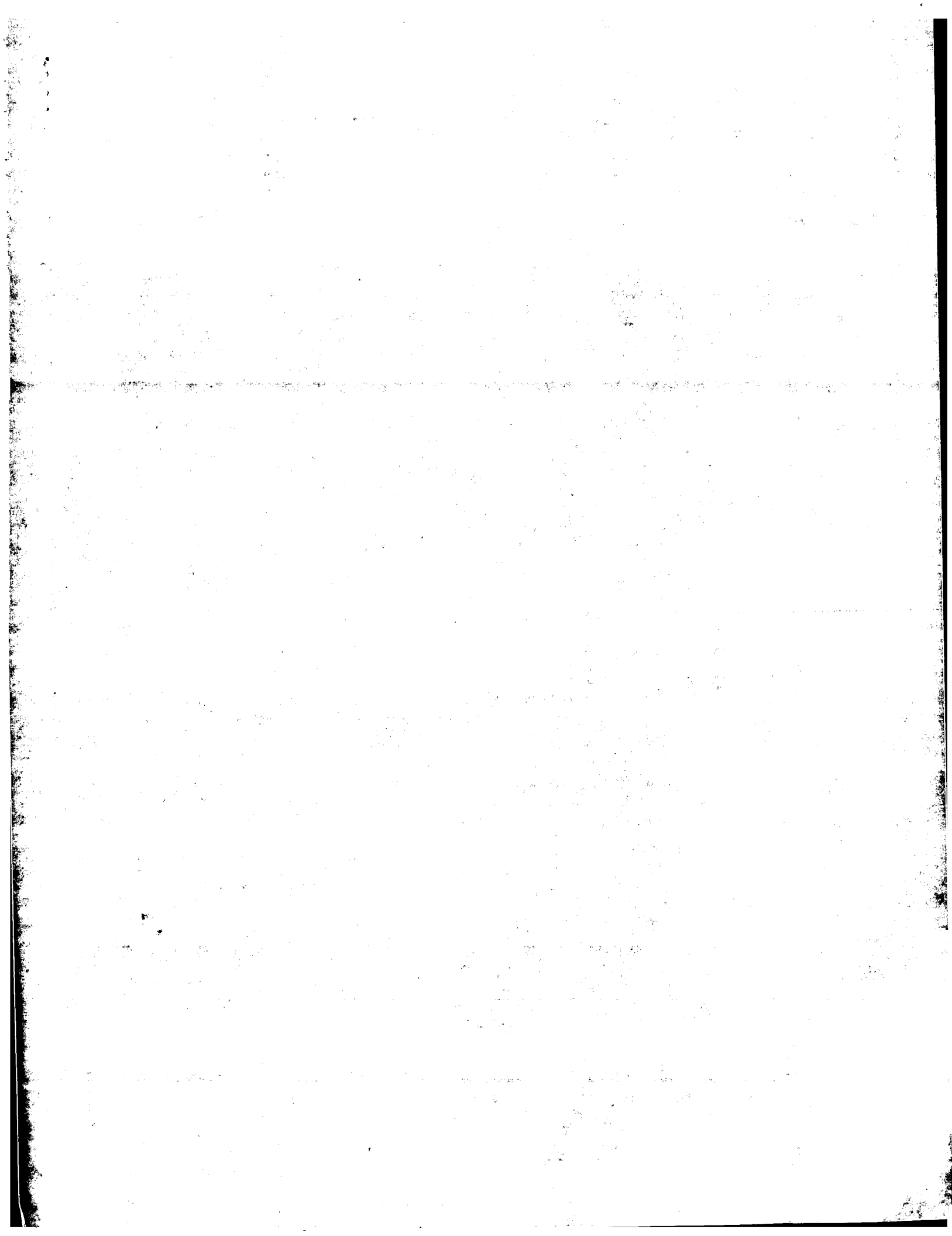
DR EMBL; U04282; AAC45541.1; -
 FT NON TER 13 13
 SO SEQUENCE 13 AA; 1407 MM; 08FAB3930E0BC720 CRC64;

Query Match 21.68; Score 24; DB 2; Length 13;
 Best Local Similarity 57.18; Pred. No. 1.4e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels

0 Gaps 0;

OY 2 LLQMDFG 8
 : 1 : 111
 Db 6 ILVLDVG 12

Search completed: December 21, 2000, 08:37:55
 Job time: 288 sec



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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:31:50 ; Search time 99.91 Seconds
(without alignments)
3.355 Million cell updates/sec

Title: US-08-934-367-35
Perfect score: 96
Sequence: 1 TTYQASYSKKLFLSLDFQ 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 87906

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/2/1aa/5A-COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5B-COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PTCUS-COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	33.4	9	1	US-08-454-207A-43	Sequence 43, Appl
2	33.3	17	5	5266328-11	Patent No. 5266328
3	30.2	18	3	US-09-100-414B-26	Sequence 26, Appl
4	29.2	18	3	US-09-100-414B-30	Sequence 30, Appl
5	28.1	19	1	US-07-654-839-5	Sequence 5, Appl
6	27.1	9	1	US-08-454-207A-45	Sequence 45, Appl
7	27.1	9	1	US-08-454-207A-30	Sequence 30, Appl
8	27.1	9	1	US-08-454-207A-41	Sequence 41, Appl
9	27.1	9	1	US-08-454-207A-44	Sequence 44, Appl
10	27.1	14	4	PCT-US95-06077-5	Sequence 4, Appl
11	27.1	15	2	US-08-195-874-2	Sequence 2, Appl
12	27.1	15	3	US-08-484-905-26	Sequence 26, Appl
13	27.1	15	3	US-08-481-985B-26	Sequence 26, Appl
14	27.1	15	4	PCT-US95-01671-2	Sequence 2, Appl
15	27.1	16	1	US-08-305-871A-9	Sequence 9, Appl
16	27.1	20	1	US-08-218-025A-81	Sequence 81, Appl
17	26.0	9	1	US-08-454-207A-29	Sequence 29, Appl
18	26.0	9	1	US-08-454-207A-31	Sequence 31, Appl
19	26.0	9	1	US-08-454-207A-32	Sequence 32, Appl
20	26.0	9	1	US-08-454-207A-33	Sequence 33, Appl
21	26.0	9	1	US-08-454-207A-34	Sequence 34, Appl
22	26.0	9	1	US-08-454-207A-35	Sequence 35, Appl
23	26.0	9	1	US-08-454-207A-36	Sequence 36, Appl
24	26.0	9	1	US-08-454-207A-37	Sequence 37, Appl
25	26.0	9	1	US-08-454-207A-38	Sequence 38, Appl
26	26.0	9	1	US-08-454-207A-39	Sequence 39, Appl
27	26.0	9	1	US-08-454-207A-40	Sequence 40, Appl
28	26.0	9	3	US-08-159-339A-78	Sequence 78, Appl

29	25	26.0	10	1	US-08-454-207A-2	Sequence 2, Appl
30	25	26.0	10	1	US-08-454-207A-5	Sequence 5, Appl
31	25	26.0	10	2	US-08-456-112B-42	Sequence 42, Appl
32	25	26.0	10	3	US-08-159-339A-77	Sequence 77, Appl
33	25	26.0	11	2	US-08-310-912A-117	Sequence 117, App
34	25	26.0	11	4	PCT-US95-04589-117	Sequence 117, App
35	25	26.0	13	4	PCT-US94-01234-47	Sequence 47, App
36	25	26.0	14	2	US-09-133-774-9	Sequence 9, Appl
37	25	26.0	14	3	US-09-303-862-9	Sequence 9, Appl
38	25	26.0	17	1	US-07-992-288-4	Sequence 4, Appl
39	25	26.0	17	1	US-07-989-764-4	Sequence 4, Appl
40	25	26.0	18	1	US-08-233-203-10	Sequence 10, Appl
41	25	26.0	18	1	US-08-182-483A-25	Sequence 25, Appl
42	25	26.0	18	1	US-08-243-879A-24	Sequence 24, Appl
43	25	26.0	18	3	US-08-499-523-45	Sequence 45, Appl
44	25	26.0	18	3	US-09-100-414B-24	Sequence 24, Appl
45	25	26.0	20	2	US-08-564-972-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-454-207A-43
: Sequence 43, Application US/08454207A
: Patent No. 5710123
: GENERAL INFORMATION:
: APPLICANT: Heaver, George A.
: APPLICANT: Kruszyński, Marian
: TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
: NUMBER OF SEQUENCES: 70
: CORRESPONDENCE ADDRESS:
: ADDRESS: Woodcock Washburn Kurtz MacKiewicz & No. 5710123rls LLP
: STREET: One Liberty Place - 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: U.S.A.
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch disk, 1.44 MB
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WordPerfect 6.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/454, 207A
: FILING DATE: 09-JUN-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/12110
: FILING DATE: 13-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/997, 771
: FILING DATE: 18-DEC-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Dianne B. Elderkin
: REGISTRATION NUMBER: 28,598
: REFERENCE/DOCKET NUMBER: CCOR-0183
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-568-3100
: TELEFAX: 215-568-3439
: INFORMATION FOR SEQ ID NO: 43:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-08-454-207A-43

Query Match 34.4% ; Score 33 ; DB 1 ; Length 9 ;
Best Local Similarity 100.0% ; Pred. No. 1.2e+05 ;
Matches 7 ; Conservative 0 ; Mismatches 0 ; Gaps 0 ;
Indels 0 ;
QY 8 SKKLFL 14

Db 1 SKKKLFL 7

RESULT 2
5266328-11

; Patent No. 5266328
; APPLICANT: SKUBITZ, AMY P.N.; FURCHT, LEO T.
; TITLE OF INVENTION: LAMININ CHAIN POLYPEPTIDES FROM
; THE CARBOXY TERMINAL GLOBULAR DOMAIN
; NUMBER OF SEQUENCES: 14
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/573,672
; FILING DATE: 27-AUG-1990
; SEQ ID NO:11:
; LENGTH: 17
5266328-11

Query Match 33.3%; Score 32; DB 5; Length 17;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 TVQASYSKKLF 13
Db 6 TVKTEYIKRAAF 17

RESULT 3
US-09-100-414B-26

; Sequence 26, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y1
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-26

Query Match 30.2%; Score 29; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KKKLFL 14
Db 1 KKKLFL 6

RESULT 4

US-09-100-414B-30
; Sequence 30, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y1
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-30

Query Match 30.2%; Score 29; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KKKLFL 14
Db 1 KKKLFL 6

RESULT 5

US-07-654-839-5
; Sequence 5, Application US/07654839
; Patent No. 5372933
; GENERAL INFORMATION:
; APPLICANT: Zamarron, Concepcion
; APPLICANT: Plow, Edward F
; APPLICANT: Ginsberg, Mark H
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST
; RECEPTOR-INDUCED BINDING SITES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESS: Patent Counsel
; STREET: 10666 No. 5372933ch Torrey Pines Road., Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA

COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/654,839
FILING DATE: 19910213
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,753
FILING DATE: 03-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/415,029
FILING DATE: 29-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Bingham, Douglas A
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: SCRO367P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-07-654-839-5

Query Match 29.2%; Score 28; DB 1; Length 19;
Best Local Similarity 38.3%; Pred. NO. 1.3e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 7 YSKKLFLLDF 19
| | | | : : : |
Db 1 YSMKTKTKIIF 13

RESULT 6
US-08-454-207A-45
Sequence 45, Application US/08454207A
Patent No. 5710123
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123rls LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,207A
FILING DATE: 09-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12110
FILING DATE: 13-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/997,771

FILING DATE: 18-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0183
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-454-207A-45

Query Match 28.1%; Score 27; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. NO. 1.2e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 SKKKLFL 14
| | | | |
Db 1 SKKKLIL 7

RESULT 7
US-08-454-207A-30
Sequence 30, Application US/08454207A
Patent No. 5710123
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123rls LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,207A
FILING DATE: 09-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12110
FILING DATE: 13-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/997,771
FILING DATE: 18-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0183
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-454-207A-30

Query Match 27.1%; Score 26; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. NO. 1.2e+05;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 8 SKKKLFLSL 16
| | | | |
Db 1 SKKKLALCI 9

RESULT 8
US-08-454-207A-41
; Sequence 41, Application US/08454207A
; Patent No. 5710123
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszyński, Marian
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,207A
; FILING DATE: 09-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12110
; FILING DATE: 13-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/997,771
; FILING DATE: 18-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0183
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-454-207A-41

Query Match 27.1%; Score 26; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.2e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 8 SKKKLFLSL 15
| | | | |
Db 1 SKKKLALFL 8

RESULT 9
US-08-454-207A-44
; Sequence 44, Application US/08454207A
; Patent No. 5710123
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszyński, Marian
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123ris LLP

; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,207A
; FILING DATE: 09-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12110
; FILING DATE: 13-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/997,771
; FILING DATE: 18-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0183
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-454-207A-44

Query Match 27.1%; Score 26; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.2e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 SKKKLFL 14
| | | | |
Db 1 SKKKLHL 7

RESULT 10
PCT-US95-06077-5
; Sequence 5, Application PC/TUS9506077
; GENERAL INFORMATION:
; APPLICANT: Immunobiology Research, Institute Inc.
; TITLE OF INVENTION: Vaccine Interdiction of Extracellular
; TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus
; TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patenlin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06077
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/247,991
; FILING DATE: 23-MAY-1994

ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IR144PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-06077-5

Query Match 27.1%; Score 26; DB 4; Length 14;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 6 SYSKKK 11
|| |||
Db 1 SYKKK 6

RESULT 11
US-08-195-874-2

; Sequence 2, Application US/08195874
; Patent No. 5817308

; GENERAL INFORMATION:

; APPLICANT: Scott, David W.

; APPLICANT: Zambidis, Elias T.

; TITLE OF INVENTION: Tolerogenic Fusion Proteins of

; TITLE OF INVENTION: Tolerogenic Fusion Proteins of

; TITLE OF INVENTION: Tolerogenic Fusion Proteins of

; TITLE OF INVENTION: Tolerogenic Fusion Proteins of

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; TITLE OF INVENTION: Tolerogenic Fusion Proteins of

; TITLE OF INVENTION: Tolerogenic Fusion Proteins of

; TITLE OF INVENTION: Tolerogenic Fusion Proteins of

Oy 3 VOASYSKKK 11
::: || |||
Db 7 LKAIYKKK 15

RESULT 12
US-08-484-905-26

; Sequence 26, Application US/08484905
; Patent No. 5976551

; GENERAL INFORMATION:

; APPLICANT: Mottez, Estelle

; APPLICANT: Abastado, Jean-Pierre

; APPLICANT: Kourilsky, Philippe

; TITLE OF INVENTION: An Altered Major Histocompatibility

; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the

; TITLE OF INVENTION: Determinant

; TITLE OF INVENTION: Determinant

; TITLE OF INVENTION: Determinant

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; TITLE OF INVENTION: Determinant

```

; APPLICANT: Kourilsky, Phillipe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-481-985B-26

Query Match      27.1%; Score 26; DB 3; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 VOASYSKKK 11
       :| | | | |
Db      7 LKAIVKKK 15

RESULT 14
PCT-US95-01671-2
; Sequence 2, Application PC/TUS9501671
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; TITLE OF INVENTION: Inducing Tolerance With Tolerogenic
; TITLE OF INVENTION: Fusion Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: United States of America
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01671
; FILING DATE: 10-FEB-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kevin W. Raasch
; REGISTRATION NUMBER: 35,651
; REFERENCE/DOCKET NUMBER: 850.114M01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-01671-2

Query Match      27.1%; Score 26; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 VOASYSKKK 11
       :| | | | |
Db      7 LKAIVKKK 15

RESULT 15
US-08-305-871A-9
; Sequence 9, Application US/08305871A
; Patent No. 5736142
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Gaeta, Federico
; APPLICANT: Grey, Howard M.
; APPLICANT: Sidney, John
; APPLICANT: Alexander, Jeffrey L.
; TITLE OF INVENTION: Alteration of Immune Response Using Pan
; TITLE OF INVENTION: DR-Binding Peptides
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/305,871A
; FILING DATE: 14-SEP-1994
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,101
; FILING DATE: 14-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-0062-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
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: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-305-871A-9

Query Match 27.1%; Score 26; DB 1; Length 6;
Best Local Similarity 55.6%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels

0; Gaps 0;

OY 3 VQASYSKK 11
: : I I I I I
Db 8 LKAIYKKK 16

Search completed: December 21, 2000, 08:31:50
Job time: 373 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2000, 08:30:08 ; Search time 112.59 seconds

(without alignments)
11.273 Million cell updates/sec

Title: US-08-934-367-35

Sequence: 1 TTVOASYSKKKFLSLDPRO 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_65:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	30	31.2	18	2	S14560	probable heme-bind
2	28	29.2	14	2	S13864	methyl coenzyme M
3	26	27.1	14	4	I52618	hemoglobin beta ch
4	25	26.0	6	2	A61411	amelotin - rat
5	24	25.0	17	2	I49593	cystic fibrosis tr
6	24	25.0	17	2	I84733	gene CFTR protein
7	23	24.0	19	2	A49192	transhyretin - bu
8	23	24.0	20	2	S39049	cytochrome-binding
9	22	22.9	13	2	PH0786	T-cell receptor al
10	22	22.9	15	2	S65717	prostaglandin D-sy
11	22	22.9	16	2	PA0046	protein OAI00044 -
12	22	22.9	15	2	S34444	blaz protein - Sta
13	22	22.9	18	2	S54272	CYC 75 protein - h
14	21	21.9	13	2	G22565	R-phycocyanin ga
15	21	21.9	14	2	S29209	avenin alpha-2 - o
16	21	21.9	14	2	A44920	2-halobenzoate 1,2
17	21	21.9	15	2	PN0662	dystrophin-associa
18	21	21.9	16	2	B45895	T-cell surface gly
19	21	21.9	17	2	S32587	L-ascorbate peroxi
20	21	21.9	17	2	A35550	adenocortical cel
21	21	21.9	19	2	S59717	hypothetical prote
22	21	21.9	20	2	H49034	nuclear antigen EB
23	20	20.8	15	2	S03955	acidic fibroblast
24	20	20.8	16	2	S01669	rRNA N-glycosidase
25	20	20.8	16	2	S02473	coat protein VPI -
26	20	20.8	16	2	S70331	endosperm protein,
27	20	20.8	18	2	S45373	translation elonga
28	20	20.8	18	2	S29108	glutathione trans
29	20	20.8	20	2	S63602	glutathione S-tran

30	20	20.8	20	2	PI0192	Ig lambda 2 chain
31	20	20.8	20	2	A44921	hydroxypruvate re
32	20	20.8	20	2	S46479	retinoid-X-recepto
33	19	19.8	9	3	PC7076	spectrin alpha cha
34	19	19.8	10	2	A13687	caerulein-like pep
35	19	19.8	12	2	S26556	T-cell receptor be
36	19	19.8	13	2	S47365	T-cell antigen rec
37	19	19.8	14	2	S14336	mastoparan B - hor
38	19	19.8	14	2	A47421	ribosomal protein
39	19	19.8	15	2	S36890	hypothetical prote
40	19	19.8	17	2	S61451	Ig heavy chain DJ
41	19	19.8	17	2	PH1331	neurofibromatosis-
42	19	19.8	18	2	B35910	cyclin C - mouse (
43	19	19.8	18	2	S48863	serpin MSZCI - whe
44	19	19.8	19	2	S43652	flagellar sheath p
45	19	19.8	19	2	A47689	

ALIGNMENTS

RESULT 1
S14560
probable heme-binding protein - garden pea chloroplast (fragment)
C:Species: chloroplast Pisum sativum (garden pea)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 11-Jan-2000
C:Accession: S14560
R:Smith, A.G.; Wilson, R.J.; Kaethner, T.M.; Willey, D.L.; Gray, J.C.
submitted to the EMBL Data Library, October 1990
A:Reference number: S14557
A:Accession: S14560
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18 <SMD>
A:Cross-references: EMBL:X54750; NID:g12194; PID:g12198
C:Genetics:
A:Genome: chloroplast
C:Superfamily: maize chloroplast protein cema
C:Keywords: chloroplast; heme; transmembrane protein

Query Match 31.2% Score 30; DB 2; Length 18;
Best local similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 8 SKKKLFLSL 17
DB 2 AKKKAFLPL 11
RESULT 2
S13864
methyl coenzyme M reductase (EC 1.8.-.-) II alpha chain - Methanobacterium thermoauto
C:Species: Methanobacterium thermoautotrophicum
A:Variety: strain Marburg
C>Date: 19-Mar-1997 #sequence_revision 13-Sep-1998 #text_change 30-Oct-1998
C:Accession: S13864
R:Rospert, S.; Linder, D.; Ellermann, J.; Thauer, R.K.
Eur. J. Biochem. 194, 871-877, 1990
A>Title: Two genetically distinct methyl-coenzyme M reductases in Methanobacterium th
A:Reference number: S13864; MUID:91099370
A:Accession: S13864
A:Molecule type: protein
A:Residues: 1-14 <ROS>
A:Experimental source: strain Marburg
A:Keywords: methanogenesis; oxidoreductase

Query Match 29.2% Score 28; DB 2; Length 14;
Best local similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 9 KKKLFLSL 17

Db 3 EKKLFKLAL 11

RESULT 3

152618 hemoglobin beta chain thalassemia mutant Portuguese - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence_revision 11-Jul-1996 #text_change 20-Apr-2000

C:Accession: 152618

R:Oner, R.; Oner, C.; Wilson, J.B.; Tamagnini, G.P.; Ribeiro, L.M.; Huisman, T.H.

Br. J. Haematol. 79, 306-310, 1991

A:Title: Dominant beta-thalassemia trait in a Portuguese family is caused by a deletion

A:Reference number: 152618; MUID:92068764

A:Accession: 152618

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-14 <ONE>

A:Cross-references: GB:S68042; NID:g239717; PIDN:AAB20440.1; PID:g239718

C:Genetics:

A:Gene: GDB:HB

A:Cross-references: GDB:119297; OMIM:141900

A:Map position: 11p15.4-11p15.4

Query Match

27.1%; Score 26; DB 4; Length 14;

Best Local Similarity 71.4%; Pred. No. 4.5e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 VOASYSK 9

111111

Db 3 VOAAAYK 9

RESULT 4

A61411 amelelin - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999

C:Accession: A61411

R:Burzynski, S.R.

Anal. Biochem. 70, 359-365, 1976

A:Title: Sequential analysis in subnanomolar amounts of peptides. Determination of the s

A:Reference number: A61411; MUID:76182447

A:Accession: A61411

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-6 <BUR>

C:Keywords: pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

26.0%; Score 25; DB 2; Length 6;

Best Local Similarity 83.3%; Pred. No. 1.8e+05;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 QASYSK 9

111111

Db 1 QAGYSK 6

RESULT 5

149593 cystic fibrosis transmembrane conductance regulator - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999

C:Accession: I49593

R:Denamur, E.; Chehab, F.F.

Hum. Mol. Genet. 3, 1089-1094, 1994

A:Title: Analysis of the mouse and rat CFTR promoter regions.

A:Reference number: I49593; MUID:95072572

A:Accession: I49593

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-17 <RES>

A:Cross-references: GB:L04873; NID:g414726; PIDN:AAA73562.1; PID:g553892

C:Genetics:

A:Gene: CFTR

C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding casse

Query Match

25.0%; Score 24; DB 2; Length 17;

Best Local Similarity 41.2%; Pred. No. 1.2e+03;

Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 3 VOASYSKKLFSLDLF 19

111111111111111111

Db 1 MQKSPLEKASFSIKLFF 17

RESULT 6

184733 gene CFTR protein - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999

C:Accession: 184733

R:Denamur, E.; Chehab, F.F.

Hum. Mol. Genet. 3, 1089-1094, 1994

A:Title: Analysis of the mouse and rat CFTR promoter regions.

A:Reference number: I49593; MUID:95072572

A:Accession: 184733

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-17 <RES>

A:Cross-references: GB:L26098; NID:g425185; PIDN:AAA73561.1; PID:g915270

C:Genetics:

A:Gene: CFTR

C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding casse

Query Match

25.0%; Score 24; DB 2; Length 17;

Best Local Similarity 41.2%; Pred. No. 1.2e+03;

Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 3 VOASYSKKLFSLDLF 19

111111111111111111

Db 1 MQKSPLEKASFSIKLFF 17

RESULT 7

A49192 transthyretin - bullfrog (fragment)

N:Alternate names: 3,5,3'-L-triiodothyronine-specific binding protein

C:Species: Rana catesbeiana (bullfrog)

C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995

C:Accession: A49192

R:Yamauchi, K.; Kasahara, T.; Hayashi, H.; Horiuchi, R.

Endocrinology 132, 2254-2261, 1993

A:Title: Purification and characterization of a 3,5,3'-L-triiodothyronine-specific bi

A:Reference number: A49192; MUID:93258653

A:Accession: A49192

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <YAM>

A:Experimental source: tadpole plasma

A:Note: sequence extracted from NCBI backbone (NCBIP:130235)

Query Match

24.0%; Score 23; DB 2; Length 19;

Best Local Similarity 45.5%; Pred. No. 1.9e+03;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 8 SKKKLFSLDL 18

111111111111111111

Db 7 SKXPLWVKVLD 17

RESULT 8
S39049
cytotoxin-binding protein - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 18-Feb-1994 #sequence_revision 19-Apr-1996 #text_change 16-Feb-1997
C:Accession: S39049
R:Rutledge, F.; Mohr, M.; Grimmig, M.; Leidecker, R.; Linder, D.
Eur. J. Biochem. 217, 1123-1128, 1993
A:Title: Pseudomonas aeruginosa cytotoxin-binding protein in rabbit erythrocyte membrane
A:Reference number: S39049; MUID:94039134
A:Accession: S39049
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <LUP>
C:Superfamily: lens fiber membrane major intrinsic protein

Query Match 24.0%; Score 23; DB 2; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 9 KKKLF 13
|||:|
Db 5 KKKTF 9

RESULT 9
PH0786
T-cell receptor alpha chain (17) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0786
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846
A:Accession: PH0786
A:Molecule type: mRNA
A:Residues: 1-13 <CNS>
A:Cross-references: EMBL:X60889
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 22.9%; Score 22; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 5 ASYSKKLF 13
|||:|:|
Db 4 SAVANKMIF 12

RESULT 10
S65717
prostaglandin D-synthase - rat (fragment)
N:Alternate names: prostaglandin-H2 D-isomerase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 31-Oct-1997
C:Accession: S65717
R:Giacomelli, S.; Leone, M.G.; Grima, J.; Silvestrini, B.; Cheng, C.Y.
Biochim. Biophys. Acta 1310, 269-276, 1996
A:Title: Astrocytes synthesize and secrete prostaglandin D synthetase in vitro.
A:Reference number: S65716; MUID:96177373
A:Accession: S65717
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <GIA>
C:Superfamily: lipocalin; lipocalin homology

Query Match 22.9%; Score 22; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 TVQASYSKKK 11
|||:|:|
Db 3 TVQPRFQDDK 12

RESULT 11
PA0046
protein OAI00044 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0046; PA0042
R:Kano, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensi
A:Reference number: PA0001
A:Accession: PA0046
A:Molecule type: protein
A:Residues: 1-15 <RAM>
A:Experimental source: stem

Query Match 22.9%; Score 22; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 10 KKLFLSLDF 18
|||:|:|
Db 4 KKGFLAVSD 12

RESULT 12
S34444
blaz protein - Staphylococcus aureus plasmid p1258 (fragment)
C:Species: Staphylococcus aureus
C:Date: 22-Nov-1993 #sequence_revision 09-Mar-1996 #text_change 07-May-1999
C:Accession: S34444
R:Wang, P.Z.; Projan, S.J.; Novick, R.P.
Nucleic Acids Res. 19, 4000, 1991
A:Title: Nucleotide sequence of beta-lactamase regulatory genes from staphylococcal p
A:Reference number: S34444; MUID:91319567
A:Accession: S34444
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-16 <MAN>
A:Cross-references: EMBL:M62650
A:Experimental source: strain RN11
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
C:Genetics:
A:Gene: blaZ
A:Genome: plasmid p1258

Query Match 22.9%; Score 22; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.4e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 10 KKLFLSLDF 19
|||:|:|
Db 6 KQLOLKITTF 15

RESULT 13
S54272
CTC 75 protein - human
C:Species: Homo sapiens (man)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C:Accession: S54272
R:Gensch, E.; Eckerskorn, C.; Lottspeich, F.; Herzog, C.; Kuehn, K.; Poeschl, E.
EMBO J. 14, 791-800, 1995

A:Title: Purification of the sequence-specific transcription factor CTCBF, involved in t
A:Reference number: S54272; MUID:95188883
A:Accession: S54272
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-18 <GEN>

Query Match 22.9%; Score 21; DB 2; Length 18;
Best Local Similarity 33.3%; Pred. No. 2.6e+03;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTVQASYSKKL 12
| | : | | : | |
Db 6 STGKVEYSEEL 17

RESULT 14
G22565
R-phycoerythrin gamma-B chain - red alga (Gastrocionium coulteri) (fragment)
C:Species: Gastrocionium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: G22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: G22565
A:Molecule type: protein
A:Residues: 1-13 <KLO>

Query Match 21.9%; Score 21; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 2.8e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTVQASYSK 9
| | | : | |
Db 5 TVPQAAFEK 13

RESULT 15
S29209
avenin alpha-2 - oat (fragment)
N:Alternate names: CIP-3; coeliac immunoreactive protein 3
C:Species: Avena sativa (oat)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C:Accession: S29209
R:Roche, A.; Collila, F.; Ortiz, M.L.; Mendez, E.
FEBS Lett. 310, 37-40, 1992
A:Title: Identification of the three major coeliac immunoreactive proteins and one alpha
A:Reference number: S29207; MUID:92405739
A:Accession: S29209
A:Molecule type: protein
A:Residues: 1-14 <ROC>
A:Experimental source: endosperm
C:Superfamily: gliadin
C:Keywords: prolamin; seed

Query Match 21.9%; Score 21; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTVQASYSKK 10
| | | : | |
Db 2 TTVQYNPSEQ 11

Search completed: December 21, 2000, 08:30:08
Job time: 272 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:33:00 ; Search time 62.7 Seconds
(without alignments)
10.191 Million cell updates/sec

Title: US-08-934-367-35
Perfect score: 96
Sequence: 1 TTVQASYSKKLFLSLDFQ 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues
Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	24	25.0	18 1 UC21_MAIZE	P80627 zea mays (m
2	23	24.0	12 1 PA21_MICM	P23072 micriturus fu
3	23	24.0	20 1 CPBX_CAVPO	P34033 cavia porce
4	22	22.9	20 1 VR90_BORPE	P81549 bordetella
5	21	21.9	10 1 XYNB_DICB4	P80717 dictyoglomu
6	21	21.9	20 1 M117_BOVIN	P35451 bos taurus
7	21	21.9	20 1 TL18_SPTOL	P25336 spinaclia ol
8	20	20.8	12 1 PA2B_VIRBO	P31859 viperia beru
9	20	20.8	15 1 FGFI_CANPA	P18651 canis famli
10	20	20.8	16 1 RIPK_TRIKI	P16093 trichosanth
11	19	19.8	8 1 B44K_PORGI	P81886 porphyromon
12	19	19.8	14 1 MAST_VESBA	P21654 vespa basal
13	19	19.8	15 1 EFLA_MICCR	P81266 micropililis
14	19	19.8	16 1 R16_VIBPR	Q36715 vibrio prot
15	19	19.8	19 1 PRSL_DESHN	P13066 desulfovibr
16	19	19.8	20 1 STYA_STYCL	P81469 styela clav
17	18	18.8	9 1 ULAE_HUMAN	P31931 homo sapien
18	18	18.8	13 1 UVRD_SALTY	Q05311 salmonella
19	18	18.8	13 1 YPE2_LACTC	P42021 lactococcus
20	18	18.8	16 1 ARCD_PSEPU	P41147 pseudomonas
21	18	18.8	17 1 ATP1_PAVLU	P28529 pavlova lut
22	18	18.8	19 1 UP24_UPEIN	P81207 uperoleia i
23	18	18.8	20 1 AMP_FUSNU	P12073 fusobacteri
24	18	18.8	20 1 CRP_MUSCA	P13094 mustelus ca
25	17	17.7	8 1 CCKN_MACEU	P10366 macropus eu
26	17	17.7	11 1 TKN_ELEMO	P01293 eleodone mos
27	17	17.7	12 1 NO40_SOTBN	P35960 glycine max
28	17	17.7	14 1 MAST_VESMA	P42050 vespa manda
29	17	17.7	14 1 MAST_VESXA	P01515 vespa xanth
30	17	17.7	14 1 UC34_MAIZE	P80640 zea mays (m
31	17	17.7	15 1 CBPB_PROAT	P19628 protopteris
32	17	17.7	17 1 B01L_MRCPE	P10521 megabombus
33	17	17.7	18 1 NODD_RHITO	Q32838 rhizobium i

34	17	17.7	18 1 RL23_HAICU	P05975 halobacteri
35	17	17.7	20 1 CATF_LACTRA	P81422 actineobact
36	17	17.7	20 1 RIPX_CUCPE	P80750 cucurbita p
37	16	16.7	8 1 ARH_MELML	P25423 melonlontha
38	16	16.7	8 1 COXG_RAT	P80430 rattus norv
39	16	16.7	8 1 CPD1_ENTFA	P13269 enterococcu
40	16	16.7	10 1 COXM_RAT	P80431 rattus norv
41	16	16.7	10 1 PNEU_RAT	P21996 rattus norv
42	16	16.7	11 1 CS15_BACSU	P81095 bacillus su
43	16	16.7	11 1 OXB2_YEAST	P99013 saccharomyc
44	16	16.7	14 1 MAST_VESLE	P01514 vespa lew
45	16	16.7	14 1 RS19_PPMBP	Q52093 pigeon pea

ALIGNMENTS

RESULT 1				
UC21_MAIZE	ID	UC21_MAIZE	STANDARD:	PRT: 18 AA.
AC P80627;				
DT 01-OCT-1996 (Rel. 34, Created)				
DT 01-OCT-1996 (Rel. 34, Last sequence update)				
DT 15-JUL-1999 (Rel. 38, Last annotation update)				
DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLLEOPTILE (SPOT 443)				
DE (FRAGMENT)				
OS Zea mays (Maize).				
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;				
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.				
RN [1]				
RP SEQUENCE.				
RC TISSUE=COLEOPTILE;				
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,				
RA Penollet J.-C., Zivy M., de Vienne D.;				
RT "The maize two dimensional gel protein database: towards an integrated				
RT genome analysis program.";				
RL Theor. Appl. Genet. 93:997-1005(1996).				
CC -I- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN				
CC PROTEIN IS: 5.9; ITS MW IS: 26.5 KDA.				
CC -I- SIMILARITY: TO L-ASCORBATE PEROXIDASES.				
CC HSSP: P48534; IAPX.				
DR MAIZE-2DPAGE; P80627; COLEOPTILE.				
DR MAIZEDB: 123953; -.				
FT NON_TER 1 1				
FT NON_TER 18 18				
SEQ SEQUENCE 18 AA; 1938 MM; F32F6FEF038BABBA CRC64;				
Query Match				
Best local similarity 25.0%; Score 24; DB 1; Length 18;				
Matches 5; Conservative 71.4%; Pred. No. 3.7e+02;				
Mismatches 2; Indels 0; Gaps 0;				
QY 2 TTVQASYS 8				
Db 6 TVSAEYS 12				
RESULT 2				
PA21_MICFM	ID	PA21_MICFM	STANDARD:	PRT: 12 AA.
AC P25072;				
DT 01-MAY-1992 (Rel. 22, Created)				
DT 01-MAY-1992 (Rel. 22, Last sequence update)				
DT 15-DEC-1998 (Rel. 37, Last annotation update)				
DE PHOSPHOLIPASE A2 ISOZYME 1 (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE				
DE 2-ACYLHYDROLASE) (FRAGMENT).				
OS Micriturus fulvius microgalbatus (Mexican coral snake).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Lepidosauilia; Squamata; Scleroglossa; Serpentes; Colubroidae;				
OC Elapidae; Elapinae; Micriturus.				
RN [1]				
RP SEQUENCE.				
RC TISSUE=VENOM;				

RX MEDLINE: 79255521.
RA Pessani L.D., Alagon A.C., Fletcher P.L. Jr., Varela M.J., Julia J.Z.;
RT "Purification and characterization of a phospholipase A2 from the
venom of the coral snake, Micrurus fulvius microgabineus (Brown and
Smith).";
RL Biochem. J. 179:603-606(1979).
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-
PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
DR INTERPRO: IPR001211; -;
DR PROSITE: PS00118; PA2_HIS_PARTIAL.
DR PROSITE: PS00119; PA2_ASP_PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Venom.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1398 MW; CC21992A899F039 CRC64;

Query Match 24.0%; Score 23; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 15 SLDDFQ 20
|||:|
Db 1 SLBKF 6

RESULT 3
CPBX_CAVPO STANDARD; PRT; 20 AA.
AC P34033;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME P450IIB (EC 1.14.14.1) (FRAGMENT).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RC STRAIN-HARTLEY, TISSUE-LIVER.
RX MEDLINE: 91054472.
RA Narimatsu S., Akutsu Y., Matsunaga T., Watanabe K., Yamamoto I.,
RA Yoshimura H.;
RT "Purification of a cytochrome P450 isozyme belonging to a subfamily
of P450 IIB from liver microsomes of guinea pigs";
RL Biochem. Biophys. Res. Commun. 172:607-613(1990).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. THIS ISOZYME IS ACTIVE
UPON P-NITROANISOLE, ANILINE, D-BENZPHETAMINE, DELTA(9)-
TETRAHYDROCANNABINOL (THC) AND STRYCHNINE.
CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
OXIDIZED FLAVOPROTEIN + H(2)O.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR PIR: A36154; A36154.
DR INTERPRO: IPR001128; -;
DR PROSITE: PS00086; CYTOCHROME_P450; PARTIAL.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2259 MW; 78DC81280C970A55 CRC64;

Query Match 24.0%; Score 23; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 12 LFLSL 17
|||:|
Db 7 LFLALL 12

RESULT 4
VR90_BORPE STANDARD; PRT; 20 AA.
AC P81549;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VIRULENCE-ASSOCIATED OUTER MEMBRANE PROTEIN VIR90 (FRAGMENT).
GN VIR90.
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
OC Bordetella.
RN [1]
RP SEQUENCE.
RC STRAIN-TOHAMA 1;
RX MEDLINE: 99179239.
RA Passerini de Rossi B.N., Friedman L.E., Gonzalez Flecha F.L.,
RA Castello P.R., Franco M.A., Rossi J.P.F.C.;
RT "Identification of Bordetella pertussis virulence-associated outer
membrane proteins.";
RL FEMS Microbiol. Lett. 172:9-13(1999).
KW Outer membrane; Virulence.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2116 MW; D24E1CDCA665206C CRC64;

Query Match 22.9%; Score 22; DB 1; Length 20;
Best Local Similarity 57.1%; Pred. No. 9.4e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 TVQASYS 8
||:|
Db 11 TVGEYS 17

RESULT 5
XYNB_DICB4 STANDARD; PRT; 10 AA.
AC P80717;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ENDO-1,4-BETA-XYLANASE B (EC 3.2.1.8) (XYLANASE B)
DE (1,4-BETA-D-XYLAN XYLANOXYDROLASE B) (FRAGMENT).
OS Dictyoglomus sp. (strain B4A).
OC Bacteria; Dictyoglomus group; Dictyoglomus.
RN [1]
RP SEQUENCE.
RA Adamsen A.K., Jacobsen S., Ahning B.K.;
RL Submitted (OCT-1996) TO THE SWISS-PROT data bank
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
LINKAGES IN XYLANS.
CC -1- PATHWAY: XYLAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL
HYDROLASES).
DR INTERPRO: IPR001000; -;
DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; PARTIAL.
KW Xylan degradation; Hydrolase; Glycosidase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; 45543322AA720A1A3 CRC64;

Query Match 21.9%; Score 21; DB 1; Length 10;
Best Local Similarity 55.6%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 10 KKLFLSLD 18
||:|
Db 2 KKLTLDLKD 10

RESULT 6
MIL7_BOVIN STANDARD: PRT: 20 AA.
AC P35451;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 17 KDA MILK GLYCOPROTEIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RC TISSUE-MILK;
RX MEDLINE: 93308294.
RA Seerensen E.S., Petersen T.E.;
RT "Purification and characterization of three proteins isolated from
the protease peptone fraction of bovine milk";
RL J. Dairy Res. 60:189-197(1993).
CC -1- PPM: N-GLYCOSYLATED.
CC -1- SIMILARITY: TO CAMEL WHEY PROTEIN.
KW Glycoprotein; Milk.
FT NON_TER 1
FT NON_TER 20
SO SEQUENCE 20 AA: 2233 MW: 4CCAS89404C62C27 CRC64;

Query Match 21.9%; Score 21; DB 1; Length 20;
Best Local Similarity 35.3%; Pred. No. 1.4e+03;
Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
OY 1 TTVOASYSKKKFLSL 17
Db 1 SSXQPGSONPKPLSL 17

RESULT 7
TL18_SPTOL STANDARD: PRT: 20 AA.
AC P82536;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE THYLAKOID LUMENAL 18 KDA PROTEIN (P18) (FRAGMENT).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
OC Caryophyllales; Chenopodiaceae; Spinacia.
RN [1]
RP SEQUENCE.
RA Kieselbach T., Bystedt M., Schroeder W.P.;
RL Submitted (May-2000) to the SWISS-PROT data bank.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 20
FT NON_TER 20
SO SEQUENCE 20 AA: 2192 MW: 752C21963FA9FA64 CRC64;

Query Match 21.9%; Score 21; DB 1; Length 20;
Best Local Similarity 30.8%; Pred. No. 1.4e+03;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 TTVOASYSKKKFL 13
Db 5 TPLOSKVTNKVVF 17

RESULT 8
PA2B_VIPBO STANDARD: PRT: 12 AA.
AC P31859;
DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PHOSPHOLIPASE A2, BASIC (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE
DE 2-ACYLHYDROLASE) (FRAGMENT).
OS Vipera berus orientalis (Viper).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Vipera.
RN [1]
RP SEQUENCE.
RC TISSUE-VENOM;
RX MEDLINE: 74128698.
RA Delori P.J.;
RT "Purification and physicochemical, chemical and biological properties
of a toxic A2 phospholipase isolated from the venom of viperidae
snakes: Vipera berus";
RL Biochimie 55:1031-1045(1973).
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
2-ACYL GROUPS IN 3-SN-PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O -> 1-ACYLGLYCERYL-
PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
DR INTERPRO: IPR001211; .
DR PROSITE: PS00118; PA2_HIS; PARTIAL.
DR PROSITE: PS00119; PA2_ASP; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Venom.
FT NON_TER 12
FT NON_TER 12
SO SEQUENCE 12 AA: 1412 MW: D054351A89969879 CRC64;

Query Match 20.8%; Score 20; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 15 SLDF 19
Db 1 SLDF 5

RESULT 9
FGF1_CANFA STANDARD: PRT: 15 AA.
AC P18651;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HEPARIN-BINDING GROWTH FACTOR 1 (HBGF-1) (ACIDIC FIBROBLAST GROWTH
DE FACTOR) (AFGF) (ALPHA-ENDOTHELIAL CELL GROWTH FACTOR) (FRAGMENT).
GN FGF1 OR FGF-1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE.
RA Quinkler M., Maasberg M., Bernotat-Danilewski S., Luethe N.,
RA Sharma H.S., Schaper W.;
RT "Isolation of heparin-binding growth factors from bovine, porcine and
canine hearts";
RL Eur. J. Biochem. 181:67-73(1989).
CC -1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN
VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
CONCENTRATION OF THESE 2 GROWTH FACTORS.
CC -1- SUBUNIT: MONOMER.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN, ALTHOUGH LESS STRONGLY
THAN DOES BEGF.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
DR PIR: S03955; S03955.
DR HSSP: P05230; 2AXM.
DR INTERPRO: IPR002209; .
DR PROSITE: PS00247; HBGF_FGF; PARTIAL.
KW Growth factor; Mitogen; Vascularization; Heparin-binding.

FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1732 MW; 53CC9A3CADDDDA1 CRC64;

Query Match
Best Local Similarity 20.8%; Score 20; DB 1; Length 15;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 SYSKKL 12
DB 1 NYMKPL 7

RESULT 10
RIPK_TRIKI
ID RIPK_TRIKI STANDARD; PRT; 16 AA.
AC P16093;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE RIBOSOME-INACTIVATING PROTEIN TRICHOKIRIN (RNA N-GLYCOSIDASE)
DE (EC 3.2.2.22) (FRAGMENT).
OS Trichosanthos kirilowi (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Cucurbitales; Cucurbitaceae; Trichosanthes.
[1]
RN SEQUENCE.
RP TISSUE=SEED;
RX MEDLINE; 89005108.
RA Casellas P., Dussosoy D., Falasca A.I., Barbieri L.,
RA Guillemot J.C., Ferrara P., Bologna A., Cennini P., Stirpe F.;
RT "Trichosanthos kirilowi Maximowicz. Purification, partial
RT characterisation and use for preparation of immunotoxins."
RL Eur. J. Biochem. 176:581-588(1988).
CC -1- CATALYTIC ACTIVITY: ENDOPHYLISIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- PTM: GLYCOSYLATED.
CC -1- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
CC PROTEINS. BELONGS TO TYPE 1 RIP.
DR PIR: S01669; S01669.
DR INTERPRO: IPR001574; -
DR PROSITE: PS00275; SHIGA_RICIN; PARTIAL.
KW Protein synthesis inhibitor; Hydrolase; Toxin; Glycoprotein.
KW NON_TER 16
SQ SEQUENCE 16 AA; 1605 MW; 5E26847F345935A2 CRC64;

Query Match
Best Local Similarity 20.8%; Score 20; DB 1; Length 16;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 ASYSK 9
DB 12 ASYK 16

RESULT 11
B44K_PORGI
ID B44K_PORGI STANDARD; PRT; 8 AA.
AC P81886;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 44 KDA IMMUNOGENIC PROTEIN (FRAGMENT).
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; CFB group; Bacteroidaceae; Porphyromonas.
[1]
RN SEQUENCE.
RP STRAIN=VPB 3492;
RX MEDLINE; 20198497.
RA Norris J.M., Love D.N.;

RT "Serum antibody responses of cats to soluble whole cell antigens of
RT feline porphyromonas gingivalis."
RL Vet. Microbiol. 73:37-49(2000).
CC -1- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
KW Antigen.
FT NON_TER 8
SQ SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;

Query Match
Best Local Similarity 19.8%; Score 19; DB 1; Length 8;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 ASYSKKL 12
DB 1 APYOKRNI 8

RESULT 12
MAST_VESBA
ID MAST_VESBA STANDARD; PRT; 14 AA.
AC P21654;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE MASTOPARAN B.
OS Vespa basalis (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vespoidea; Vespidae; Vespinae; Vespa.
[1]
RN SEQUENCE.
RP TISSUE=VENOM;
RX MEDLINE; 91174755.
RA Lo C.-L., Hwang L.-L.;
RT "Structure and biological activities of a new mastoparan isolated
RT from the venom of the hornet vespa basalis."
RL Biochem. J. 274:453-456(1991).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
CC THAT COUPLE TO PHOSPHOLIPASE C.
DR PIR: S14336; S14336.
KW Mast cell degranulation; Venom; Amidation.
KW MOD_RES 14
FT MOD_RES 14
SQ SEQUENCE 14 AA; 1613 MW; D35944CA193A19A2 CRC64;

Query Match
Best Local Similarity 19.8%; Score 19; DB 1; Length 14;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 SYSKKL 12
DB 8 SWAKVL 14

RESULT 13
EPIA_MTCR
ID EPIA_MTCR STANDARD; PRT; 15 AA.
AC P81266;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (FRAGMENT).
OS Microplitis croceipes.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Ichneumonidae; Braconidae; Microgasterinae; Microplitis.
[1]
RN SEQUENCE.
RP MEDLINE; 99033459.
RX Stuart M.K.;
RT "An antibody diagnostic for hymenopteran parasitism is specific for a
RT homologue of elongation factor-1 alpha.";

```

RL Arch. Insect Biochem. Physiol. 39:1-8(1998).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
CC AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
CC BIOSYNTHESIS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR
CC EF-TU/EF-1A SUPERFAMILY.
CC INTERPRO: IPR000795; -.
DR PROSITE: PS00301; EFACOR_GTP, PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 15
SQ SEQUENCE 15 AA: 1670 MW: 1E87DA05B09B3751 CRC64;

Query Match 19.8% Score 19; DB 1; Length 15;
Best Local Similarity 20.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 8 SKKRLFLSL 17
   :|:|:|:|:|:
Db 1 AKKIHINIV 10

RESULT 14
RL6_VIBPR STANDARD; PRT; 16 AA.
ID 056715:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 50S RIBOSOMAL PROTEIN L6 (FRAGMENT).
GN RPLF.
OS Vibrio proteolyticus (Aeromonas proteolytica).
NC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15338;
RX MEDLINE: 97149305.
RA Settequist R.A., Smith G.K., Oakley T.H., Lee Y.H., Fox G.E.
RT "Sequence, overproduction and purification of Vibrio proteolyticus
RT ribosomal protein L18 for in vitro and in vivo studies.";
RL Gene 183;237-242(1996).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
CC LOCATED AT THE AMINOACYL-TRNA BINDING SITE OF THE
CC PEPTIDYLTRANSFERASE CENTER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L6P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U08943; AAB41328.1; -.
DR INTERPRO: IPR002358; -.
DR PROSITE: PS00525; RIBOSOMAL_L6.1; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1
SQ SEQUENCE 16 AA: 1935 MW: ABC19078DF581B6C CRC64;

Query Match 19.8% Score 19; DB 1; Length 16;
Best Local Similarity 44.4%; Pred. No. 2.5e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 VQASYSKKK 11
   :|:|:|
Db 8 VRTKARKKK 16

RESULT 15

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PHSL_DESBN STANDARD; PRT; 19 AA.
ID PHSL_DESBN
AC P13066;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PERIPLASMIC [NIFSE] HYDROGENASE LARGE SUBUNIT (EC 1.18.99.1) [NIFSE]
DE HYDROGENYLASE LARGE CHAIN (FRAGMENT).
OS Desulfovibrio baculatus (strain Norway 4).
NC Bacteria; Proteobacteria; delta subdivision; Desulfomicrobium.
RN [1]
RP SEQUENCE.
RX MEDLINE: 88106446.
RA Prickril B.C., He S.H., Li C., Menon N., Choi E.S., Przybyla A.E.,
RA Dervartanian D.V., Peck H.D. Jr., Faugue G., Le Gall J., Teixeira M.,
RA Moura I., Moura J.J.G., Patil D., Huynh B.H.;
RT "Identification of three classes of hydrogenase in the genus,
RT Desulfovibrio.";
RL Biochem. Biophys. Res. Commun. 149:369-377(1987).
CC -1- CATALYTIC ACTIVITY: 2 REDUCED FERREDOXIN + 2 H(+) = 2 OXIDIZED
CC FERREDOXIN + H(2).
CC -1- COFACTOR: ONE NICKEL ION, TWO 4FE-4S CLUSTERS AND ONE
CC SELENOCYSTEINE.
CC -1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL SUBUNIT.
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE [NIFE]/[NIFSE] HYDROGENASE LARGE
CC SUBUNIT FAMILY.
DR PIR: H27480; H27480.
DR INTERPRO: IPR001501; -.
DR PROSITE: PS00507; NI_HGNASE_L_1; PARTIAL.
DR OXIDOREDUCTASE; Periplasmic; Nickel; Selenum; Selenocysteine.
KW NON_TER 19
FT SEQUENCE 19 AA: 1942 MW: 2BFCD2D360F00367 CRC64;

Query Match 19.8% Score 19; DB 1; Length 19;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 ASYSKKKL 12
   :|:|:|
Db 7 AADGKKKI 14

Search completed: December 21, 2000, 08:33:00
Job time: 443 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:35:40 ; Search time : 57.2 Seconds

(Without alignments)
11.880 Million cell updates/sec

Title: US-08-934-367-35

Perfect score: 96
Sequence: 1 TTVAQSYSKKFLSLDFQ 20

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	27.1	18	3 002414	002414 aspergillus
2	26	27.1	19	2 09RLU4	09RLU4 lactococcus
3	25	26.0	18	11 P97522	P97522 rattus norv
4	24	25.0	15	3 09URE0	09URE0 saccharomyc
5	24	25.0	15	4 09UCH4	09UCH4 homo sapien
6	24	25.0	18	2 006514	006514 escherichia
7	24	24.0	20	2 09RAE9	09RAE9 rhodospseudo
8	23	24.0	17	2 P78199	P78199 escherichia
9	23	24.0	18	2 056610	056610 vibrio chol
10	23	24.0	18	11 09QVBO	09QVBO rattus sp.
11	23	24.0	20	6 09T518	09T518 otycolagus
12	23	24.0	20	8 P82138	P82138 spinacia ol
13	23	24.0	20	11 008806	008806 mus musculu
14	22	22.9	15	4 P78533	P78533 homo sapien
15	22	22.9	16	4 09UD41	09UD41 homo sapien
16	22	22.9	16	6 09TRA2	09TRA2 sus scrofa
17	22	22.9	17	11 09Z170	09Z170 mus musculu
18	22	22.9	19	4 09UMK9	09UMK9 homo sapien
19	22	22.9	19	6 09TRF3	09TRF3 macropus gl

20	21	21.9	9	2 045852	045852 clostridium
21	21	21.9	12	11 054970	054970 mus musculu
22	21	21.9	14	2 09R506	09R506 burkholderi
23	21	21.9	18	11 09QUZ8	09QUZ8 rattus sp.
24	21	21.9	19	3 092321	092321 saccharomyc
25	21	21.9	20	2 049448	049448 mycoplasma
26	21	21.9	20	9 037868	037868 bacterioph
27	21	21.9	20	12 086935	086935 human herpe
28	21	21.9	20	12 086936	086936 human herpe
29	21	21.9	20	12 086937	086937 human herpe
30	21	21.9	20	12 086938	086938 human herpe
31	21	21.9	20	12 086939	086939 human herpe
32	21	21.9	20	12 086940	086940 human herpe
33	21	21.9	20	12 086941	086941 human herpe
34	21	21.9	20	12 086942	086942 human herpe
35	20.5	21.4	19	13 09PRP1	09PRP1 gallus gall
36	20	20.8	13	11 062354	062354 mus musculu
37	20	20.8	13	11 062355	062355 mus musculu
38	20	20.8	15	2 068425	068425 buchiera ap
39	20	20.8	15	2 09R470	09R470 pseudomonas
40	20	20.8	16	2 047605	047605 escherichia
41	20	20.8	16	2 09R410	09R410 spiroplasma
42	20	20.8	16	10 09S8A4	09S8A4 secale cere
43	20	20.8	16	12 079458	079458 human immun
44	20	20.8	17	8 09Z177	09Z177 trisoculus
45	20	20.8	18	2 046390	046390 clostridium

ALIGNMENTS

RESULT 1					
002414	002414	PRELIMINARY;	PRT;	18 AA.	
ID	002414				
AC	002414				
DT	01-NOV-1996 (TREMUREL. 01, Created)				
DT	01-NOV-1996 (TREMUREL. 01, Last sequence update)				
DT	01-NOV-1998 (TREMUREL. 08, Last annotation update)				
DE	OROTIDINE-5'-MONOPHOSPHATE DECARBOXYLASE (FRAGMENT).				
GN	PRG.				
OS	Aspergillus awamori.				
OC	Eukaryota; Fungi; Ascomycota; Eurotiiales; Trichocomaceae;				
OC	anamorphic Trichocomaceae; Aspergillus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 96031709.				
RA	Gouka R.J., Hessing J.G., Stam H., Musters W., Hondel C.A.;				
RT	"A novel strategy for the isolation of defined pyrg mutants and the				
RT	development of a site-specific integration system for Aspergillus				
RT	awamori.";				
RL	Curr. Genet. 27:536-540(1995).				
DR	EMBL; S79674; AAB3350.1; -.				
FT	NON_TER	1			
FT	SEQUENCE	18 AA;	1891 MW;	E1A0E34C7D23688E CRC64;	
SO					
Query Match	27.1%	Score 26;	DB 3;	Length 18;	
Best Local Similarity	41.2%	Pred. No. 8.1e+02;			
Matches 7;	Conservative 1;	Mismatches 9;	Indels 0;	Gaps 0;	
QY	2 TVQASYSKKKFLSLD 18				
Db	11111111111111111111				
	2 TVSADVTTKELDLAD 18				
RESULT 2					
09RLU4	09RLU4	PRELIMINARY;	PRT;	19 AA.	
ID	09RLU4				
AC	09RLU4				
DT	01-MAY-2000 (TREMUREL. 13, Created)				
DT	01-MAY-2000 (TREMUREL. 13, Last sequence update)				
DT	01-MAY-2000 (TREMUREL. 13, Last annotation update)				
DE	NISG PROTEIN (FRAGMENT).				

```

GN NISC.
OS Lactococcus lactis.
OG Plasmid pLEB513.
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-N8; TRANSPOSON-TN5481;
RA Immonen T., Mahlstrom G., Takala T., Saris P.E.J.;
RT "Evidence for a mosaic structure of the Tn5481 in Lactococcus lactis
RT N8."
RL DNA Seq. 9:245-261(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-N8; TRANSPOSON-TN5481;
RA Immonen T., Saris P.E.J.;
RT "Characterization of the nisFEG operon of the nisin Z producing
RT Lactococcus lactis subsp. lactis N8 strain."
RL DNA Seq. 9:263-274(1998).
DR EMBL; AJ000993; CAA0441.1; -.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 19 AA; 2139 MW; 6A429DC80E673613 CRC64;

Query Match
Best Local Similarity 27.1%; Score 26; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTVOASYSKKLL 12
   | : : ||| :
DB 7 TTIIVALSKKKI 18

RESULT 3
P97522 PRELIMINARY; PRT; 18 AA.
AC P97522;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DE 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE CETR GENE.
GN CETR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RA Vuillaume S., Denamur E.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X95927; CAA65168.1; -.
SQ SEQUENCE 18 AA; 2158 MW; 5C5855056C1CE6DE CRC64;

Query Match
Best Local Similarity 26.0%; Score 25; DB 11; Length 18;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 VOASYSKKLLFLSLDFQ 20
   | | : | : | : | :
DB 1 WKSPLKASFSKLFER 18

RESULT 4
Q09RE0 PRELIMINARY; PRT; 15 AA.
AC Q09RE0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE TYPE II TOPOISOMERASE, TOPOISOMERASE II.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;

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OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RA Elisea S.H., Hsiung Y., Nitiss J.L., Osteroff N.;
RL J Biol. Chem. 270:1913-1920(1995).
SQ SEQUENCE 15 AA; 2094 MW; 0A6A37F6E81E85F6 CRC64;

Query Match
Best Local Similarity 25.0%; Score 24; DB 3; Length 15;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 YSKKKLFLS 15
   | | : | : |
DB 2 YKKRKYDYS 10

RESULT 5
Q09UCH4 PRELIMINARY; PRT; 15 AA.
AC Q09UCH4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE NATURAL KILLER ENHANCING FACTOR, NKEF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 93215001.
RA Shau H., Gupta R.K., Golub S.H.;
RT "Identification of a natural killer enhancing factor (NKEF) from human
RT Cell. Immunol. 147:1-11(1993).
RL Cell. Immunol. 147:1-11(1993).
SQ SEQUENCE 15 AA; 1738 MW; 4909DA793D382BF CRC64;

Query Match
Best Local Similarity 25.0%; Score 24; DB 4; Length 15;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 VOAFQCKVNVFL 14
   | | | : | : |
DB 2 VOAFQCKVNVFL 13

RESULT 6
O06514 PRELIMINARY; PRT; 18 AA.
AC O06514;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DE 01-JUL-1997 (TREMBlrel. 04, Last annotation update)
DE DNA, MOSAIC MERCURY RESISTANCE TRANSPOSABLE ELEMENT
DE (MER-OPERON)1040 BP (FRAGMENT).
GN MERP.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CH210; TRANSPOSON-TN5059;
RX MEDLINE; 97303088.
RA Nikiforov V., Kholodil G., Minakhin L., Gorlenko Z., Kalyaeva E.,
RA Mindlin S., Nikiforov V.;
RT "Intercontinental spread of promiscuous mercury-resistance transposons
RT in environmental bacteria."
RL Mol. Microbiol. 24:321-329(1997).
DR EMBL; Y09026; CAA70241.1; -.
FT NON_TER
SQ SEQUENCE 18 AA; 1899 MW; 484A2D7197814DF9 CRC64;

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Query Match 25.0%; Score 24; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 10 KKLFLSL 16
| | | | : |
DB 2 KKLFLSL 8

RESULT 7
O9R4E9 PRELIMINARY; PRT: 20 AA.
AC O9R4E9:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE COA THIOESTERASE (FRAGMENT).
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Rhodopseudomonas.
RN [1]
RP SEQUENCE.
RX MEDLINE; 96171228.
RA Kuver J., Xu Y., Gidson J.;
RT "Metabolism of cyclohexane carboxylic acid by the photosynthetic
bacterium Rhodopseudomonas palustris.";
RL Arch. Microbiol. 164:337-345(1995).
SO SEQUENCE 20 AA; 2259 MW; 870D48384D44315 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 20;
Best Local Similarity 46.2%; Pred. No. 2e+03;
Matches 6; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

OY 10 KKLFL--LSLDFQ 20
| | | : | | | :
DB 2 KSLFDLSLDFLE 14

RESULT 8
P78199 PRELIMINARY; PRT: 17 AA.
ID P78199:
AC P78199:
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE PROBABLE N-ACETYLURAMIDYL-L-ALANINE AMIDASE (EC 3.5.1.28) (FRAGMENT).
GN AM-A.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 97349980.
RA Yamamoto Y., Aliba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mitsuhashi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA Oshima T., Oyama S., Saito N., Sempel G., Satoh Y., Sivasubram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
-K12 genome corresponding to 50.0-68.8 min on the linkage map and
analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
FT EMBL; D90874; BAA16324.1; -.
SO SEQUENCE 17 AA; 2192 MW; 02EDC1B821D3431D CRC64;

Query Match 24.0%; Score 23; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 OASYSKKK 11
| : | | | :
DB 10 OKASHSKKR 17

RESULT 9
O56610 PRELIMINARY; PRT: 18 AA.
ID O56610:
AC O56610:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
DE ACCA (FRAGMENT).
GN ACCA.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C6706;
RX MEDLINE; 97074686.
RA Franco A., Peir-Eu Y., Johnson J., Barry E.M., Guerra H., Maurer R.,
RA Morris J.G.;
RT "Cloning and characterization of dnaE, encoding the catalytic subunit
of replicative DNA polymerase III, from Vibrio cholerae strain
C6706.";
RL Gene 175:281-283(1996).
DR EMBL; U30472; AAC44579.1; -.
FT NON_TER 18
SO SEQUENCE 18 AA; 2153 MW; 18BCDAD212842EF CRC64;

Query Match 24.0%; Score 23; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 2.6e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 14 LSLDFQ 20
| : | | | :
DB 3 LNFDFE 9

RESULT 10
O9QVB0 PRELIMINARY; PRT: 18 AA.
ID O9QVB0:
AC O9QVB0:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE (CA2+-Mg2+)-ATPASE (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE.
RX MEDLINE; 93054417.
RA Ezaki J., Himeno M., Kato K.;
RT "Purification and characterization of (Ca2+-Mg2+)-ATPase in rat liver
lysosomal membranes.";
RL J. Biochem. 112:33-39(1992).
SO SEQUENCE 18 AA; 2008 MW; 8314BA373ED6AA47 CRC64;

Query Match 24.0%; Score 23; DB 11; Length 18;
Best Local Similarity 44.4%; Pred. No. 2.6e+03;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 9 KKLFLSL 17
| : | | | :
DB 6 KERVFNVL 14

RESULT 11

09TS18
ID 09TS18 PRELIMINARY; PRT; 20 AA.
AC 09TS18;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CYTOTOXIN-BINDING PROTEIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94039134.
RA Lutz F., Mohr M., Grimmig M., Leidolf R., Linder D.;
RT "Pseudomonas aeruginosa cytotoxin-binding protein in rabbit erythrocyte membranes. An oligomer of 28 kDa with similarity to transmembrane channel proteins."
FT Eur. J. Biochem. 217:1123-1128(1993).
SO SEQUENCE 20 AA; 2414 MW; 40B82D7DB5283D2D CRC64;

Query Match 24.0%; Score 23; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 9 KKKLF 13
| | | | |
Db 5 KKKIF 9

RESULT 12
P82138 PRELIMINARY; PRT; 20 AA.
ID P82138;
AC 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S15 (FRAGMENT).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Caryophyllidae; Caryophyllales;
OC Chenopodiaceae; Spinacia.
RN [1]
RP SEQUENCE.
RC STRAIN-CV. ALMARO; TISSUE-LEAF;
RA Yamauchi K., von Knoblauch K., Subramanian A.R.;
RT "Identification of all the proteins in the small subunit of an RT organelle (chloroplast) ribosome."
RU J. Biol. Chem. 0:0-0(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND OTHER PLASTIDS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- SIMILARITY: BELONGS TO THE S15P FAMILY OF RIBOSOMAL PROTEINS.
DR INTERPRO: IPR000589; -
DR PROSITE: PS00362; RIBOSOMAL_S15; PARTIAL.
KM Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 20
SO SEQUENCE 20 AA; 2294 MW; B613012072A648A3 CRC64;

Query Match 24.0%; Score 23; DB 8; Length 20;
Best Local Similarity 44.4%; Pred. No. 2.9e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 9 KKKLFSL 17
| | | | |
Db 2 KKNFSIVY 10

RESULT 13
O08806 PRELIMINARY; PRT; 20 AA.
ID O08806

AC 008806;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE SERINE PROTEINASE INHIBITOR 14 (SERINE PROTEINASE INHIBITOR MNR26 (FRAGMENT)).
GN Sp14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA Sun J., Ooms L., Bird C.H., Sutton V.R., Trapani J.A., Bird P.I.;
RU J. Biol. Chem. 0:0-0(0).
DR EMBL; 096709; AAB57821.1; -
DR MGD; MGI:894672; Sp14.
FT NON_TER 1 1
FT NON_TER 20 20
SO SEQUENCE 20 AA; 2039 MW; 38571040F8263692 CRC64;

Query Match 24.0%; Score 23; DB 11; Length 20;
Best Local Similarity 46.7%; Pred. No. 2.9e+03;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 3 VOASYSKKKLFSL 17
| | | | |
Db 4 VAASAGKILFFSSMW 18

RESULT 14
P78533 PRELIMINARY; PRT; 15 AA.
ID P78533;
AC 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE DEOXYGUANOSINE KINASE (EC 2.7.1.113) (FRAGMENT).
GN DGR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Johansson M., Karlsson A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + DEOXYGUANOSINE = ADP + dGMP.
DR EMBL; U62042; AAB48932.1; -
KM Transferase.
FT NON_TER 15
SO SEQUENCE 15 AA; 1706 MW; 53575609CC614F8E CRC64;

Query Match 22.9%; Score 22; DB 4; Length 15;
Best Local Similarity 71.4%; Pred. No. 3.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 11 KLFSL 17
| | | | |
Db 5 RFLSRL 11

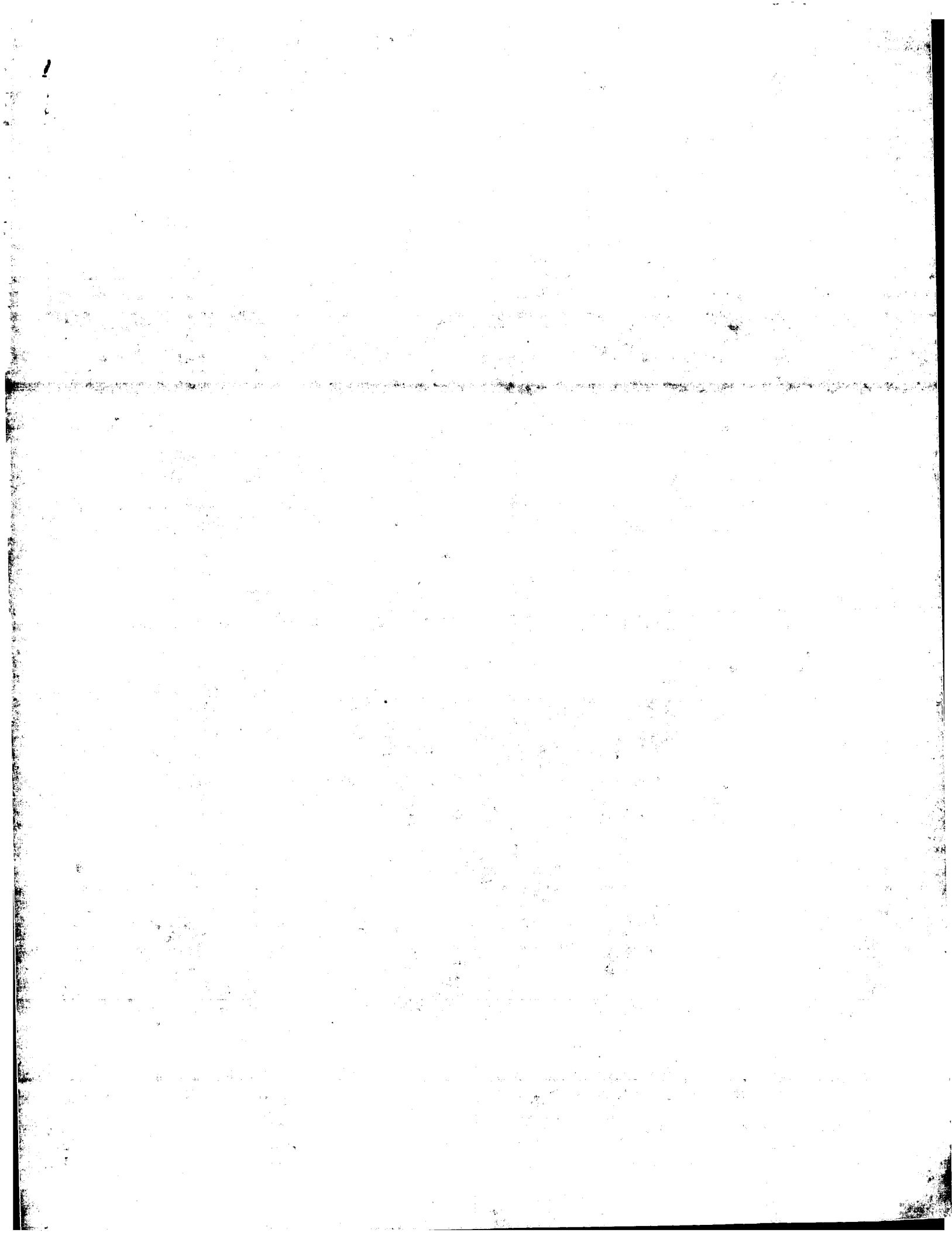
RESULT 15
Q9UD41 PRELIMINARY; PRT; 16 AA.
ID Q9UD41;
AC 09UD41;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE BETA-ISOPORN THYROID HORMONE RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95105146.
 RA Flynn T.R., Hollenberg A.N., Cohen O., Menke J.B., Usala S.J.,
 RA Tolin S., Hegarty M.K., Wondistord F.E.;
 RT "A novel C-terminal domain in the thyroid hormone receptor selectively
 RT mediates thyroid hormone inhibition.";
 RL J. Biol. Chem. 269:32713-32716(1994).
 SQ SEQUENCE 16 AA; 1920 MW; 79A831A4F3C8E22F CRC64;

Query Match 22.9%; Score 22; DB 4; Length 16;
 Best Local Similarity 40.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 11 KLFLSLDDFQ 20
 || : : |
 DB 4 KLIMKVTDLQ 13

Search completed: December 21, 2000, 08:35:40
 Job Time: 603 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:31:50 ; Search time 99.91 Seconds
(without alignments)
3.355 Million cell updates/sec

Title: US-08-934-367-36

Perfect score: 109
Sequence: 1 LLLHHQGEREPGMIKOLFVN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 1676186 residues

Total number of hits satisfying chosen parameters: 87906

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: Issued_patents-AA:*
2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backblast1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	30.3	14	1 US-08-311-611A-40	Sequence 40, Appl
2	33	30.3	14	1 US-08-372-783-40	Sequence 40, Appl
3	33	30.3	14	1 US-08-372-105-40	Sequence 40, Appl
4	33	30.3	14	1 US-08-306-473A-40	Sequence 40, Appl
5	33	30.3	14	1 US-08-209-762-40	Sequence 40, Appl
6	33	30.3	14	1 US-08-473-344-40	Sequence 40, Appl
7	33	30.3	14	2 US-08-621-803-39	Sequence 39, Appl
8	33	30.3	14	2 US-08-465-443A-40	Sequence 40, Appl
9	33	30.3	14	2 US-08-621-259A-13	Sequence 13, Appl
10	33	30.3	14	3 US-09-119-263-40	Sequence 40, Appl
11	33	30.3	14	4 PCT-US94-02465-40	Sequence 40, Appl
12	33	30.3	14	4 PCT-US95-00498-40	Sequence 40, Appl
13	33	30.3	14	4 PCT-US95-00656-40	Sequence 40, Appl
14	33	30.3	14	4 PCT-US95-09262-13	Sequence 13, Appl
15	31	28.4	10	2 US-08-621-803-227	Sequence 227, App
16	31	28.4	10	2 US-08-621-259A-219	Sequence 219, App
17	31	28.4	11	2 US-08-621-803-228	Sequence 228, App
18	31	28.4	11	2 US-08-621-259A-220	Sequence 220, App
19	31	28.4	12	2 US-08-621-803-230	Sequence 230, App
20	31	28.4	12	2 US-08-621-259A-222	Sequence 222, App
21	31	28.4	13	1 US-08-261-660A-33	Sequence 33, Appl
22	31	28.4	13	1 US-08-261-660A-42	Sequence 42, Appl
23	31	28.4	13	4 PCT-US94-06931-33	Sequence 33, Appl
24	31	28.4	13	4 PCT-US94-06931-33	Sequence 42, Appl
25	31	28.4	14	1 US-08-311-611A-15	Sequence 15, Appl
26	31	28.4	14	1 US-08-311-611A-33	Sequence 33, Appl
27	31	28.4	14	1 US-08-311-611A-34	Sequence 34, Appl
28	31	28.4	14	1 US-08-311-611A-35	Sequence 35, Appl

29	31	28.4	14	1 US-08-311-611A-36	Sequence 36, Appl
30	31	28.4	14	1 US-08-311-611A-44	Sequence 44, Appl
31	31	28.4	14	1 US-08-311-611A-45	Sequence 45, Appl
32	31	28.4	14	1 US-08-311-611A-46	Sequence 46, Appl
33	31	28.4	14	1 US-08-311-611A-81	Sequence 81, Appl
34	31	28.4	14	1 US-08-311-611A-89	Sequence 89, Appl
35	31	28.4	14	1 US-08-311-611A-91	Sequence 91, Appl
36	31	28.4	14	1 US-08-311-611A-106	Sequence 106, App
37	31	28.4	14	1 US-08-311-611A-107	Sequence 107, App
38	31	28.4	14	1 US-08-311-611A-109	Sequence 109, App
39	31	28.4	14	1 US-08-311-611A-110	Sequence 110, App
40	31	28.4	14	1 US-08-311-611A-122	Sequence 122, App
41	31	28.4	14	1 US-08-311-611A-142	Sequence 142, App
42	31	28.4	14	1 US-08-372-783-15	Sequence 15, Appl
43	31	28.4	14	1 US-08-372-783-33	Sequence 33, Appl
44	31	28.4	14	1 US-08-372-783-34	Sequence 34, Appl
45	31	28.4	14	4 PCT-US95-09262-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-08-311-611A-40
Sequence 40, Application US/08311611A
Patent No. 5523288
GENERAL INFORMATION:
APPLICANT: Cohen, Jonathan
APPLICANT: Kung, Ada H.C.
TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial
TITLE OF INVENTION: Infection by Administration of
TITLE OF INVENTION: Bactericidal/Permeability-Increasing
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,611A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,401
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/125,651
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 32251
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "BPI.38"

US-08-311-611A-40

Query Match 30.3%; Score 33; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 GWIKOLF 18
11:111
DB 5 GWLAOLF 11

RESULT 2
US-08-372-783-40
; Sequence 40, Application US/08372783
; Patent No. 5578572
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; APPLICANT: Lambert, Lewis H.
; APPLICANT: Little, Roger G.
; TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
; TITLE OF INVENTION: Materials
; NUMBER OF SEQUENCES: 237
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,783
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rih-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.38"
US-08-372-783-40

Query Match 30.3%; Score 33; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 12 GWIKOLF 18
11:111

DB 5 GWLAOLF 11

RESULT 3
US-08-372-105-40
; Sequence 40, Application US/08372105
; Patent No. 5627153
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.
; APPLICANT: Lim, Edward
; APPLICANT: Lambert, Lewis H.
; APPLICANT: Scannon, Patrick J.
; TITLE OF INVENTION: Anti-Fungal Materials and Methods
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,105
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rih-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.38"
US-08-372-105-40

Query Match 30.3%; Score 33; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 12 GWIKOLF 18
11:111
DB 5 GWLAOLF 11

RESULT 4
US-08-306-473A-40
; Sequence 40, Application US/08306473A
; Patent No. 5652332
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.

TITLE OF INVENTION: Biologically Active Peptides from
TITLE OF INVENTION: Functional Domains of Bactericidal/
TITLE OF INVENTION: Permeability-Increasing Protein and
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 226
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: Suite 3000, 10 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,473A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,1133-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: "BPI.38"
US-08-306-473A-40

Query Match 30.3%; Score 33; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 GWIKOLF 18
11:111
Db 5 GWLAQLF 11

RESULT 5
US-08-209-762-40
Sequence 40, Application us/08209762
Patent No. 5733872
GENERAL INFORMATION:
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Biologically Active Peptides from
TITLE OF INVENTION: Functional Domains of Bactericidal/Permeability-Increasing
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,762
FILING DATE: 11-JAN-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5733872nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,1133
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: "BPI.38"
US-08-209-762-40

Query Match 30.3%; Score 33; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 GWIKOLF 18
11:111
Db 5 GWLAQLF 11

RESULT 6
US-08-473-344-40
Sequence 40, Application US/08473344
Patent No. 5763567
GENERAL INFORMATION:
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Biologically Active Peptides from
TITLE OF INVENTION: Functional Domains of Bactericidal/Permeability-Increasing
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,344
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,473
FILING DATE: 15-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,762
FILING DATE: 11-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,1133-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "BPI.38"
US-08-473-344-40

Query Match 30.3%; Score 33; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 GWIKOLF 18
11: 111
Db 5 GWLAOLF 11

RESULT 7
US-08-621-803-39
Sequence 39, Application US/08621803
Patent No. 5851802
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,803
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.38"
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: //label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-39

Query Match 30.3%; Score 33; DB 2; Length 14;
e . 7 3

Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 GWIKOLF 18
11: 111
Db 5 GWLAOLF 11

RESULT 8
US-08-485-445A-40
Sequence 40, Application US/08485445A
Patent No. 5856438
GENERAL INFORMATION:
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Biologically Active Peptides from
TITLE OF INVENTION: Functional Domains of Bactericidal/
TITLE OF INVENTION: Permeability-Increasing Protein and
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 226
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: Suite 3400, 500 West Madison Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,445A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11018US08/100-224.P4.C1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-707-8889
TELEFAX: 312-707-9155
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "BPI.38"
US-08-485-445A-40

Query Match 30.3%; Score 33; DB 2; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 GWIKOLF 18
11: 111
Db 5 GWLAOLF 11

RESULT 9
US-08-621-259A-13
Sequence 13, Application US/08621259A
Patent No. 5858974
GENERAL INFORMATION:

APPLICANT: Little II, Roger G
APPLICANT: Lim, Edward
APPLICANT: Padem, Mitchell B.
TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES: 252
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,259A
FILING DATE: 21-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/504,841
FILING DATE: 20-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11021US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: "XMP.38"
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-13

Query Match 30.3% Score 33; DB 2; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWIKOLF 18
II: III
Db 5 GWIAQLF 11

RESULT 10
US-09-119-263-40
Sequence 40, Application US/09119263
GENERAL INFORMATION:
APPLICANT: Horwitz, Arnold H.
APPLICANT: Lambert, Lewis H.
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
TITLE OF INVENTION: Materials
NUMBER OF SEQUENCES: 237
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois

COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,263
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/758,116
FILING DATE:
APPLICATION NUMBER: 08/372,783
FILING DATE:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rio-laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27129/32415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: "XMP.38"
US-09-119-263-40

Query Match 30.3% Score 33; DB 3; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWIKOLF 18
II: III
Db 5 GWIAQLF 11

RESULT 11
PCT-US94-02465-40
Sequence 40, Application PC/TUS9402465
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Biologically Active Peptides from
TITLE OF INVENTION: Functional Domains of Bactericidal/Permeability-Increasing
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/02465
;; FILING DATE: 11-JAN-1994
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Noonan, Kevin E
;; REGISTRATION NUMBER: 35,303
;; REFERENCE/DOCKET NUMBER: 93,1133
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000
;; TELEFAX: 312-715-1234
;; TELE: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 40:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: misc.feature
;; OTHER INFORMATION: "BPI.38"
PCT-US94-02465-40

Query Match 30.3%; Score 33; DB 4; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 GWIKOLF 18
11:111
DB 5 GWLAOLF 11

RESULT 12
PCT-US95-00498-40
; Sequence 40, Application PC/TUS9500498
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
; NUMBER OF INVENTION: Materials
; CORRESPONDENCE ADDRESSES: 237
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00498
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELE: 25-3856
; INFORMATION FOR SEQ ID NO: 40:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: misc.feature
;; OTHER INFORMATION: "XMP.38"
PCT-US95-00498-40

Query Match 30.3%; Score 33; DB 4; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 GWIKOLF 18
11:111
DB 5 GWLAOLF 11

RESULT 13
PCT-US95-00656-40
; Sequence 40, Application PC/TUS9500656
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Materials and Methods
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELE: 25-3856
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: "XMP.38"
PCT-US95-00656-40

Query Match 30.3%; Score 33; DB 4; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWIKOLF 18
11: 111
Db 5 GWLAOLF 11

RESULT 14
PCT-US95-09262-13
; Sequence 13, Application PC/TUS9509262
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09262
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/10040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.38"
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-13

Query Match 30.3%; Score 33; DB 4; Length 14;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWIKOLF 18
11: 111
Db 5 GWLAOLF 11

RESULT 15
US-08-621-803-227
; Sequence 227, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 227:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.388"
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-227

Query Match 28.4%; Score 31; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 GWIKOLF 18
11: 111
Db 1 GWLAOLF 7

Search completed: December 21, 2000, 08:31:50
Job time: 373 sec

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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:30:08 ; Search time 112.59 Seconds

(without alignments)
11.273 Million cell updates/sec

Title: US-08-934-367-36
Perfect score: 109
Sequence: 1 LLLHLQGEREPGWIKQLFTN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	28.4	18	2	G02018
2	30	27.5	16	2	PH1790
3	29	26.6	10	2	S39030
4	27	24.8	15	2	PH1788
5	25	22.9	17	2	PH1802
6	25	22.9	17	2	PH1822
7	25	22.9	18	2	F49215
8	24	22.0	4	2	A34626
9	24	22.0	8	2	A61348
10	24	22.0	8	2	A33995
11	24	22.0	8	2	A55310
12	24	22.0	8	2	A58620
13	24	22.0	10	2	A43405
14	24	22.0	10	2	A60421
15	24	22.0	10	2	S08997
16	24	22.0	10	2	S08998
17	24	22.0	10	2	A26381
18	24	22.0	10	2	B33995
19	24	22.0	15	2	A26228
20	24	22.0	15	2	PH1329
21	24	22.0	15	2	PH1329
22	24	22.0	16	2	S38976
23	24	22.0	19	2	PT0282
24	24	22.0	20	2	S29212
25	23	21.1	7	2	A47687
26	23	21.1	7	2	A61081
27	23	21.1	11	2	S68649
28	23	21.1	15	2	S67975
29	23	21.1	16	1	A49761
	23	21.1	17	2	PH0778

30	23	21.1	18	2	S71592	serine proteinase
31	23	21.1	19	2	PH1339	Ig heavy chain DJ
32	22	20.2	9	2	S78426	52.5K protein - sp
33	22	20.2	9	2	G56978	collagen alpha 1(I
34	22	20.2	11	2	D56979	collagen alpha 1(I
35	22	20.2	11	2	PD0442	NIRSNAP2 protein -
36	22	20.2	12	2	PD0776	NAOH dehydrogenase
37	22	20.2	13	2	A28505	neurotensin-like p
38	22	20.2	14	2	PH1347	Ig heavy chain DJ
39	22	20.2	14	2	PH1311	Ig heavy chain DJ
40	22	20.2	14	2	PH1321	Ig heavy chain DJ
41	22	20.2	14	2	PH1305	Ig heavy chain DJ
42	22	20.2	14	2	PH1306	Ig heavy chain DJ
43	22	20.2	15	2	PT0222	Ig heavy chain CDR
44	22	20.2	15	2	PH1314	Ig heavy chain DJ
45	22	20.2	15	2	PH1310	Ig heavy chain DJ

ALIGNMENTS

RESULT 1
G02018
proteasome chain LMP7 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 22-Jun-1999
C:Accession: G02018
R:Kin, T.
submitted to the EMBL Data Library, July 1995
A:Reference number: G09054
A:Accession: G02018
A:Status: preliminary; translated from GR/EMBL/DDhJ
A:Molecule type: DNA
A:Residues: 1-18 <Kin>
A:Cross-references: EMBL:U32862; NID:g1045468; PIDN:AAA80234.1; PID:g1045469
C:Genetics:
A:Gene: LMP7
C:Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 28.4%; Score 31; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 REPGWIK 15
DB 4 KEDGWVK 10

RESULT 2
PH1790
T cell receptor alpha chain V region (clone 2PBL v alpha 24-6) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1790
R:Porcellini, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blo

A:Reference number: PH1754; MUID:93301585
A:Accession: PH1790
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <POR>

Query Match 27.5%; Score 30; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HLQGEREP 11
DB 1 HLQGERGP 8

```
RESULT 3
S39030
lysyl-bradykinin - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 19-Apr-1996
C:Accession: S39030
R:Conlon, J.M.; Olson, K.R
FEBS Lett. 334, 75-78, 1993
A:Title: Purification of a vasoactive peptide related to lysyl-bradykinin from trout pla
A:Reference number: S39030; MUID:94039817
A:Accession: S39030
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <CON>

Query Match          26.6%; Score 29; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 EREPGW 13
: |||
Db 1 KRPGW 6

RESULT 4
PH1788
T cell receptor alpha chain V region (clone 2PBu V alpha 24-4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1788
R:Porcell, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585
A:Accession: PH1788
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <POR>

Query Match          24.8%; Score 27; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 HLCGER 10
: |||
Db 1 HLCGERQ 7

RESULT 5
PH1802
T cell receptor alpha chain V region (clone 3PBu V alpha 24-8) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1802
R:Porcell, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585
A:Accession: PH1802
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-17 <POR>

Query Match          22.9%; Score 25; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 HLCGER 9
: |||
Db 1 HLCGER 6

RESULT 6
PH1822
T cell receptor alpha chain V region (clone 5PBu V alpha 24-5) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1822
R:Porcell, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blo
A:Reference number: PH1754; MUID:93301585
A:Accession: PH1822
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-17 <POR>

Query Match          22.9%; Score 25; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HLCGER 9
: |||
Db 1 HLCGER 6

RESULT 7
F49215
urease (EC 3.5.1.5) small chain Urea - Helicobacter mustelae (ATCC 43772) (fragment)
C:Species: Helicobacter mustelae
C>Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 30-May-1997
C:Accession: F49215
R:Turbell, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.
Infect. Immun. 60, 5259-5266, 1992
A:Title: Purification and characterization of the urease enzymes of Helicobacter spec
A:Reference number: A49215; MUID:93084378
A:Accession: F49215
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <TUR>
A:Note: sequence extracted from NCBI backbone (NCBIRP:119487)
C:Superfamily: urease 20k chain; urease 11k chain homology; urease 12k chain homology
C:Keywords: hydrolase

Query Match          22.9%; Score 25; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLLHLCGE 8
: |||
Db 9 MMLHYAGE 16

RESULT 8
A34626
RPCH-related neuropeptide - ferruginous spindie
C:Species: Fusinus ferrugineus (ferruginous spindie)
C>Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C:Accession: A34626
R:Kuroki, Y.; Kanda, T.; Kubota, T.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake,
Biochem. Biophys. Res. Commun. 167, 273-279, 1990
A:Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A:Reference number: A34626; MUID:90179762
A:Accession: A34626
A:Status: preliminary
A:Molecule type: protein
```

A:Residues: 1-4 <KUR>
C:Keywords: neuropeptide

Query Match 22.0%: Score 24; DB 2; Length 4;
Best Local Similarity 100.0%: Pred. No. 1.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGW 13
Db 2 PGW 4

RESULT 9
A61348

red pigment-concentrating hormone - northern shrimp
N:Alternate names: blanching hormone
C:Species: *Pandalus borealis* (northern shrimp)
C:Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C:Accession: A61348; S07139
R:Perlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A:Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A:Reference number: A61348; MUID:72228738
A:Accession: A61348
A:Molecule type: protein
A:Residues: 1-8 <PER>
R:Perlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A:Title: Structure of the red-pigment-concentrating hormone of the shrimp, *Pandalus borealis*.
A:Reference number: S07139; MUID:75054965
A:Accession: S07139
A:Molecule type: protein
A:Residues: 'E', 2-8 <PER2>
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C:Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pig-
C:Superfamily: adipokinetin hormone
C:Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 22.0%: Score 24; DB 2; Length 8;
Best Local Similarity 100.0%: Pred. No. 1.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGW 13
Db 6 PGW 8

RESULT 10
A33995

adipokinetin hormone - black horse fly
C:Species: *Tabanus atratus* (black horse fly)
C:Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997
C:Accession: A33995
R:Jeffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A:Title: Primary structure of two neuropeptide hormones with adipokinetin and hypotrehal
A:Reference number: A33995; MUID:90046758
A:Accession: A33995
A:Molecule type: protein
A:Residues: 1-8 <JAF>
C:Superfamily: adipokinetin hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 22.0%: Score 24; DB 2; Length 8;
Best Local Similarity 100.0%: Pred. No. 1.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGW 13
Db 6 PGW 8

RESULT 11
S55310

adipokinetin hormone - damselfly (*Pseudagrion inconspicuum*)
N:Alternate names: Psi-AKH
C:Species: *Pseudagrion inconspicuum*
C:Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
C:Accession: S55310
R:Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A:Title: A novel adipokinetin octapeptide found in the damselflies *Pseudagrion inco*
A:Reference number: S55310; MUID:94379987
A:Accession: S55310
A:Molecule type: protein
A:Residues: 1-8 <JAN>
C:Superfamily: adipokinetin hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 22.0%: Score 24; DB 2; Length 8;
Best Local Similarity 100.0%: Pred. No. 1.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGW 13
Db 6 PGW 8

RESULT 12
A58620

adipokinetin hormone - damselfly (*Ischnura senegalensis*)
C:Species: *Ischnura senegalensis*
C:Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
C:Accession: A58620
R:Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A:Title: A novel adipokinetin octapeptide found in the damselflies *Pseudagrion inco*
A:Reference number: S55310; MUID:94379987
A:Accession: A58620
A:Molecule type: protein
A:Residues: 1-8 <JAN>
C:Superfamily: adipokinetin hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 22.0%: Score 24; DB 2; Length 8;
Best Local Similarity 100.0%: Pred. No. 1.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGW 13
Db 6 PGW 8

RESULT 13
A43405

6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2,6-bisphosphate 2-phosphatase (EC
C:Species: *Bos primigenius taurus* (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Mar-2000
C:Accession: A43405
R:Ventura, F.; Rosa, J.L.; Ambrosio, S.; Pilakis, S.J.; Bartons, R.
J. Biol. Chem. 267, 17939-17943, 1992
A:Title: Bovine Brain 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase. Evidence

A:Reference number: A43405; MUID:92388154
A:Accession: A43405
A:Molecule type: protein
A:Residues: 1-10 <VEN>
C:Superfamily: 6-phosphofructo-2-kinase / fructose-2,6-bisphosphate 2-phosphatase; phosph
C:Keywords: phosphoric monoester hydrolase; phosphotransferase

Query Match 22.0%; Score 24; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 HLOGE 8
11:11
DB 5 HLKGE 9

RESULT 14

A60421
hypertrehalosemic hormone - German cockroach
N:Alternate names: Bld-HrTH
C:Species: Blattella germanica (German cockroach)
C>Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 31-Oct-1997
C:Accession: A60421; S09137
R:Veestra, J.A.; Camps, F.
Neuropeptides 15, 107-109, 1990
A>Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, Blatt
A:Reference number: A60421; MUID:91179584
A:Accession: A60421
A:Molecule type: protein
A:Residues: 1-10 <VEE>
R:Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A>Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpor
entails and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A:Reference number: S08995; MUID:90253659
A:Accession: S09137
A:Molecule type: protein
A:Residues: 1-10 <GAE>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 22.0%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PGW 13
11:11
DB 6 PGW 8

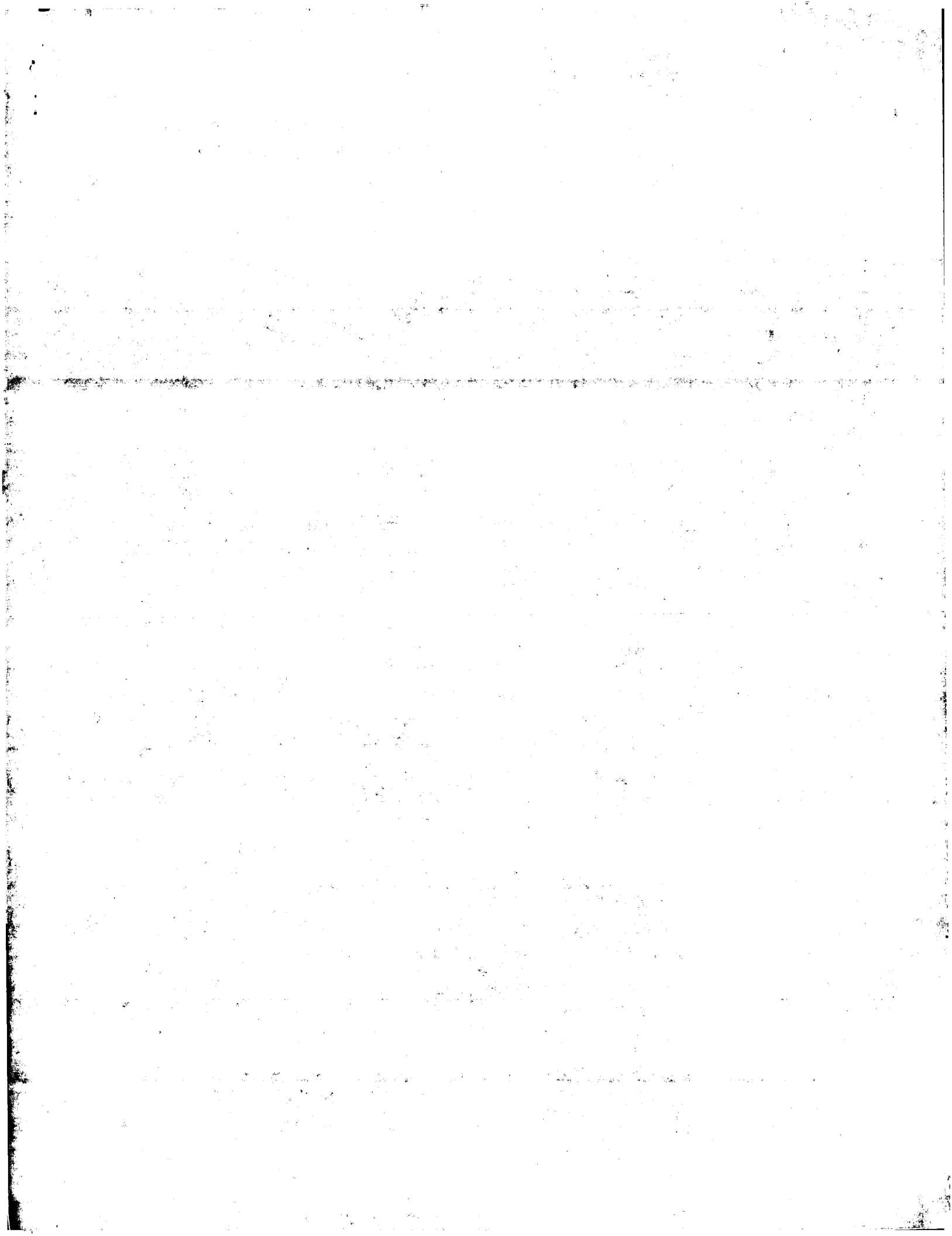
RESULT 15

S08997
hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)
C:Species: Gromphadorina portentosa
C>Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 24-Oct-1997
C:Accession: S08997
R:Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A>Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpor
entails and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A:Reference number: S08995; MUID:90253659
A:Accession: S08997
A:Molecule type: protein
A:Residues: 1-10 <GAE>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 22.0%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PGW 13
11:11
DB 6 PGW 8

Search completed: December 21, 2000, 08:30:08
Job time: 272 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:33:00 ; Search time 52.7 Seconds

(without alignments)
10.191 Million cell updates/sec

Title: US-08-934-367-36
Perfect score: 109
Sequence: 1 LLLHLQGEREPGWIKQLFTN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues
Total number of hits satisfying chosen parameters: 1083

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	25.7	19	1 TRP3_LEUMA	P81735 leucophaea
2	24	22.0	8	1 AKH_TABAT	P14595 tabanus atr
3	24	22.0	8	1 RPCH_PANBO	P08939 pandanus bo
4	24	22.0	10	1 HTF_NAUCI	P10939 nauphoeta c
5	24	22.0	10	1 HTF_TABAT	P14596 tabanus atr
6	24	22.0	10	1 AROQ_AME	P46380 amycolatops
7	23	21.1	16	1 LPK1_LOCHI	P20404 locusta mlg
8	22	20.2	13	1 BRK_PARID	P42717 parapolydia
9	22	20.2	13	1 NEUT_CHICK	P13724 gallus gall
10	21	19.3	10	1 QZOG_COMTE	P80466 comanona t
11	21	19.3	13	1 CXET_COMTE	P81755 comus texti
12	21	19.3	17	1 CHH3_BOMMO	P20729 bombyx mori
13	21	19.3	20	1 CRCC_SPILO	P30806 spinacia ol
14	20	18.3	12	1 PORD_METT	P80903 methanobact
15	20	18.3	13	1 HPAL_RANES	P32415 rana esculie
16	20	18.3	14	1 CAT2_FASHE	P80342 fasciola he
17	20	18.3	15	1 TAL_TREBR	P34070 tremella br
18	20	18.3	19	1 CAT3_FASHE	P80532 fasciola he
19	20	18.3	19	1 LANA_ACTUG	P56650 actinoplane
20	20	18.3	20	1 CAT1_FASHE	P09093 fasciola he
21	19.5	17.9	20	1 COG1_PARC	P55576 ratius norv
22	19	17.4	7	1 UH11_RAT	P55576 petromyzon
23	19	17.4	10	1 GON1_PETMA	P20367 oncorhynch
24	19	17.4	10	1 GON3_ONCKE	P27429 squalus aca
25	19	17.4	10	1 GONL_SQUAC	P47881 elm yellow
26	19	17.4	12	1 RS19_ELYEP	P43173 ascatis suu
27	19	17.4	13	1 FARB_ASCSU	P41536 rana tempor
28	19	17.4	13	1 NEUT_RANVE	P46828 clover proi
29	19	17.4	14	1 RS19_CLOPP	P48878 loofah wilt
30	19	17.4	14	1 RS19_LOWBP	P80907 methanobact
31	19	17.4	15	1 VORA_METT	P15506 bos taurus
32	19	17.4	18	1 NPA_BOVIN	P14471 equus caball
33	19	17.4	19	1 FIBB_HORSE	

34	19	17.4	19	1 PYRB_PSEFL	P56585 pseudomonas
35	19	17.4	20	1 COG1_CHIOP	P34153 chionoecete
36	18	16.5	8	1 AKH_LIBAU	P25418 libellula a
37	18	16.5	8	1 CCKN_MACEU	P30369 macropus eu
38	18	16.5	8	1 HTF1_PERAM	P04548 periplaneta
39	18	16.5	8	1 HTF2_PERAM	P04549 periplaneta
40	18	16.5	8	1 HTF_TENMO	P25419 tenebrio mo
41	18	16.5	8	1 UF06_MOUSE	P38644 mus musculu
42	18	16.5	10	1 CAER_LITXA	P56264 litorea xan
43	18	16.5	10	1 HTF1_ROMMI	P18110 romalea mic
44	18	16.5	10	1 HTF2_CARMO	P11385 carausius m
45	18	16.5	11	1 BRK_MEGFL	P12797 megascolla

ALIGNMENTS

RESULT 1
TRP3_LEUMA STANDARD: PRT: 19 AA.

AC P81735:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TACHYKININ-RELATED PEPTIDE 3 (LEMRP 3).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
RN [1]

RP SEQUENCE.
RC TISSUE=MIDGUT.
RX MEDLINE: 97053012.
RA Muren J.E., Naessel D.R.:
RT "Isolation of five tachykinin-related peptides from the midgut of
RT the cockroach Leucophaea maderae: existence of N-terminally extended
RT isoforms.";
RL Regul. Pept. 65:185-196(1996).

CC -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -1- TISSUE SPECIFICITY: MIDGUT.

CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD.RES 19
SQ SEQUENCE 19 AA: 1930 MW: 9985471A011625E5 CRC64:

Query Match 25.7%; Score 28; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 7 GEREPG 12
11111

DB 2 GERAPG 7

RESULT 2
AKH_TABAT STANDARD: PRT: 8 AA.

AC P14595:
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH) (DIPTERAN CORPORA CARDIACA FACTOR I)
DE (DCC 1).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
OC Tabanidae; Tabanus.
RN [1]

RP SEQUENCE.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE: 90046758.

RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hypertrehalosemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC GLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE GLYCERIDES AS AN ENERGY SOURCE.
 CC -1- SIMILARITY: BELONGS TO THE AKH / RHTH / RPCH FAMILY.
 DR PIR: A33955; A33955.
 DR INTERPRO: IPR002047; -.
 DR PROSITE: PS00256; AKH; 1.
 KM Neuropeptide; Amidation; Flight.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 22.0%; Score 24; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGW 13
 Db 6 PGW 8

RESULT 3
 RPCH_PANBO STANDARD; PRT; 8 AA.
 AC P08939;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE RED PIGMENT CONCENTRATING HORMONE (RPCH).
 OS Pandanus borealis (Northern red shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidae;
 OC Pandalidae; Pandalus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 75054965.
 RA Fernlund P.;
 RT "Structure of the red-pigment-concentrating hormone of the shrimp,
 RT Pandanus borealis.";
 RL Biochim. Biophys. Acta 371:304-311(1974).
 CC -1- FUNCTION: THIS HORMONE ADAPTS THE ANIMAL TO LIGHT BACKGROUNDS BY
 CC STIMULATING CONCENTRATION OF THE PIGMENT OF ITS RED BODY-
 CC CHROMATOPHORES.
 CC -1- SIMILARITY: BELONGS TO THE AKH / RHTH / RPCH FAMILY.
 DR PIR: S07139; S07139.
 DR INTERPRO: IPR002047; -.
 DR PROSITE: PS00256; AKH; 1.
 KM Pigment; Hormone; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 948 MW; 86786775B9C44736 CRC64;

Query Match 22.0%; Score 24; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGW 13
 Db 6 PGW 8

RESULT 4
 HTF_NAUCI STANDARD; PRT; 10 AA.
 ID HTF_NAUCI

AC P10939;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPERTREHALOSAEMIC HORMONE (HTH) (HYPERTREHALOSAEMIC NEUROPEPTIDE).
 OS Nauphoeta cinerea (Cinereous cockroach),
 OS Leucophaea maderae (Maderia cockroach),
 OS Blattella germanica (German cockroach),
 OS Gromphadorhina portentosa (Cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberoidea; Blaberidae; Nauphoeta.
 RN [1]
 RP SEQUENCE.
 RC SPECIES=N.CINEREA; TISSUE=CORPORA CARDIACA;
 RX MEDLINE: 87100208.
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Amino acid sequence of a hypertrehalosaemic neuropeptide from the
 RT corpus cardiaca of the cockroach, Nauphoeta cinerea.";
 RL Biochem. Biophys. Res. Commun. 141:774-781(1986).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=L.MADERAE, G.PORIENTOSA, AND B.GERMANICA;
 RX MEDLINE: 90253659.
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
 RT and of the stick insect Extatosoma titatum assigned by tandem fast
 RT atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=B.GERMANICA;
 RX MEDLINE: 91179584.
 RA Veenstra J.A., Camps F.;
 RT "Structure of the hypertrehalosemic neuropeptide of the German
 RT cockroach, Blattella germanica.";
 RL Neuropeptides 15:107-109(1990).
 CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / RHTH / RPCH FAMILY.
 DR PIR: A26381; A26381.
 DR PIR: S08997; S08997.
 DR PIR: S08998; S08998.
 DR PIR: S09137; S09137.
 DR PIR: A60421; A60421.
 DR INTERPRO: IPR002047; -.
 DR PROSITE: PS00256; AKH; 1.
 KM Neuropeptide; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1092 MW; 056236786775B9C4 CRC64;

Query Match 22.0%; Score 24; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGW 13
 Db 6 PGW 8

RESULT 5
 HTF_TABAT STANDARD; PRT; 10 AA.
 ID HTF_TABAT
 AC P14596;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE HYPERTREHALOSAEMIC FACTOR (HTHF) (DIPTERAN CORPORA CARDIACA FACTOR II)

DE (DCC II).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
OC Tabanidae; Tabanus.
RN [1]
RP SEQUENCE.
RC TISSUE-CORPORA CARDIACA;
RX MEDLINE: 90046758.
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RT Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYPH OF INSECTS).
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RCH FAMILY.
DR PIR: B33995; B33995.
DR INTERPRO: IPR002047; .
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
FT SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;

Query Match 22.0%; Score 24; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PGM 13
Db 6 PGM 8

RESULT 6
AROO_AMYME STANDARD; PRT: 20 AA.
ID AROO_AMYME
AC P46380;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10) (3-DEHYDROQUINASE)
DE (TYPE II DHQASE) (FRAGMENT).
GN AROO.
OS Amycolatopsis methanolica.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Pseudonocardiales; Pseudonocardiaceae;
OC Amycolatopsis.
RN [1]
RP SEQUENCE.
RC STRAIN-NCIB 11946;
RX MEDLINE: 93123995.
RA Eversink G.J.W., Hessels G.I., Vrijbloed J.W., Coggins J.R.,
RT Dijkhuizen L.;
RT "Purification and characterization of a dual function
RT 3-dehydroquinate dehydratase from Amycolatopsis methanolica.";
RT J. Gen. Microbiol. 138:2449-2457(1992).
CC -1- FUNCTION: CATALYZE A TRANS-DEHYDRATION VIA AN ENOLATE
CC INTERMEDIATE. IS INVOLVED IN BOTH THE CATABOLISM OF QUINATE AND
CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS. HAS A TEMPERATURE
CC OPTIMAL OF 76 DEGREES CELSIUS AND PH OPTIMAL OF 9.0. TYPE II
CC ENZYMES ARE THERMOSTABLE.
CC -1- CATALYTIC ACTIVITY: 3-DEHYDROQUINATE = 3-DEHYDROSHIKIMATE + H(2)O.
CC -1- PATHWAY: THIRD STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
CC -1- SUBUNIT: HOMODODECAMER.
CC -1- SIMILARITY: BELONGS TO THE TYPE-II 3-DEHYDROQUINASE FAMILY.
DR INTERPRO: IPR001874; .
DR PROSITE: PS01029; DEHYDROQUINASE-II, PARTIAL.
KW Quinate metabolism; Aromatic amino acid biosynthesis; Lyase.

FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2197 MW; C24AA1B3E5CFD0A CRC64;
Query Match 22.0%; Score 24; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 GEREP 11
Db 15 GKREP 19

RESULT 7
LPR1_LOCM1 STANDARD; PRT: 16 AA.
ID LPR1_LOCM1
AC P20404;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE LOCUSTAPYROKININ 1 (LOW-PK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;
OC Acridoidea; Acrididae; Locusta.
RN [1]
RP SEQUENCE.
RC TISSUE-CORPORA CARDIACA;
RX MEDLINE: 91224474.
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, primary structure, and synthesis of locustapyrokinin: a
RT myotropic peptide of Locusta migratoria.";
RL Gen. Comp. Endocrinol. 81:97-104(1991).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR: A49761; A49761.
DR INTERPRO: IPR001484; .
DR PROSITE: PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 16 16 AMIDATION.
FT SEQUENCE 16 AA; 1827 MW; A7178BBDCAAFD6 CRC64;

Query Match 21.1%; Score 23; DB 1; Length 16;
Best Local Similarity 57.1%; Pred. No. 8e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 GWIKOLF 18
Db 6 GWPOOPF 12

RESULT 8
BRK_PARID STANDARD; PRT: 13 AA.
ID BRK_PARID
AC P42717;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE WASPKININ.
OS Parapolybia indica.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoecrita; Aculeata;
OC Vespidae; Vespidae; Polistinae; Parapolybia.
RN [1]
RP SEQUENCE.
RC TISSUE-VENOM.
RA Toki T., Yasuhara T., Nakajima T.;
RT "Isolation and sequential analysis of peptides on the venom sac of
RT Parapolybia indica.";
RL Eisel Dobutsu 39:105-111(1988).

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CC -1- FUNCTION: SMOOTH MUSCLE CONTRACTION.
KM Bradykinin; Vasodilator.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1573 MW; 2673CB3D83ECC867 CRC64;

Query Match
Best Local Similarity 20.2%; Score 22; DB 1; Length 13;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 QGEREPGW 13
   1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1 QZKRPPGF 8

RESULT 9
NEUT_CHICK
ID NEUT_CHICK STANDARD; PRT; 13 AA.
AC P13724;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE NEUROTENSIN (NT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN 111
RP SEQUENCE.
RX MEDLINE; 88063566.
RA Iwabuchi H., Komori S., Ohashi H., Kimura S.;
RT "The amino acid sequence of a smooth muscle-contracting peptide from
RT chicken rectum. Identity to chicken neurotensin."
RL Jpn. J. Pharmacol. 44:455-459(1987).
CC -1- FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE.
DR PIR; A28505; A28505.
KM Vasoactive.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1608 MW; 4C949E71AC410DD3 CRC64;

Query Match
Best Local Similarity 20.2%; Score 22; DB 1; Length 13;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 LHIQGEREP 11
   1 1 1 1 1 1 1 1 1 1 1 1 1
Db 2 LHVNRARRP 10

RESULT 10
QZOG_COMTE
ID QZOG_COMTE STANDARD; PRT; 10 AA.
AC P80466;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE QUINOLINE 2-OXIDOREDUCTASE, GAMMA CHAIN (EC 1.-.-.-) (FRAGMENT).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
RN 111
RP SEQUENCE.
RX STRAIN-63.
RC MEDLINE; 96035889.
RA Schach S., Tshisudaka B., Fetzner S., Lingens F.;
RT "Quinolone 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation."
RL Eur. J. Biochem. 232:536-544(1995).
CC -1- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-
CC 1,2-DIHYDROQUINOLINE.
CC -1- COFACTOR: FAD AND MOLYBDENUM.
CC -1- PATHWAY: FIRST STEP IN THE DEGRADATION OF QUINOLINE AND

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CC (3-METHYL-)-QUINOLINE.
CC -1- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
CC TWO GAMMA CHAINS (PROBABLE).
KM Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1153 MW; C848CE6443B1DC6 CRC64;

Query Match
Best Local Similarity 19.3%; Score 21; DB 1; Length 10;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 LQGEREP 11
   1 1 1 1 1 1 1 1 1 1
Db 2 IQAEKNP 8

RESULT 11
CXET_COMTE
ID CXET_COMTE STANDARD; PRT; 13 AA.
AC P81755;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPSILON-CONOTOXIN TXIX.
OS Conus textile (Cloth-of-gold cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
RN 111
RP SEQUENCE; CARBOHYDRATE-LINKAGE SITE THR-10, AND STRUCTURE BY NMR.
RC TISSUE-VENOM;
RX MEDLINE; 99254114.
RA Rigby A.C., Lucas-Munier E., Kalme D.E., Czerviec E., Hambe B.,
RA Dahlqvist I., Fossier P., Baux G., Roepstorff P., Boleja J.D.,
RA Furtie B.C., Furtie B., Stenflo J.P.;
RT "A conotoxin from Conus textile with unusual posttranslational
RT modifications reduces presynaptic Ca2+ influx."
RL Proc. Natl. Acad. Sci. U.S.A. 96:5758-5763(1999).
CC -1- FUNCTION: CONOTOXIN WHICH ACTS AT PRESYNAPTIC MEMBRANES, BLOCKING
CC THE CALCIUM CHANNELS.
CC -1- PTM: O-GLYCAN CONSISTS OF THE DISACCHARIDE GAL-GALNAC.
DR PDB; 1WCR; 08-JUN-99.
KM Presynaptic neurotoxin; Calcium channel inhibitor; Venom; Vitamin K;
KM Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Bromination;
KM 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 9
FT MOD_RES 1 1 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 4 4 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 7 7 BROMINATION.
FT MOD_RES 13 13 HYDROXYLATION.
FT CARBOHYD 10 10 O-LINKED (GALNAC.-.-.).
SQ SEQUENCE 13 AA; 1388 MW; 386C9E1C74AFA378 CRC64;

Query Match
Best Local Similarity 19.3%; Score 21; DB 1; Length 13;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 EPGW 13
   1 1 1 1 1 1 1 1 1 1 1 1 1
Db 4 EDGW 7

RESULT 12
CHH3_BOMO
ID CHH3_BOMO STANDARD; PRT; 17 AA.
AC P20729;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE CHORION CLASS HIGH-CYSTEINE HCA PROTEIN 13 PRECURSOR (HC-A.13)
DE (FRAGMENT).

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OS Bombyx mori (Silk moth).
 OC Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta;
 OC Pterygota: Neoptera: Endopterygota: Lepidoptera: Glossata: Ditylaria;
 OC Bombycoidea: Bombycidae: Bombyx.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 8508311.
 RA Rodakis G.C., Lecanidou R., Eickbush T.H.;
 RT "Diversity in a chorion multigene family created by tandem
 RT duplications and a putative gene conversion event.";
 RL J. Mol. Evol. 20:265-273(1984).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF MANY FROM THE EGGSHELL OF THE
 CC SILK MOTH.
 CC -1- SIMILARITY: MEMBER OF THE ALPHA-BRANCH OF CHORION PROTEIN TO WHICH
 CC BELONG CLASSES A, CA AND HCA.
 CC -----
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 CC -----
 CC EMBL: X01068; CAB57790.1; -
 DR PIR: B23219; B23219.
 KM Eggshell; Chorion; Repeat; Multigene family; Signal.
 FT SIGNAL. 1
 FT NON_TER 17
 FT 17
 SQ SEQUENCE 17 AA: 1913 MW: 56634508C535C9C CRC64;

Query Match 19.3%; Score 21; DB 1; Length 17;
 Best Local Similarity 71.4%; Pred. No. 1.7e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLLHLOG 7
 111 :11
 Db 7 LLLCVQG 13

RESULT 13
 ID CRTG_SPTOL STANDARD; PRT; 20 AA.
 AC P30806;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE CALRETTICULIN-LIKE PROTEIN (FRAGMENT).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta;
 OC Magnoliophyta: eudicotyledons: core eudicots: Caryophyllales;
 OC Caryophyllales: Chenopodiaceae: Spinacia.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-LEAF.
 RX MEDLINE: 93176159.
 RA Menegazzi P., Guzzo F., Balzan B., Martani P., Treves S.;
 RT "Purification of calreticulin-like protein(s) from spinach leaves.";
 RL Biochem. Biophys. Res. Commun. 190:1130-1135(1993).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM.
 CC -1- PFM: GLYCOSTYLATED.
 CC -1- SIMILARITY: BELONGS TO THE CALRETTICULIN FAMILY.
 CC PIR: PC1241; PC1241.
 DR INTERPRO: IPR001580; -
 DR PROSITE: PS00803; CALRETTICULIN_1; PARTIAL.
 DR PROSITE: PS00804; CALRETTICULIN_2; PARTIAL.
 DR PROSITE: PS00805; CALRETTICULIN_REPEAT; PARTIAL.
 KW Endoplasmic reticulum; Calcium-binding; Glycoprotein.
 FT NON_TER 20
 FT 20
 SQ SEQUENCE 20 AA: 2645 MW: 00FABAC9DEDCB0F CRC64;

Query Match 19.3%; Score 21; DB 1; Length 20;
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 EPGW 13
 111 :11
 Db 9 EDGW 12

RESULT 14
 ID PORD_METTM STANDARD; PRT; 12 AA.
 AC P80903;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PYRUVATE SYNTHASE SUBUNIT PORD (EC 1.2.7.1) (PYRUVATE OXIDOREDUCTASE
 DE DELTA CHAIN) (PORD) (PYRUVIC-FERREDOXIN OXIDOREDUCTASE DELTA SUBUNIT)
 DE (FRAGMENT).
 CN PORD.
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
 OC Archaea: Euryarchaeota: Methanobacteriales; Methanobacteriaceae;
 OC Methanobacterium.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 97261844.
 RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
 RT "Structures and functions of four anaerobic 2-oxoacid oxidoreductases
 RT in Methanobacterium thermoautotrophicum.";
 RL Eur. J. Biochem. 244:862-868(1997).
 CC -1- FUNCTION: THE PH OPTIMUM IS PH 10.0 AND THE OPTIMAL TEMPERATURE
 CC IS 80 DEGREES CELSIUS.
 CC -1- CATALYTIC ACTIVITY: PYRUVATE + COA + OXIDIZED FERREDOXIN -
 CC ACETYL-COA + CO(2) + REDUCED FERREDOXIN.
 CC -1- COFACTOR: BINDS TWO 4FE-4S CLUSTERS (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
 CC GAMMA CHAIN.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
 KM Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
 FT NON_TER 12
 FT 12
 SQ SEQUENCE 12 AA: 1241 MW: 2D54065D1BD1ADD8 CRC64;

Query Match 18.3%; Score 20; DB 1; Length 12;
 Best Local Similarity 75.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 9 REPG 12
 111 :11
 Db 9 KEFG 12

RESULT 15
 ID HPAL_RANES STANDARD; PRT; 13 AA.
 AC P32415;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE HEMOLYTIC PROTEIN A1 (FRAGMENT).
 OS Rana esculenta (Edible frog).
 OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
 OC Amphibia: Batrachia: Anura: Neobatrachia: Ranoidae; Rana.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-SKIN SECRETION.
 RX MEDLINE: 90198965.
 RA Simmaco M., de Biase D., Severini C., Alta M., Ersamer G.F.,
 RA Barra D., Bossa F.;
 RT "Purification and characterization of bioactive peptides from skin
 RT extracts of Rana esculenta.";
 RL Biochim. Biophys. Acta 1033:318-323(1990).

CC -!- FUNCTION: SHOWS HEMOLYTIC ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- TISSUE SPECIFICITY: SKIN.
 DR PIR; S09018; S09018.
 KW Amphibian skin; Amidation; Hemolysis.
 FT MOD_RES 13 13 AMIDATION.
 FT NON_TER 13 13
 SO SEQUENCE 13 AA; 1390 MW; C6BA768B9DFE587D CRC64;

Query Match 18.3%; Score 20; DB 1; Length 13;
 Best Local Similarity 57.1%; Pred. No. 1.9e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 12 GWIKOLF 18
 I : |||
 Db 7 GILSQLF 13

Search completed: December 21, 2000, 08:33:00
 Job time: 443 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:35:40 ; Search time 157.2 Seconds
(without alignments)
11.880 Million cell updates/sec

Title: US-08-934-367-36

Sequence: 1 LLLHGEREPGKIKQLFTN 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_14:*
2: sp_archaea:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	26.6	10	13	09PRZ1 oncorhynchu
2	29	26.6	20	4	09UC71 homo sapien
3	28	25.7	9	13	09PRJ4 lepisosteus
4	28	25.7	14	5	018502 schistosoma
5	27	24.8	20	2	09RAW5 heliobacte
6	26	23.9	11	7	077893 oreochromis
7	26	23.9	17	8	09X313 prochloroc
8	26	23.9	17	8	09T2R9 solanum tub
9	25.5	23.4	19	4	09UCG3 homo sapien
10	25	22.9	14	4	016045 homo sapien
11	25	22.9	18	2	09R5F6 heliobacte
12	25	22.9	18	13	09PRM7 xenopus. ac
13	25	22.9	19	4	044850 borrelia bu
14	25	22.9	19	4	09UJ18 homo sapien
15	24	22.0	12	12	012088 caprine art
16	24	22.0	12	12	012074 caprine art
17	24	22.0	12	12	012076 caprine art
18	24	22.0	12	12	012078 caprine art
19	24	22.0	12	12	012080 caprine art

20	24	22.0	12	12	012082	012082 caprine art
21	24	22.0	12	12	012084	012084 caprine art
22	24	22.0	12	12	012086	012086 caprine art
23	24	22.0	12	12	012090	012090 caprine art
24	24	22.0	12	12	012092	012092 caprine art
25	24	22.0	12	12	012094	012094 caprine art
26	24	22.0	12	12	012106	012106 caprine art
27	24	22.0	12	12	012108	012108 caprine art
28	24	22.0	12	12	012110	012110 caprine art
29	24	22.0	12	12	012112	012112 caprine art
30	24	22.0	12	12	012114	012114 caprine art
31	24	22.0	12	12	012116	012116 caprine art
32	24	22.0	12	12	012118	012118 caprine art
33	24	22.0	15	2	046963	046963 escherichia
34	24	22.0	15	5	09YXC8	09YXC8 locusta mag
35	24	22.0	16	4	09UCX9	09UCX9 homo sapien
36	24	22.0	16	4	09UCH1	09UCH1 homo sapien
37	24	22.0	19	2	047079	047079 escherichia
38	24	22.0	19	10	09S8W5	09S8W5 avena sativ
39	24	22.0	19	12	093210	093210 porcine clr
40	24	22.0	11	5	09V7K6	09V7K6 drosophila
41	23	21.1	11	7	077892	077892 oreochromis
42	23	21.1	11	7	077906	077906 oreochromis
43	23	21.1	11	7	077918	077918 pseudotroph
44	23	21.1	13	4	09Y674	09Y674 homo sapien
45	23	21.1	17	6	09TR78	09TR78 didelphis m

ALIGNMENTS

RESULT 1
ID 09PRZ1 PRELIMINARY: PRT: 10 AA.
AC 09PRZ1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE LYSYL-BRADYKININ-VASOACTIVE PEPTIDE KALIDIN HOMOLOG.
OS Oncohychnus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncohychnus.
RN [1]
RP SEQUENCE.
RX MEDLINE: 94039817.
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from trout plasma."
RL FEBS Lett. 334:75-78(1993).
SO SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 26.6%; Score 29; DB 13; Length 10;

Best Local Similarity 66.7%; Pred. No. 2.2e+02; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 EREPGW 13

Db 1 KRPGW 6

RESULT 2
ID 09UC71 PRELIMINARY: PRT: 20 AA.

AC 09UC71:
DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE FILAGGRIN (FRAGMENT).

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]
RP SEQUENCE:
RX MEDLINE: 95337087.
RA Thulin C.D., Walsh K.A.:
RT "Identification of the amino terminus of human flaggrin using
RT differential LC/MS techniques: implications for profilaggrin
RT processing."
RL Biochemistry 34:8687-8692(1995).
SQ SEQUENCE 20 AA; 2199 MW; 0FD0856B199AB332 CRC64;

Query Match 26.6%; Score 29; DB 4; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 4 HLOGREPWC 13
| | | | |
Db 5 HROSESHCW 14

RESULT 3
O9PRJ4 PRELIMINARY; PRT; 9 AA.
ID O9PRJ4:
AC O9PRJ4:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE BRADYKININ.
OS Lepisosteus osseus (Long-nosed gar), and Amia calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;
OC Lepisosteus.
RN [1]
RP SEQUENCE.
RX MEDLINE: 95380361.
RA Conlon J.M., Platack B., Maria L.E., Youson J.H., Olson K.R.:
RT "Isolation and biological activity of [Trp5]bradykinin from the plasma
RT of the phylogenetically ancient fish, the bowfin and the longnosed
RT gar."
RL Peptides 16:485-489(1995).
SQ SEQUENCE 9 AA; 1099 MW; 3393D775A3786777 CRC64;

Query Match 25.7%; Score 28; DB 13; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 RPPGW 13
| | | | |
Db 1 RPPGW 5

RESULT 4
O18502 PRELIMINARY; PRT; 14 AA.
ID O18502:
AC O18502:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-AUG-1998 (TREMblrel. 07, Last annotation update)
DE LYSOPHOSPHOLIPASE HOMOLOG (FRAGMENT).
GN SMPPLH.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EGYPTIAN;
RA Hamdan F.F., Ribeiro P.:
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF006679; AAC62255.1; -.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1541 MW; 48B847C2E5D89177 CRC64;

Query Match 25.7%; Score 28; DB 5; Length 14;
Best Local Similarity 38.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 LLLHLOGREPWC 13
| | | | |
Db 2 IFLHGLDPTCHGW 14

RESULT 5
O9R4W5 PRELIMINARY; PRT; 20 AA.
ID O9R4W5:
AC O9R4W5:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE 30 KDA MAJOR HEAT SHOCK PROTEIN (FRAGMENT).
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE.
RX MEDLINE: 95020803.
RA Yokota K., Hirai Y., Haque M., Hayashi S., Isogai H., Sugiyama T.,
RA Nagamachi E., Tsukada Y., Fujii N., Oguma K.:
RT "Heat shock protein produced by Helicobacter pylori."
RL Microbiol. Immunol. 38:403-405(1994).
DR INTERPRO: IPR002026; -.
DR PRAM: PF00347; urease_gamma; 1.
SQ SEQUENCE 20 AA; 2302 MW; 29C9DFBFD6D21805 CRC64;

Query Match 24.8%; Score 27; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 9.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LLLHLOGE 8
| | | | |
Db 11 LMLHYAGE 18

RESULT 6
O77893 PRELIMINARY; PRT; 11 AA.
ID O77893:
AC O77893:
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE MHC CLASS II B LOCUS 10 (FRAGMENT).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
OC Percormorpha; Perciformes; Labroidae; Cichlidae; Oreochromis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98315113.
RA Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska Z.,
RA Snelmann H., Figueroa F., Klein J.:
RT "Linkage relationships and haplotype polymorphism among cichlid Mhc
RT class II B loci."
RL Genetics 149:1527-1547(1998).
DR EMBL: AF050003; AAC41342.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1296 MW; 68775B73786B572B CRC64;

Query Match 23.9%; Score 26; DB 7; Length 11;
Best Local Similarity 50.0%; Pred. No. 7.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 13 WIKOLF 18
Db 1 WIRELY 6

RESULT 7
09X313

ID 09X313 PRELIMINARY; PRT; 17 AA.

AC 09X313; 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DE CYTOCHROME B (FRAGMENT).

OS Prochlorococcus sp.

OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;

RN [1]

RP SEQUENCE FROM N.A.

RA Urbach E., Chisholm S.W.; "Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream";

RT Limnol. Oceanogr. 43:1615-1630(1998).

DR EMBL; AF070176; AAD20791.1; -

FT NON_TER

SO SEQUENCE 17 AA; 1953 MW; 630843039ADD51B4 CRC64;

Query Match 23.9%; Score 26; DB 2; Length 17;

Best Local Similarity 33.3%; Pred. No. 1.1e+03;

Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 LHLHLOGREP 12
Db 1 LMLHLDXDRKG 12

RESULT 8
09T2R9

ID 09T2R9 PRELIMINARY; PRT; 17 AA.

AC 09T2R9; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE CYTOCHROME-C REDUCTASE 55 KDA SUBUNIT (EC 1.10.2.2) (FRAGMENT).

OS Solanum tuberosum (Potato).

OC Magnoliophyta; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; Asteridae; eusterids I; Solanales;

RN [1]

RP SEQUENCE.

RA Braun H.P., Kruff V., Schmitz U.K.;

RL Planca 193:99-106(1994).

SO SEQUENCE 17 AA; 1758 MW; F95F7BF7940F5F21 CRC64;

Query Match 23.9%; Score 26; DB 8; Length 17;

Best Local Similarity 57.1%; Pred. No. 1.1e+03;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LHLHLOG 7
Db 4 LMLHLDG 10

RESULT 9
09UCG3

ID 09UCG3 PRELIMINARY; PRT; 19 AA.

AC 09UCG3; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE ALPHA-2-PLASMIN INHIBITOR (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP SEQUENCE.

RA Bangert K., Johnson A.H., Christensen U., Thorsen S.;

RT "Different N-terminal forms of alpha-2-plasmin inhibitor in human plasma";

RL Biochem. J. 291:623-625(1993).

SO SEQUENCE 19 AA; 2065 MW; 41352BF04D1EEA9 CRC64;

Query Match 23.4%; Score 25.5; DB 4; Length 19;

Best Local Similarity 63.6%; Pred. No. 1.5e+03;

Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 2 LHLHLOGREP 12
Db 10 LKL-GNOEPG 19

RESULT 10
016045

ID 016045 PRELIMINARY; PRT; 14 AA.

AC 016045; 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE D3 DOPAMINE RECEPTOR (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RA Nagai Y., Ueno S., Saeki Y., Soga F., Yanagihara T.;

RT "Expression of the D3 dopamine receptor gene and a novel variant transcript generated by alternative splicing in human peripheral blood lymphocytes";

RT Biochem. Biophys. Res. Commun. 194:368-374(1993).

DR EMBL; S63845; CAB32270.1; -

FT NON_TER

SO SEQUENCE 14 AA; 1586 MW; EA310BEFE94CF1B1 CRC64;

Query Match 22.9%; Score 25; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LHLHLOG 6
Db 9 LHLHLOG 13

RESULT 11
09R5F6

ID 09R5F6 PRELIMINARY; PRT; 18 AA.

AC 09R5F6; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE UREASE SMALL SUBUNIT (FRAGMENT).

OS Helicobacter mustelae.

OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;

RN [1]

RP SEQUENCE.

RA Turbett G.R., Hoj P.B., Horne R., Mee B.J.;

RT "Purification and characterization of the urease enzymes of

RT Helicobacter species from humans and animals."
 RL Infect. Immun. 60:5259-5266(1992).
 SO SEQUENCE 18 AA; 2060 MW; 29C8E0AB77E21805 CRC64;

Query Match 22.9%; Score 25; DB 2; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LHLHGE 8
 Db 9 KMLHAGE 16

RESULT 12
 Q9PRM7 PRELIMINARY; PRT; 18 AA.
 AC Q9PRM7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE ACID THIOL PROTEASE (FRAGMENT).
 OS Xenopus.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 RN [1]
 RX MEDLINE; 96417001.
 RA Miyata S., Kihara H.K.;
 RT "Cathepsin L-like protease from Xenopus embryos that is stimulated by
 nucleoside phosphates and nucleic acids."
 RL Zool. Sci. 12:771-774(1995).
 SO SEQUENCE 18 AA; 2060 MW; AIDCB106B341504 CRC64;

Query Match 22.9%; Score 25; DB 13; Length 18;
 Best Local Similarity 57.1%; Pred. No. 1.7e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 9 REPGWIK 15
 Db 8 REGYVK 14

RESULT 13
 Q44850 PRELIMINARY; PRT; 19 AA.
 AC Q44850;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBlrel. 01, Last annotation update)
 DE HYPOTHEICAL PROTEIN (FRAGMENT).
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-297;
 RA Akins D.R., Popova T., Brusca J., Goldberg M.L., Li M., Baker S.C.,
 RL Norgard M.V., Radolf J.D.;
 RL Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U31425; AAA64901.1; -.
 KW Hypothetical protein.
 FT NON_TER 19
 SO SEQUENCE 19 AA; 2321 MW; C821BF312DBA1512 CRC64;

Query Match 22.9%; Score 25; DB 2; Length 19;
 Best Local Similarity 50.0%; Pred. No. 1.8e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 2 LHLGGEREP 11
 Db 1 LHLGGEREP 1

Db 4 LHLGSLHP 13

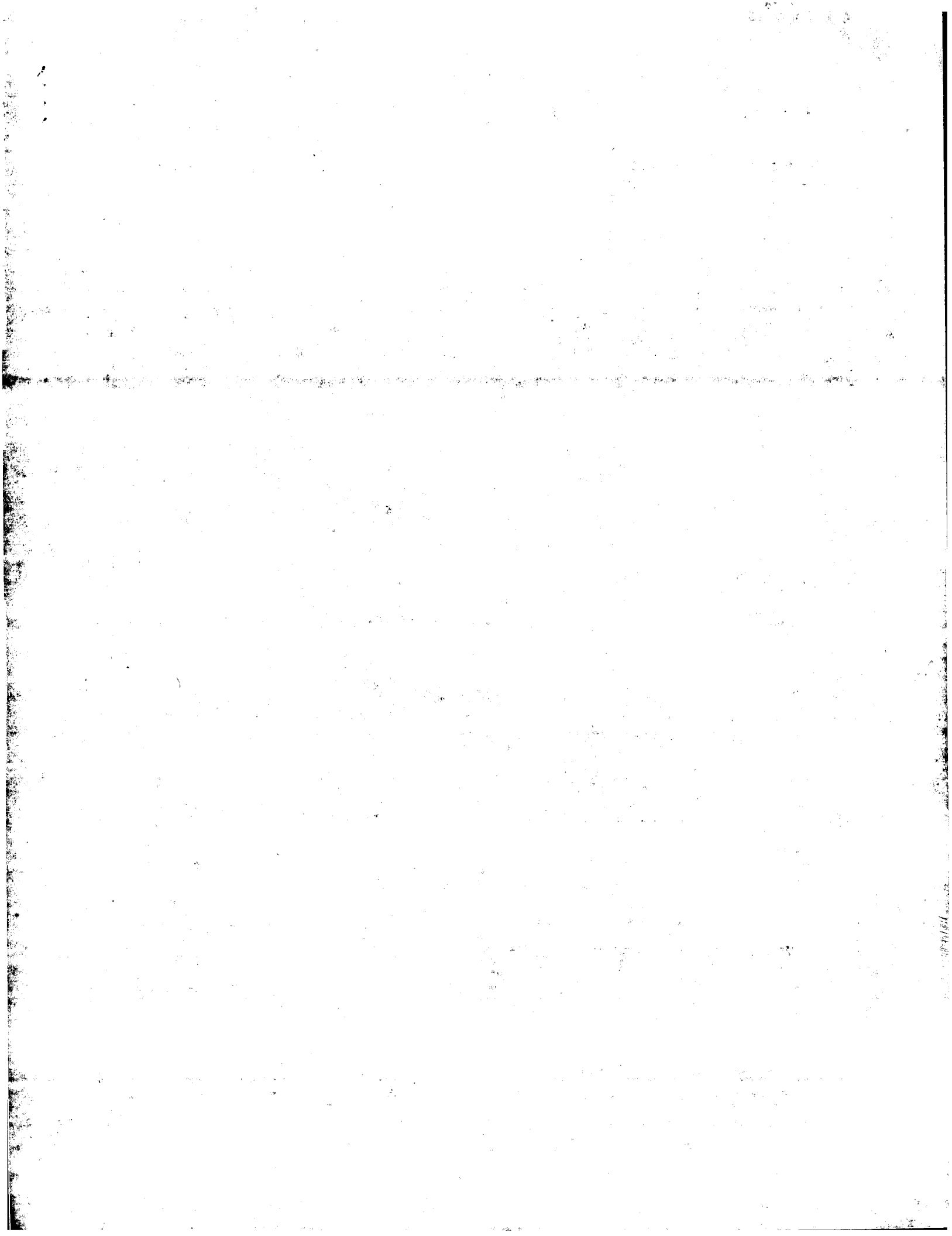
RESULT 14
 Q90J18 PRELIMINARY; PRT; 19 AA.
 AC Q90J18;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE DJ33A15.2 (PROSTAGLANDIN E RECEPTOR (EP3e)) (FRAGMENT).
 GN PTGER3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Frankland J.;
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031429; CAB52457.1; -.
 KW Receptor.
 FT NON_TER 1
 SO SEQUENCE 19 AA; 2245 MW; 142450379B298FEC CRC64;

Query Match 22.9%; Score 25; DB 4; Length 19;
 Best Local Similarity 44.4%; Pred. No. 1.8e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 3 LHLGGEREP 11
 Db 8 LHLVGKXP 16

RESULT 15
 O12088 PRELIMINARY; PRT; 12 AA.
 AC O12088;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
 DE TAT PROTEIN (FRAGMENT).
 GN TAT.
 OS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Turelli P., Guiguen F., Mornex J.F., Vigne R., Querat G.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U81435; AAB60824.1; -.
 FT NON_TER 1
 SO SEQUENCE 12 AA; 1279 MW; 4B90BB1E8644EB7 CRC64;

Query Match 22.0%; Score 24; DB 12; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 PGW 13
 Db 8 PGW 10

Search completed: December 21, 2000, 08:35:40
 Job time: 603 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:31:50 ; Search time 99.91 Seconds
(without alignments)
3.355 Million cell updates/sec

Title: US-08-934-367-37
Perfect score: 104
Sequence: 1 NITGEXAMLLGOVKYGLHN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 87906

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/p/odata/2/1aa/5A-COMB.pep:*
3: /cgn2_6/p/odata/2/1aa/5B-COMB.pep:*
4: /cgn2_6/p/odata/2/1aa/6-COMB.pep:*
5: /cgn2_6/p/odata/2/1aa/PCUUS-COMB.pep:*
6: /cgn2_6/p/odata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	27.9	12	1 US-08-164-618-20	Sequence 20, Appl
2	29	27.9	14	1 US-08-159-340A-17	Sequence 17, Appl
3	27	26.0	10	2 US-08-706-702-21	Sequence 21, Appl
4	27	26.0	10	3 US-08-706-706-21	Sequence 21, Appl
5	27	26.0	13	1 US-08-306-231-9	Sequence 9, Appl
6	27	26.0	13	1 US-08-355-888A-25	Sequence 25, Appl
7	27	26.0	13	1 US-08-693-697-25	Sequence 25, Appl
8	27	26.0	13	3 US-08-693-696-25	Sequence 25, Appl
9	26	25.0	15	2 US-08-484-905-28	Sequence 28, Appl
10	26	25.0	15	3 US-08-481-985B-28	Sequence 28, Appl
11	26	25.0	15	5 5304631-8	Patent No. 5304631
12	26	25.0	15	5 5304631-16	Patent No. 5304631
13	26	25.0	16	1 US-08-218-025A-12	Sequence 12, Appl
14	26	25.0	17	2 US-08-182-067-14	Sequence 14, Appl
15	26	25.0	17	2 US-08-465-313-14	Sequence 14, Appl
16	26	25.0	17	5 5304631-5	Patent No. 5304631
17	26	25.0	20	2 US-08-466-975A-12	Sequence 12, Appl
18	26	25.0	20	2 US-08-466-975A-13	Sequence 13, Appl
19	26	25.0	20	2 US-08-391-671A-12	Sequence 12, Appl
20	26	25.0	20	2 US-08-391-671A-13	Sequence 13, Appl
21	26	25.0	20	2 US-08-475-634D-2	Sequence 2, Appl
22	26	25.0	20	3 US-08-467-902A-12	Sequence 12, Appl
23	26	25.0	20	3 US-08-467-902A-13	Sequence 13, Appl
24	25	24.0	15	2 US-08-480-190-77	Sequence 77, Appl
25	25	24.0	15	2 US-08-488-379-77	Sequence 77, Appl
26	25	24.0	15	4 PCT-US93-07545-77	Sequence 77, Appl
27	25	24.0	16	2 US-08-480-190-76	Sequence 76, Appl
28	25	24.0	16	2 US-08-488-379-76	Sequence 76, Appl

29	25	24.0	16	4 PCT-US93-07545-76	Sequence 76, Appl
30	25	24.0	17	1 US-07-894-212A-3	Sequence 3, Appl
31	25	24.0	18	1 US-07-893-928A-3	Sequence 3, Appl
32	25	24.0	18	2 US-08-480-190-192	Sequence 192, App
33	25	24.0	18	2 US-08-488-379-192	Sequence 192, App
34	25	24.0	18	4 PCT-US93-07545-192	Sequence 192, App
35	25	24.0	19	2 US-08-480-190-74	Sequence 74, Appl
36	25	24.0	19	2 US-08-480-190-75	Sequence 75, Appl
37	25	24.0	19	2 US-08-488-379-74	Sequence 74, Appl
38	25	24.0	19	2 US-08-488-379-75	Sequence 75, Appl
39	25	24.0	19	2 US-08-696-944-3	Sequence 3, Appl
40	25	24.0	19	4 PCT-US93-07545-74	Sequence 74, Appl
41	25	24.0	19	4 PCT-US93-07545-75	Sequence 75, Appl
42	25	24.0	20	2 US-08-480-190-191	Sequence 191, App
43	25	24.0	20	2 US-08-749-852-55	Sequence 55, App
44	25	24.0	20	2 US-08-488-379-191	Sequence 191, App
45	25	24.0	20	4 PCT-US93-07545-191	Sequence 191, App

ALIGNMENTS

RESULT 1
US-08-164-618-20
: Sequence 20, Application US/08164618
: Patent No. 5408036
: GENERAL INFORMATION:
: APPLICANT: Ghadiri, M. Reza
: TITLE OF INVENTION: Isolated Metallopolypeptides:
: TITLE OF INVENTION: Compositions and Synthetic Methods
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Goldsmith, Shore, Sutter &
: ADDRESSEE: Milanow, Ltd.
: STREET: 180 No. 5408036th Stetson, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/164,618
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/769,621
: FILING DATE:
: APPLICATION NUMBER: 07/591,988
: FILING DATE: October 2, 1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Gamson, Edward G.
: REGISTRATION NUMBER: 29,381
: REFERENCE/DOCKET NUMBER: SCRF 231.0
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 616-5400
: TELEFAX: (312) 616-5460
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 12 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-164-618-20

Query Match 27.9% Score 29: DB 1: Length 12:
Best Local Similarity 71.4% Pred. No. 40:
Matches 5: Conservative 1: Mismatches 0: Gaps 0:

OY 14 VKYGLN 20
111111
Db 3 VKHGSN 9

RESULT 2

US-08-159-340A-17
; Sequence 17, Application US/08159340A
; Patent No. 5565352
; GENERAL INFORMATION:
; APPLICANT: Hochstrasser, Mark
; APPLICANT: Papa, Ferioz
; TITLE OF INVENTION: DEUBIQUITINATING ENZYME: COMPOSITIONS
; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,340A
; FILING DATE: 24-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:112/HYL
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-340A-17

Query Match 27.9%; Score 29; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 14 VKYGLN 20
111111
Db 8 VKHGSN 14

RESULT 3

US-08-706-702-21
; Sequence 21, Application US/08706702
; Patent No. 5948614
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Deb K.
; TITLE OF INVENTION: Cloned DNA Polymerases from Thermotoga
; TITLE OF INVENTION: maritima and Mutants Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,702
; FILING DATE: 06-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/689,807
; FILING DATE: 14-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/537,400
; FILING DATE: 02-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/576,759
; FILING DATE: 21-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/537,397
; FILING DATE: 02-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/525,057
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.2800006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-706-702-21

Query Match 26.0%; Score 27; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ITGKAM 9
111111
Db 3 ITGDKML 10

RESULT 4

US-08-706-706-21
; Sequence 21, Application US/08706706
; Patent No. 6015668
; GENERAL INFORMATION:
; APPLICANT: Hughes, A. John
; TITLE OF INVENTION: Chatterjee, Deb K.
; TITLE OF INVENTION: Cloned DNA Polymerases from Thermotoga and
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,706

FILED DATE: 06-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/689,807
FILING DATE: 14-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537,400
FILING DATE: 02-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/370,190
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,423
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,759
FILING DATE: 21-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537,397
FILING DATE: 02-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/525,057
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.2800005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-706-706-21

Query Match 26.0%; Score 27; DB 3; Length 10;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 ITGKXAM 9
Db 3 ITGDKML 10
RESULT 5
US-08-306-231-9
Sequence 9, Application US/08306231
Patent No. 5643748
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HEMATOPOIETIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,231
FILING DATE: 14-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Polissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-076
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-306-231-9

Query Match 26.0%; Score 27; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVKTGL 18
Db 3 QIRYGL 8

RESULT 6
US-08-355-888A-25
Sequence 25, Application US/08355888A
Patent No. 5763211
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/355,888A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Polissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown

MOLECULE TYPE: peptide
US-08-355-888A-25

Query Match 26.0%; Score 27; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVRYGL 18
I:::|||
Db 3 QIRYGL 8

RESULT 7
US-08-693-697-25
Sequence 25, Application US/08693697
Patent No. 5869610

GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,697
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0037-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556

TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-693-697-25

Query Match 26.0%; Score 27; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVRYGL 18
I:::|||
Db 3 QIRYGL 8

RESULT 8
US-08-693-696-25
Sequence 25, Application US/08693696
Patent No. 6005080
GENERAL INFORMATION:

APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,696
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/355,888
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 7225-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-693-696-25

Query Match 26.0%; Score 27; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVRYGL 18
I:::|||
Db 3 QIRYGL 8

RESULT 9
US-08-484-905-28
Sequence 28, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:

APPLICANT: Motez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for using the
TITLE OF INVENTION: Determinant
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Polter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-905-28

Query Match 25.0%; Score 26; DB 2; Length 15;
Best Local Similarity 38.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 TGEKAMMLGQVK 15
11 :|||:
Db 3 TSEGCROTLGQLQ 15

RESULT 10
US-08-481-985B-28
Sequence 28, Application US/08481985B
Patent No. 6011146
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W., Suite 700
City: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-985B-28

Query Match 25.0%; Score 26; DB 3; Length 15;
Best Local Similarity 38.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 TGEKAMMLGQVK 15
11 :|||:
Db 3 TSEGCROTLGQLQ 15

RESULT 11
5304631-8
Patent No. 5304631
APPLICANT: SPENART, JOHN M.; HAHN, KARL W.; KLIS, WISLAW A.
TITLE OF INVENTION: SYNTHETIC HELIZYME ENZYMES
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/464,932
FILING DATE: 16-JAN-1990
SEQ ID NO: 8
LENGTH: 15
5304631-8

Query Match 25.0%; Score 26; DB 5; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 5 EKAMMLGQVK 15
111 :|||:
Db 2 EKAKLLEELK 12

RESULT 12
5304631-16
Patent No. 5304631
APPLICANT: SPENART, JOHN M.; HAHN, KARL W.; KLIS, WISLAW A.
TITLE OF INVENTION: SYNTHETIC HELIZYME ENZYMES
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/464,932
FILING DATE: 16-JAN-1990
SEQ ID NO: 16
LENGTH: 15
5304631-16

Query Match 25.0%; Score 26; DB 5; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 5 EKAMMLGQVK 15
111 :|||:
Db 2 EKAKLLEELK 12

RESULT 13
US-08-218-025A-12
Sequence 12, Application US/08218025A
Patent No. 5556744
GENERAL INFORMATION:
APPLICANT: Weiner, David B.
APPLICANT: Ugen, Kenneth E.
APPLICANT: Williams, William V.
TITLE OF INVENTION: Methods and Compositions for Diagnosing
TITLE OF INVENTION: and Treating Certain HIV Infected Patients
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: P.O. Box 457, 321 No. 55567441stow Road
CITY: Spring House
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,025A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 07/891,451
FILING DATE: 29-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST33A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-218-025A-12

Query Match 25.0%; Score 26; DB 1; Length 16;
Best local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 NITGEKAM 9
1:11111
DB 8 NVTSENFNM 16

RESULT 14
US-08-182-067-14
Sequence 14, Application US/08182067
Patent No. 5985279
GENERAL INFORMATION:
APPLICANT: WALDMANN, HERMAN
APPLICANT: SIMS, MARTIN
APPLICANT: CROME, SCOTT
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg Ernst & Kurz
STREET: Suite 701-F, 555 Thirteenth St., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,067
FILING DATE: 23-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01289
FILING DATE: 15-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9115364.3
FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1786-118A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-182-067-14

Query Match 25.0%; Score 26; DB 2; Length 17;
Best local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 GOVKYG 17
1:111
DB 7 GETKYG 12

RESULT 15
US-08-465-313-14
Sequence 14, Application US/08465313
Patent No. 5997867
GENERAL INFORMATION:
APPLICANT: WALDMANN, HERMAN
APPLICANT: SIMS, MARTIN J.
APPLICANT: CROME, J. SCOTT
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: TWO MILLITTA DRIVE
CITY: LEXINGTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,313
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/182,067
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01289
FILING DATE: 15-JUL-1992
PRIOR APPLICATION DATA:

```

: APPLICATION NUMBER: GB 9115364.3
: FILING DATE: 16-JUL-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: BROOK, DAVID E.
: REGISTRATION NUMBER: 22,592
: REFERENCE/DOCKET NUMBER: LYNX91-01A2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 861-6240
: TELEFAX: (617) 861-9540
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 17 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-465-313-14

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Query Match      25.0%; Score 26; DB 2; Length 17;
Best Local Similarity 65.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 GGVKYG 17
   1: 111
Db 7 GGVKYG 12

```

Search completed: December 21, 2000, 08:31:50
Job time: 373 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:30:08 ; Search time 112.59 Seconds
(without alignments)
11.273 Million cell updates/sec

Title: US-08-934-367-37
Perfect score: 104
Sequence: 1 NITGEKAMMLGQVKYGLHN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	25.0	18	2	I52623 hypothetical prote
2	26	23.1	15	2	PA0091 methionine adenosy
3	24	23.1	15	2	PC4213 hphb protein - Com
4	24	22.1	16	2	PH1475 T-cell receptor be
5	23	22.1	9	2	A11497 transaldolase (EC
6	23	22.1	10	2	S74147 glyceraldehyde-3-P
7	23	22.1	15	2	PH0797 T-cell receptor al
8	23	22.1	20	2	S04961 malate dehydrogena
9	23	22.1	20	2	S04058 malate dehydrogena
10	23	22.1	20	2	B44835 gDHPeptide 4,6-de
11	23	22.1	20	2	PH1338 1g heavy chain DJ
12	22	21.2	12	2	S23168 2 protein - guinea
13	22	21.2	14	2	JN0390 histamine-releasin
14	22	21.2	14	2	S72217 D-arabinose 1-dehy
15	22	21.2	15	2	A49887 transcription fact
16	22	21.2	16	2	S02455 DNA-invertase - ph
17	22	21.2	16	2	PH0773 T-cell receptor be
18	22	21.2	16	2	PH1476 T-cell receptor be
19	22	21.2	18	2	S63487 fibrinogenolytic p
20	22	21.2	20	2	A47105 dystroglycan - chi
21	22	21.2	20	2	S10876 hypothetical prote
22	21	20.2	16	2	D45193 zinc finger protei
23	21	20.2	18	2	A41877 LcrKc - Versinia p
24	21	20.2	18	2	A49857 megakaryocyte pote
25	21	20.2	19	2	B61056 cytochrome P450 PB
26	21	20.2	20	2	PH1358 1g heavy chain DJ
27	20	19.2	9	2	G58502 kidney and bladder
28	20	19.2	12	2	PH1635 1g H chain V-D-J r
29	20	19.2	13	2	PS0325 tetrahydroderlin

30	20	19.2	13	2	PH1772 T cell receptor al
31	20	19.2	14	2	PH1332 Ig heavy chain DJ
32	20	19.2	14	2	A28018 very late antigen-
33	20	19.2	15	2	PL0143 carbon-monoxide de
34	20	19.2	15	2	A30330 neurotrophin pep -
35	20	19.2	15	2	PH1619 Ig H chain V-D-J r
36	20	19.2	15	2	PH0775 T-cell receptor al
37	20	19.2	15	2	PH0779 T-cell receptor al
38	20	19.2	15	2	PH1455 T-cell receptor al
39	20	19.2	15	2	PH0752 T-cell receptor be
40	20	19.2	18	2	A39997 group III allergen
41	20	19.2	19	2	S43657 hep90 protein homo
42	20	19.2	20	2	S11416 ribosomal protein
43	19.5	18.8	15	2	PA0106 protein QP200076 -
44	19.5	18.8	19	2	A39504 octamer-binding pr
45	19.5	18.8	20	2	nlrtrophin 3 - Rh

ALIGNMENTS

RESULT 1
I52623
hypothetical protein TCR delta [imported] - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 20-Jun-2000
C:Accession: I52623
R:Przybylski, G.; Oettle, H.; Ludwig, W.D.; Siegert, W.; Schmidt, C.A.
Br. J. Haematol. 87, 301-307, 1994
A:Title: Molecular characterization of illegitimate TCR delta gene rearrangements in
A:Reference number: I52623; MUID:95034253
A:Accession: I52623
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18 <RES>
A:Cross-references: GB:S73537; NID:G688155
C:Genetics:
A:Gene: TCRdelta

Query Match 25.0%; Score 26; DB 2; Length 18;
Best Local Similarity 41.2%; Pred. NO. 4.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 8; Gaps 1;

OY 11 LGQVKY-----GLH 19
||| |
Db 1 LGOKKSSYLWGTSGVH 17
|:|

RESULT 2
PA0091
methionine adenosyltransferase (EC 2.5.1.6) 2 - fungus (Fusarium sporotrichioides) (F
C:Species: Fusarium sporotrichioides
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-May-2000
C:Accession: PA0091
R:Chow, L.P.; Fukaya, N.; Suglura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPD, October 1994
A:Reference number: PA0051
A:Accession: PA0091
A:Molecule type: protein
A:Residues: 1-15 <CHO>
C:Keywords: S-adenosylmethionine; transferase

Query Match 23.1%; Score 24; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. NO. 8.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 3 TGEKAMMLG 12
| | | | |
Db 1 TYEKALDGLG 10

```
RESULT 3
PC4213
bphb protein - Comamonas testosteroni (fragment)
C:Species: Comamonas testosteroni
C:Date: 17-Dec-1996 #sequence_revision 21-Jan-1997 #text_change 08-Oct-1999
C:Accession: PC4213
R:Sylvestre, M.; Strolis, M.; Hurtubise, Y.; Bergeron, J.; Ahmad, D.; Shareck, F.; Barria
Gene 174, 195-202, 1996
A:Title: Sequencing of Comamonas testosteroni strain B-356-Diphenyl/chlorobiphenyl dioxy
A:Reference number: J04993; MUID:97045812
A:Accession: PC4213
A:Molecule type: DNA
A:Residues: 1-15 <STL>
A:Cross-references: GB:U47637; NID:91245151; PID:MAC44530.1; PID:91245156
A:Experimental source: strain B-356
A:Genetics:
A:Gene: bphb

Query Match 23.1%; Score 24; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 8.1e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ITGERKAMLLG 12
|||||:|
Db 3 LTGERVALITGG 13

RESULT 4
PH1475
T-cell receptor beta chain (clone 223/5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1475
R:Casanova, J.L.; Martinon, F.; Gounier, H.; Barra, C.; Pannetier, C.; Regnault, A.; KC
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatih
A:Reference number: PH1430; MUID:93171821
A:Accession: PH1475
A:Molecule type: mRNA
A:Residues: 1-16 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 23.1%; Score 24; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGERKAMLLG 12
|||||:|
Db 7 TGERERLFFG 16

RESULT 5
A11497
transaldolase (EC 2.2.1.2) III - Yeast (Pichia jadinii) (fragment)
C:Species: Pichia jadinii, Candida utilis
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 30-Sep-1993
C:Accession: A11497
R:Tsolas, O.; Sun, S.C.
Arch. Biochem. Biophys. 167, 525-533, 1975
A:Title: Isolation of a peptide containing a histidinyl-cysteiny sequence from the acti
A:Reference number: A11497; MUID:75145197
A:Accession: A11497
A:Molecule type: protein
A:Residues: 1-9 <TSO>
C:Keywords: transferase

Query Match 22.1%; Score 23; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.8e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 YGLH 19
|||||
Db 1 YGTH 4

RESULT 6
S74147
glyceroldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C:Accession: S74147
R:Fukuda, A.; Osawa, T.; Hiltoml, K.; Uchida, K.
Arch. Biochem. Biophys. 333, 419-426, 1996
A:Title: 4-Hydroxy-2-nonenal cytotoxicity in renal proximal tubular cells: protein mo
A:Reference number: S74147; MUID:96404942
A:Accession: S74147
A:Molecule type: protein
A:Residues: 1-10 <FGK>
A:Experimental source: LLC-PK1 cells (renal tubular epithelial cells)
C:Keywords: NAD; oxidoreductase

Query Match 22.1%; Score 23; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 GQKRYGLH 19
|||||:|
Db 1 GKRYGVGN 8

RESULT 7
PH0797
T-cell receptor alpha chain (PF2.10.1 V-alpha-3.AN5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0797
R:Casanova, J.L.; Romero, P.; Widmann, C.; Koutilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility comple
A:Allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846
A:Accession: PH0797
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: EMBL:X60903
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 22.1%; Score 23; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 NITGERKAMLLG 12
|||||:|
Db 4 SITGNTKRLIFG 15

RESULT 8
S04961
malate dehydrogenase (EC 1.1.1.37) - Kibdelosporangium aridum (fragment)
C:Species: Kibdelosporangium aridum
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Aug-1994
C:Accession: S04961
R:Rommel, T.O.; Hund, H.K.; Spehl, A.R.; Lingens, F.
Biol. Chem. Hoppe-Seyler 370, 763-768, 1989
A:Title: Purification and N-terminal amino-acid sequences of bacterial malate dehydro
A:Reference number: S04956; MUID:89374824
A:Accession: S04961
A:Molecule type: protein
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A:Residues: 1-20 <ROM>
C:Superfamily: L-lactate dehydrogenase
C:Keywords: oxidoreductase; tricarboxylic acid cycle

Query Match 22.1%; Score 23; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 GOVKYGL 18
||: ||
Db 14 GOIGYAL 20

RESULT 9
S04958
maleate dehydrogenase (EC 1.1.1.37) - Microtetraspora glauca (fragment)
C:Species: Microtetraspora glauca
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Aug-1994
C:Accession: S04958
R:Rommel, T.O.; Hund, H.K.; Speth, A.R.; Lingens, F.
Biol. Chem. Hoppe-Seyler 370, 763-768, 1989
A:Title: Purification and N-terminal amino-acid sequences of bacterial maleate dehydrogenase
A:Reference number: S04956; MUID:89374824
A:Accession: S04958
A:Molecule type: protein
A:Residues: 1-20 <ROM>
C:Superfamily: L-lactate dehydrogenase
C:Keywords: oxidoreductase; tricarboxylic acid cycle

Query Match 22.1%; Score 23; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 GOVKYGL 18
||: ||
Db 11 GOIGYAL 17

RESULT 10
B44835
dTDPglucose 4,6-dehydratase (EC 4.2.1.46) - Streptomyces peucetius (fragment)
C:Species: Streptomyces peucetius
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: B44835
R:Thompson, M.W.; Strohl, W.R.; Floss, H.G.
J. Gen. Microbiol. 138, 779-786, 1992
A:Title: Purification and characterization of TDP-D-glucose 4,6-dehydratase from anthracis
A:Reference number: A44835; MUID:92268857
A:Accession: B44835
A:Molecule type: protein
A:Residues: 1-20 <THO>
A:Cross-references: PIDN:AAB2196.1; PID:g249564
A:Experimental source: ATCC 29050
A:Note: Sequence extracted from NCBI backbone (NCBIP:103673)
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 22.1%; Score 23; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 GOVKYGL 18
||: ||
Db 14 GOIGYAL 20

RESULT 11
PH1338
Ig heavy chain DJ region (clone C372-115) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: PH1338
R:Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor B1
A:Reference number: PH1302; MUID:93094761
A:Accession: PH1338
A:Molecule type: DNA
A:Residues: 1-20 <MAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match 22.1%; Score 23; DB 2; Length 20;
Best Local Similarity 30.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 8 MWLLGOVKYGL 17
::: ||:
Db 4 ILRIQLRLRYG 13

RESULT 12
S23168
Z protein - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C:Accession: S23168
R:Nicollier, M.; Roblin, S.; Cypriant, B.; Remy-Martin, J.P.; Adessi, G.L.
Eur. J. Biochem. 205, 1137-1144, 1992
A:Title: Purification and characterization of a binding protein related to the Z class
A:Reference number: S23168; MUID:92249319
A:Accession: S23168
A:Molecule type: protein
A:Residues: 1-12 <NIC>
A:Experimental source: liver
C:Function:
A:Description: binds dehydroepiandrosterone sulfate, estrone sulfate, oleic acid, cho
C:Keywords: liver; steroid binding

Query Match 21.2%; Score 22; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NITGE 5
|| ||
Db 2 NITGE 6

RESULT 13
JN0390
histamine-releasing peptide II - oriental hornet
N:Alternate names: venom protein HR-2
C:Species: Vespa orientalis (oriental hornet)
C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 23-Aug-1997
C:Accession: JN0390; S10919
R:Mitroshnikov, A.I.; Snezhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozhnov, B.V.;
Biorog. Khim. 7, 1467-1477, 1981
A:Title: Structure and properties of histamine releasing peptides from the venom of V
A:Reference number: JN0389
A:Accession: JN0390
A:Molecule type: protein
A:Residues: 1-14 <MIR>
R:Tutubayev, M.U.; Akmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.
Biochemistry (N.Y.) 53, 183-190, 1988
A:Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis.
A:Reference number: S06445
A:Accession: S10919
A:Molecule type: protein
A:Residues: 1-14 <TUI>
C:Superfamily: crabrolin
C:Keywords: amidated carboxyl end; venom
F:14/Modified site: amidated carboxyl end (Ieu) #status experimental

Query Match 21.2%; Score 22; DB 2; Length 14;
 Best Local Similarity 40.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 9 MLLGQVKYGL 18
 : : : : :
 DB 4 LILGKLVKGL 13

RESULT 14

S72217
 D-arabinose 1-dehydrogenase (NAD(P)+) (EC 1.1.1.117) - yeast (Candida albicans) (fragment)
 C:Species: Candida albicans
 C>Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 13-Mar-1998
 C:Accession: S72217
 R:Kim, S.T.; Huh, W.K.; Kim, J.Y.; Hwang, S.W.; Kang, S.O.
 Blochlm. Biophys. Acta 1297, 1-8, 1996
 A:Title: D-arabinose dehydrogenase and biosynthesis of erythroascorbic acid in Candida a
 A:Reference number: S72217; MUID:96439039
 A:Accession: S72217
 A:Molecule type: protein
 A:Residues: 1-14 <KIM>
 C:Keywords: oxidoreductase

Query Match 21.2%; Score 22; DB 2; Length 14;
 Best Local Similarity 30.8%; Pred. No. 1.7e+03;
 Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 MMLGQVKYGLHN 20
 : : : : :
 DB 1 MKLATEIDFXLNN 13

RESULT 15

A49887
 transcription factor HNF-3 beta - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 07-May-1999
 C:Accession: A49887
 R:Sasaki, H.; Hogan, B.L.M.
 Cell 76, 103-115, 1994
 A:Title: HNF-3beta as a regulator of floor plate development.
 A:Reference number: A49887; MUID:94116056
 A:Accession: A49887
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-15 <SAS>
 C:Keywords: alternative initiators; alternative splicing; transcription factor

Query Match 21.2%; Score 22; DB 2; Length 15;
 Best Local Similarity 55.6%; Pred. No. 1.8e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 AMMLGQVK 15
 : : : : :
 DB 4 ASSMLGAVK 12

Search completed: December 21, 2000, 08:30:08
 Job time: 272 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2000, 08:33:00 ; Search time 62.7 Seconds
(without alignments)
10.191 Million cell updates/sec

Title: US-08-934-367-37
Perfect score: 104
Sequence: 1 NTGKAMWLLGQVRYGLHN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 1086

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	22.1	8	AL17_CARMA	P81820 carcinus ma
2	23	22.1	9	TAL3_PICJA	F17441 pichia jadi
3	23	22.1	20	MDH_KIBAR	F19978 kibdelospor
4	23	22.1	20	MDH_MICGL	F19979 microtetras
5	22	21.2	9	AL11_CARMA	P81814 carcinus ma
6	22	21.2	14	CRBL_VESOR	F17236 vespa orien
7	22	21.2	20	LECB_IRIHO	F36231 iris hollan
8	21	20.2	8	AL16_CARMA	F18189 carcinus ma
9	21	20.2	13	CRBL_VESTR	F17231 vespa tropl
10	21	20.2	14	TEMA_RANTF	F56917 rana tempor
11	21	20.2	14	TEMA_RANTF	F56917 rana tempor
12	20	19.2	13	IDHC_PIG	F20304 sus scrofa
13	20	19.2	15	DCMM_PSECA	F19920 pseudomonas
14	20	19.2	15	DCMM_PSECH	F19917 pseudomonas
15	20	19.2	16	ARCD_PSEPU	F41147 pseudomonas
16	20	19.2	19	PHLC_STAIN	F80924 staphylococ
17	20	19.2	19	UP25_UPEIN	F82031 urocladia i
18	20	19.2	20	UCRO_EOUAR	F81247 equisetum a
19	19	18.3	10	TKSL_AEPDAE	F42634 aedes aegypt
20	19	18.3	10	TKSL_AEPDAE	F42634 aedes aegypt
21	19	18.3	14	TKSC_AEPDAE	F42633 aedes aegypt
22	19	18.3	14	TKSC_AEPDAE	F42633 aedes aegypt
23	19	18.3	15	UC18_MAIZE	F80618 zea mays (m
24	19	18.3	17	RBS_PHYPA	F80657 physcomitre
25	19	18.3	18	BOLA_MEGPE	F07495 megaphomus
26	19	18.3	18	LUXB_KRYAS	F18300 kryptophana
27	19	18.3	19	RL23_HAICU	F05978 halobacteri
28	19	18.3	20	MDH_COMAC	F80353 comamonas a
29	19	18.3	20	COG2_CHTOP	F44154 chionoecete
30	19	18.3	20	COG3_CHTOP	F44155 chionoecete
31	19	18.3	20	COG4_PARCOP	F20733 parathode
32	19	18.3	20	COG8_PARCOP	F20733 parathode
33	18	17.3	12	PA2B_VIRBO	F31855 vipeira beru

34	18	17.3	13	1	CRBL_VESMA	P17232 vespa manda
35	18	17.3	15	1	CDN5_LITCE	P82077 litorea cae
36	18	17.3	17	1	PLA2_BABA	P35634 bartonella
37	18	17.3	17	1	NU4M_TIRIU	Q36834 trichophyto
38	18	17.3	19	1	RS19_SPICI	O31159 splroplasma
39	18	17.3	20	1	ANCR_AGRBI	P33588 agkistrodon
40	18	17.3	20	1	COXO_ONCMY	P80335 oncorhynch
41	18	17.3	20	1	COXO_THIOB	P80983 thunnus obe
42	17	16.3	8	1	AL15_CARMA	P81818 carcinus ma
43	17	16.3	9	1	HUTU_KLEAE	P12381 klebsiella
44	17	16.3	10	1	CON1_ALAMI	P37041 alligator m
45	17	16.3	10	1	GS15_BACSU	P80861 bacillus su

ALIGNMENTS

RESULT 1						
ID	AL17_CARMA	STANDARD:	PRT:	8 AA.		
AC	P81820:					
DT	30-MAY-2000 (Rel. 39, Created)					
DT	30-MAY-2000 (Rel. 39, Last sequence update)					
DT	30-MAY-2000 (Rel. 39, Last annotation update)					
DE	CARCINOSTATIN 17					
OS	Carcinus maenas (Common shore crab) (Green crab).					
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;					
OC	Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;					
OC	Eubrachyura; Portunoidae; Portunidae; Carcinus.					
RN	[1]					
RP	SEQUENCE.					
RC	TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;					
RP	MEDLINE: 98121193.					
RA	Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,					
RA	Thorpe A.;					
RT	"Isolation and identification of multiple neuropeptides of the					
RT	RT allatostatin superfamily in the shore crab Carcinus maenas.";					
RL	Eur. J. Biochem. 250:727-734(1997).					
CC	-I- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.					
CC	-I- SIMILARITY: BELONGS TO THE ALATOSTATIN FAMILY.					
KW	Neuropeptide; Amidation; Multigene family.					
FT	MOD_RES 8					
FT	SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;					
Query Match						
Best Local Similarity		22.1%	Score 23;	DB 1;	Length 8;	
Matches 4;		Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;	
Oy	12 GOVKYGL 18					
	:					
Db	2 GOYSFGL 8					
RESULT 2						
ID	TAL3_PICJA	STANDARD:	PRT:	9 AA.		
AC	P17441:					
DT	01-AUG-1990 (Rel. 15, Created)					
DT	01-AUG-1990 (Rel. 15, Last sequence update)					
DT	01-FEB-1994 (Rel. 28, Last annotation update)					
DE	TRANSALDOLASE III (EC 2.2.1.2) (FRAGMENT).					
OS	Pichia jadinii (Yeast) (Candida utilis).					
OC	Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;					
OC	Saccharomycetales; Pichia.					
RN	[1]					
RP	SEQUENCE.					
RP	MEDLINE: 75145197.					
RA	Tsolas O., Sun S.C.;					
RT	"Isolation of a peptide containing a histidiny1-cysteinyl sequence					
RT	from the active center of transaldolase.";					
RL	Arch. Biochem. Biophys. 167:525-533(1975).					
CC	-I- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF					

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CC METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
CC -1- CATALYTIC ACTIVITY: SEDOHEPTULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE
CC 3-PHOSPHATE = D-FRUCTULOSE 4-PHOSPHATE + D-FRUCTULOSE 6-PHOSPHATE.
CC -1- PATHWAY: NONOXIDATIVE PART OF THE PENTOSE-PHOSPHATE PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY.
DR PIR: A11497; A11497.
DR INTERPRO: IPR001585; -.
DR PROSITE: PS00958; TRANSALDOLASE_2; PARTIAL.
DR PROSITE: PS01054; TRANSALDOLASE_1; PARTIAL.
KW Transferase; Pentose shunt.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1033 MW; 325A31A44EB1E058 CRC64;

Query Match
Best Local Similarity 22.1%; Score 23; DB 1; Length 9;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 YG1H 19
DB 1 YG1H 4

RESULT 3
MDH_KIBAR
ID MDH_KIBAR STANDARD; PRT; 20 AA.
AC P19978;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MALATE DEHYDROGENASE (EC 1.1.1.37) (FRAGMENT).
GN MDH.
OS Kibdelosporangium aridum.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
OC Kibdelosporangium.
RN [1]
RP SEQUENCE.
RX Rommel T.O., Hand H.-K., Speth A.R., Lingsens F.;
RT "Purification and N-terminal amino-acid sequences of bacterial malate
RT dehydrogenases from six actinomycetales strains and from
RT phenyllobacterium immobile, strain E."
RL Biol. Chem. Hoppe-Seyler 370:763-768(1989).
CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE + NADH.
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
DR PIR: S04961; S04961.
DR HSSP: P10584; 1BDW.
DR INTERPRO: IPR001252; -.
DR PROSITE: PS00068; MDH; PARTIAL.
KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT NON_TER 20 20
FT MOD_RES 9 9
SQ SEQUENCE 20 AA; 1989 MW; 79587E6F58C00AC9 CRC64;

Query Match
Best Local Similarity 22.1%; Score 23; DB 1; Length 20;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 GQVYGL 18
DB 14 GQ1GYAL 20

RESULT 4
MDH_MICGL
ID MDH_MICGL STANDARD; PRT; 20 AA.
AC P19979;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MALATE DEHYDROGENASE (EC 1.1.1.37) (FRAGMENT).

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GN MDH.
OS Microtetraspora glauca.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptosporangineae; Streptosporangiaceae;
OC Microtetraspora.
RN [1]
RP SEQUENCE.
RX Rommel T.O., Hand H.-K., Speth A.R., Lingsens F.;
RT "Purification and N-terminal amino-acid sequences of bacterial malate
RT dehydrogenases from six actinomycetales strains and from
RT phenyllobacterium immobile, strain E."
RL Biol. Chem. Hoppe-Seyler 370:763-768(1989).
CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE + NADH.
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
DR PIR: S04958; S04958.
DR HSSP: P10584; 1BDW.
DR INTERPRO: IPR001236; -.
DR INTERPRO: IPR001252; -.
DR PFAM: PF00056; Ldh; 1.
DR PROSITE: PS00068; MDH; PARTIAL.
KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT NON_TER 20 20
FT MOD_RES 9 9
SQ SEQUENCE 20 AA; 2065 MW; 740129BE59D01EBE CRC64;

Query Match
Best Local Similarity 22.1%; Score 23; DB 1; Length 20;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 GQVYGL 18
DB 11 GQ1GYAL 17

RESULT 5
AL11_CARMA
ID AL11_CARMA STANDARD; PRT; 9 AA.
AC P81814;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINUSSTYRIN 11.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
RN [1]
RP SEQUENCE.
RX TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
RC MEDLINE; 98121193.
RX Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaro P.P.,
RA "Isolation and identification of multiple neuropeptides of the
RA allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 9 9
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 927 MW; 832D79CDB46D861 CRC64;

Query Match
Best Local Similarity 21.2%; Score 22; DB 1; Length 9;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 GQVYGL 18
DB 3 GQVAFGL 9

RESULT 6

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CRBL_VESOR
ID CRBL_VESOR STANDARD: PRT: 14 AA.
AC P17236:
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE HISTAMINE-RELEASING PEPTIDE II (HR-II).
OS Vespa orientalis (Oriental hornet).
OC Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
OC Pterygota: Neoptera: Endopterygota: Hymenoptera: Apocrita: Aculeata:
OC Vespoidea: Vespidae: Vespinae: Vespa.
RN [1]
RP SEQUENCE.
RC TISSUE-VEINOM:
RA Miroshnikov A.I., Snezhkova L.G., Nazinov I.V., Reshetova O.I.,
RA Rozynov B.V., Gushchin I.S.;
RT "Structure and properties of histamine releasing peptides from the
RT venom of Vespa orientalis hornet."
RL Bloofg. Khim. 7:1467-1477(1981).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
CC OF NEUTROPHILS.
DR PIR: JN0390.
KM MAST cell degranulation: Chemotaxis: Venom: Amidation.
FT MOD_RES 14
SQ SEQUENCE 14 AA: 1524 MW: 22015B4ACEDEFD38 CRC64:

Query Match 21.2% Score 22: DB 1: Length 14:
Best Local Similarity 40.0%: Pred. No. 8.4e+02;
Matches 4: Conservative 4: Mismatches 2: Indels 0: Gaps 0:
QY 9 MLCGVKYL 18
Db 4 LILGKLKGL 13

RESULT 7
LECB_IRIHO
ID LECB_IRIHO STANDARD: PRT: 20 AA.
AC P36231:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE N-ACETYL-D-GALACTOSAMINE-BINDING LECTIN SUBUNIT B (A-DISACCHARIDE-
DE BINDING LECTIN SUBUNIT B) (FRAGMENT).
OS Iris hollandica (Dutch iris)
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
OC Magnoliophyta: Liliopsida: Asparagales: Iridaceae: Iris.
RN [1]
RP SEQUENCE.
RC STRAIN-CV. GOLDEN HARVEST, AND CV. PROF. BLAUW; TISSUE-BULB;
RX MEDLINE: 94171801.
RA Mc H., van Damme E.J.M., Peumans W.J., Goldstein I.J.;
RT "Isolation and characterization of an
RT N-acetyl-D-galactosamine-binding lectin from Dutch iris bulbs which
RT recognizes the blood group A disaccharide (GalNAc alpha 1-3Gal).";
RL J. Biol. Chem. 269:7666-7673(1994).
CC -1- FUNCTION: GAL / GALNAc-SPECIFIC LECTIN. AGGLUTINATES BOTH NATIVE
CC AND TRYPSIN-TREATED RABBIT ERYTHROCYTES BUT NOT HUMAN ERYTHROCYTES
CC IRRESPECTIVE OF BLOOD GROUP TYPE.
CC -1- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A AND B CHAINS.
KM LECTIN.
FT NON_TER 20
SQ SEQUENCE 20 AA: 2246 MW: DE08DA025FD17D56 CRC64:

Query Match 21.2% Score 22: DB 1: Length 20:
Best Local Similarity 50.0%: Pred. No. 1.2e+03;
Matches 4: Conservative 2: Mismatches 2: Indels 0: Gaps 0:
QY 5 EKAWMLG 12
Db 9 EETWRIIG 16

RESULT 8
AL16_CARMA
ID AL16_CARMA STANDARD: PRT: 8 AA.
AC P81819:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE CARCINUSMAENAS 16.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota: Metazoa: Arthropoda: Crustacea: Malacostraca:
OC Eumalacostraca: Eucarida: Decapoda: Pleocyemata: Brachyura:
OC Eudacchylura: Portunioidea: Portunidae: Carcinus.
RN [1]
RP SEQUENCE.
RC TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
RX MEDLINE: 98121193.
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaro P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KM Neuropeptide: Amidation: Multigene family.
FT MOD_RES 8
SQ SEQUENCE 8 AA: 813 MW: 7C286B45AB476878 CRC64:

Query Match 20.2% Score 21: DB 1: Length 8:
Best Local Similarity 57.1%: Pred. No. 8.8e+04;
Matches 4: Conservative 0: Mismatches 3: Indels 0: Gaps 0:
QY 12 GQVRYGL 18
Db 2 GPVSYGL 8

RESULT 9
CRBL_VESTR
ID CRBL_VESTR STANDARD: PRT: 13 AA.
AC P17231:
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE VESPID CHEMOTACTIC PEPTIDE T (VESP-T).
OS Vespa tropica (Hornet).
OC Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
OC Pterygota: Neoptera: Endopterygota: Hymenoptera: Apocrita: Aculeata:
OC Vespoidea: Vespidae: Vespinae: Vespa.
RN [1]
RP SEQUENCE.
RC TISSUE-VEINOM:
RA Yasuhara T., Nakajima T., Erspaer V.;
RT (In) Sakakibara S. (eds.);
RL Peptide chemistry 1982, pp. 213-218, Protein Research Foundation,
RL Osaka (1983).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
CC OF NEUTROPHILS.
CC MAST cell degranulation: Chemotaxis: Venom: Amidation.
KM MOD_RES 13
SQ SEQUENCE 13 AA: 1354 MW: 220140365DFE538 CRC64:

Query Match 20.2% Score 21: DB 1: Length 13:
Best Local Similarity 44.4%: Pred. No. 1.1e+03;
Matches 4: Conservative 3: Mismatches 2: Indels 0: Gaps 0:
QY 10 LMGVRYGL 18
Db 4 ILGKILGGL 12

RESULT 10
 ID TEMP_RANTE STANDARD: PRT: 14 AA.
 AC P56917;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TEMPORIN A.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-SKIN.
 RX MEDLINE: 97175050.
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barra D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 RT temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
 CC BACTERIA.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 CC FAMILY.
 KM Amphibian skin; Antibiotic; Amidation; Multigene family.
 FT MOD RES 14
 FT SEQUENCE 14 AA; 1469 MW; 601653612B9DECD4 CRC64;
 SQ

Query Match 20.2%; Score 21; DB 1; Length 14;
 Best Local Similarity 44.4%; Pred. No. 1.2e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 10 LIGQVKYGL 18
 I::I I:
 Db 4 LIGKVLST 12

RESULT 11
 ID TEMP_RANTE STANDARD: PRT: 14 AA.
 AC P56921;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TEMPORIN F.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-SKIN;
 RX MEDLINE: 97175050.
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barra D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 RT temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
 CC GRAM-POSITIVE BACTERIA.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 CC FAMILY.
 KM Amphibian skin; Antibiotic; Amidation; Multigene family.
 FT MOD RES 14
 FT SEQUENCE 14 AA; 1441 MW; 4D1653612B9DECC3 CRC64;
 SQ

Query Match 20.2%; Score 21; DB 1; Length 14;
 Best Local Similarity 44.4%; Pred. No. 1.2e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 10 LIGQVKYGL 18
 I::I I:
 Db 4 LIGKVLST 12

RESULT 12
 IDHC_PIG STANDARD: PRT: 13 AA.
 AC P20304;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE ISOCITRATE DEHYDROGENASE [NADP] CYTOPLASMIC (EC 1.1.1.42)
 DE (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICCH) (IDP)
 DE IDH1.
 GN Sus scrofa (Pig).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 87308293.
 RA Bailey J.M., Colman R.F.;
 RT "Isolation of the glutamyl peptide labeled by the nucleotide analogue
 RT 2-(4-bromo-2,3-dioxobutylthio)-L-N(6)-ethenoadenosine
 RT 2',5'-biphosphate in the active site of NADP+-specific isocitrate
 RT dehydrogenase.";
 RL J. Biol. Chem. 262:12620-12626(1987).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE: 87308292.
 RA Ehrlich R.S., Colman R.F.;
 RT "Characterization of an active site peptide modified by the substrate
 RT analogue 3-bromo-2-ketoglutarate on a single chain of dimeric NADP+-
 RT dependent isocitrate dehydrogenase.";
 RL J. Biol. Chem. 262:12614-12619(1987).
 CC -1- CATALYTIC ACTIVITY: ISOCITRATE + NADP(+) = 2-OXOGLUTARATE +
 CC CO(2) + NADPH.
 CC -1- SUBUNIT: HOMODIMER.
 CC PIR; A27371; A27371.
 DR PIR; A27372; A27372.
 DR INTERPRO: IPR001804; -;
 DR PROSITE: PS00470; IDH_IMDH; PARTIAL.
 KM Oxidoreductase; NADP; Tricarboxylic acid cycle.
 FT NON_TER 1
 FT ACT_SITE 5
 FT POTENTIAL 13
 FT SEQUENCE 13 AA; 1353 MW; 1B640F0B9F7C71E0 CRC64;
 SQ

Query Match 19.7%; Score 20.5; DB 1; Length 13;
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

OY 10 LIGQVKYGLHN 20
 I::I I:
 Db 2 LAGEI-HGLSN 11

RESULT 13
 ID DCMK_PSECA STANDARD: PRT: 15 AA.
 AC P19920;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE CARBON MONOXIDE OXYGENASE [CYTOCHROME B-561] MEDIUM CHAIN (EC 1.2.2.4)
 DE (FRAGMENT).
 OS Pseudomonas carboxydovorans.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Bradyrhizobium group; Oligotropha.
 RN [1]

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RP SEQUENCE.
RC STRAIN-OW5:
RX MEDLINE: 90055678.
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RL carboxydophilic bacteria."
RL Arch. Microbiol. 152:335-341(1989).
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + FERROCYTOCHROME B-561 = CO(2) +
CC 2 H(+) + FERRICCYTOCHROME B-561.
CC -1- COFACTOR: MOLYBDENUM.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR: PLO141.
KW Oxidoreductase; Molybdenum.
FT NON_TER
SQ SEQUENCE 15 AA: 1779 MW: 82D03BF93E739D63 CRC64;

Query Match 19.2%; Score 20; DB 1; Length 15;
Best Local Similarity 44.4%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 8 MMLGOVKY 16
||:|
Db 1 MMLPGHFDY 9

RESULT 14
DCMH_PSECH STANDARD; PRT; 15 AA.
ID DCMH_PSECH
AC P19917;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARBON MONOXIDE DEHYDROGENASE MEDIUM CHAIN (EC 1.2.99.2) (FRAGMENT).
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria.
CC [1]
RN SEQUENCE.
RX MEDLINE: 90055678.
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RL carboxydophilic bacteria."
RL Arch. Microbiol. 152:335-341(1989).
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
CC ACCEPTOR.
CC -1- COFACTOR: MOLYBDENUM.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR: PLO143.
KW Oxidoreductase; Molybdenum.
FT NON_TER
SQ SEQUENCE 15 AA: 1815 MW: 90508CF93E739D63 CRC64;

Query Match 19.2%; Score 20; DB 1; Length 15;
Best Local Similarity 44.4%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 8 MMLGOVKY 16
||:|
Db 1 MMLPGHFDY 9

RESULT 15
ARCD_PSEPU STANDARD; PRT; 16 AA.
ID ARCD_PSEPU
AC P41147;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ARGININE/ORNITHINE ANTIporter (FRAGMENT).
ARCD

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OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 4359;
RA Wilson S.D., Wang M., Filpula D.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES AN ELECTRONEUTRAL EXCHANGE BETWEEN ARGININE
CC AND ORNITHINE TO ALLOW HIGH-EFFICIENCY ENERGY CONVERSION IN THE
CC ARGININE DEIMINASE PATHWAY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYST FAMILY OF
CC PERMEASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U07185; AAA16963.1;
KW Transport; Amino-acid transport; Transmembrane; Inner membrane.
FT NON_TER
SQ SEQUENCE 16 AA: 1644 MW: 90B48A7C8FAA9705 CRC64;

Query Match 19.2%; Score 20; DB 1; Length 16;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 16 YGLHN 20
||||:
Db 7 YGLYD 11

```

Search completed: December 21, 2000, 08:33:00
Job time: 443 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 21, 2000, 08:35:40 ; Search time 157.2 Seconds

(without alignments)
11.880 Million cell updates/sec

Title: US-08-934-367-37

Perfect score: 104

Sequence: 1 NITGEKAMMLGQVKYGLHN 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	30.8	19	10	Q9S8G6
2	27	26.0	17	8	003888
3	27	26.0	17	10	Q9S8U7
4	25	24.0	19	2	031045
5	25	24.0	19	5	09TMD0
6	24.5	23.6	19	2	053545
7	24	23.1	11	5	09UAK8
8	23	22.1	17	6	09TQ25
9	23	22.1	19	2	09R4A3
10	23	22.1	20	3	09R5L1
11	22	21.2	8	3	005403
12	22	21.2	17	8	09T2S1
13	22	21.2	18	13	09PRM8
14	22	21.2	19	8	036277
15	22	21.2	19	10	Q9S901
16	22	21.2	20	4	09UCP6
17	22	21.2	20	6	028734
18	22	21.2	20	13	09PRM4
19	21	20.2	15	6	09TRW0

20	21	20.2	17	4	09UCF0
21	21	20.2	17	11	09Q107
22	21	20.2	18	4	09UCB2
23	21	20.2	19	2	057012
24	21	20.2	19	11	064132
25	21	20.2	19	11	09QXP9
26	21	20.2	20	2	034197
27	21	20.2	20	2	09R419
28	21	20.2	20	10	09S739
29	20	19.2	10	5	025355
30	20	19.2	11	12	084247
31	20	19.2	15	5	09TXC8
32	20	19.2	15	12	084332
33	20	19.2	16	4	09UC18
34	20	19.2	16	12	084353
35	20	19.2	17	2	052748
36	20	19.2	17	5	09TWF6
37	20	19.2	18	11	09QVBO
38	20	19.2	19	2	006140
39	20	19.2	19	2	09R4X3
40	20	19.2	19	5	09TRK7
41	20	19.2	19	12	084863
42	20	19.2	20	2	09R9A5
43	20	19.2	20	2	09R987
44	20	19.2	20	2	09R5T8
45	20	19.2	20	3	013594

ALIGNMENTS

RESULT 1
ID Q9S8G6 PRELIMINARY: PRT: 19 AA.
AC Q9S8G6:
DT 01-MAY-2000 (TREMBLREL. 13, Created)
DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLREL. 14, Last annotation update)
DE TYPE 2 LECTIN (FRAGMENT).
OS Colocasia esculenta (Elephant's ear) (Taro).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Araceae; Colocasia.
RN [1]
RP SEQUENCE.
RX MEDLINE: 95288362.
RA Van Damme E.D., Goossens K., Smeets K., van Leuven F., Verhaert P.,
RA Pennans W.J.;
RT "The major tuber storage protein of araceae species is a lectin.
RT Characterization and molecular cloning of the lectin from Arum
RT maculatum L.";
RL Plant Physiol. 107:1147-1158(1995).
SQ SEQUENCE 19 AA: 206 MW: F9C18865CA58608A CRC64:

Query Match 30.8%; Score 32; DB 10; Length 19;
Best Local Similarity 41.2%; Pred. No. 79;
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 1 NITGEKAMMLGQVKY 17
II : : : : :
Db 1 NIPFTNLLFSCGVYXG 17
RESULT 2
ID Q03888 PRELIMINARY: PRT: 17 AA.
AC Q03888:
DT 01-JUL-1997 (TREMBLREL. 04, Created)
DT 01-JUL-1997 (TREMBLREL. 04, Last sequence update)
DT 01-NOV-1998 (TREMBLREL. 08, Last annotation update)
DE NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE)
DE (TYPE I DEHYDROGENASE) (FRAGMENT).
GN NAD5.

OS Chlorogonium elongatum.
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Haematococcaceae; Chlorogonium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2E;
 RX MEDLINE; 97306270.
 RA Kroyman J., Zetsche K.;
 RT "The apocytochrome-b gene in Chlorogonium elongatum
 (Chlamydomonadaceae): an intronic G1Y-XIG ORF in green algal
 mitochondria.";
 RL Curr. Genet. 31:414-418(1997).
 CC -1- CATALYTIC ACTIVITY: NADH + ACCEPTOR = NAD(+) + REDUCED ACCEPTOR.
 CC -1- COFACTOR: FLAVOPROTEIN; IRON-SULFUR.
 DR EMBL; Y07814; CAA69147.1; -
 KW Oxidoreductase; Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 17 AA; 1844 MW; BC88B2E8E529A229 CRC64;

Query Match 26.0%; Score 27; DB 8; Length 17;
 Best Local Similarity 31.2%; Pred. No. 4.8e+02;
 Matches 5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 TGEKAMLLGQVRYGL 18
 ||:|::|
 DB 2 TGDKGLFIYHDKVSL 17

RESULT 3
 Q9S8U7 PRELIMINARY; PRT; 17 AA.
 AC Q9S8U7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE SOLANIDINE UDP-GLUCOSE GLUCOSYLTRANSFERASE, SGT-19 KDA CNBR CLEAVED
 DE FRAGMENT.
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
 OC Solanaceae; Solanum.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 93044546.
 RA Stapleton A., Allen P.V., Tao H.P., Belknap W.R., Friedman M.;
 RT "Partial amino acid sequence of potato solanidine UDP-glucose
 RT glucosyltransferase purified by new anion-exchange and size exclusion
 RT media.";
 RL Protein Expr. Purif. 3:85-92(1992).
 SQ SEQUENCE 17 AA; 1783 MW; 75BADCB0077E593C CRC64;

Query Match 26.0%; Score 27; DB 10; Length 17;
 Best Local Similarity 83.3%; Pred. No. 4.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NITGEK 6
 ||:|::|
 DB 8 NISGEK 13

RESULT 4
 Q310A5 PRELIMINARY; PRT; 19 AA.
 AC Q310A5;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE LEUA LEADER PEPTIDE.
 LEUA.
 GN Streptomyces coelicolor.
 OS

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-D132;
 RA Potter C.A., Baumberg S.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF026444; AAB82585.1; -
 SQ SEQUENCE 19 AA; 2080 MW; 1A591DC2999760D4 CRC64;

Query Match 24.0%; Score 25; DB 2; Length 19;
 Best Local Similarity 44.4%; Pred. No. 1.2e+03;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 10 LLGQVRYGL 18
 :||::|
 DB 1 MLGIMRFG 9

RESULT 5
 Q9TWD0 PRELIMINARY; PRT; 19 AA.
 AC Q9TWD0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE STALOPROTEIN I (FRAGMENT).
 OS Sphaerechinus granularis (purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
 OC Euechinoidea; Echinacea; Temnopleuruloidea; Toxopneustidae;
 OC Sphaerechinus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 96428846.
 RA Karamanos N.K., Manouras A., Anagnostides S., Makatsori E.,
 RA Tseganidis T., Antonopoulos C.A.;
 RT "Isolation, biochemical and immunological characterisation of two sea
 RT urchin glycoproteins bearing sulphated poly(styalic acid)
 RT polysaccharides rich in N-glycolyl neuraminic acid.";
 RL Biochimie 78:171-182(1996).
 SQ SEQUENCE 19 AA; 2265 MW; 38FFDEB1A033E850 CRC64;

Query Match 24.0%; Score 25; DB 5; Length 19;
 Best Local Similarity 27.3%; Pred. No. 1.2e+03;
 Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 6 KAMMLGQVRY 16
 :||::|
 DB 8 QXMLTXGEIEY 18

RESULT 6
 Q53545 PRELIMINARY; PRT; 19 AA.
 AC Q53545;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE VIRF (FRAGMENT).
 VIRF.
 GN Shigella sonnei.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Shigella.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95394812.
 RA Nakayama S., Watanabe H.;
 RT "Involvement of cpxA, a sensor of a two-component regulatory system,
 RT in the pH-dependent regulation of expression of Shigella sonnei VIRF
 RT gene.";
 RL J. Bacteriol. 177:5062-5069(1995).

DR EMBL: S79443; AAB35192.1; -
 FT NON_TER 19
 SQ SEQUENCE 19 AA: 2344 MW: 52A53B9DAAEFCF4 CRC64;

Query Match 23.6%; Score 24.5; DB 2; Length 19;
 Best Local Similarity 38.9%; Pred. No. 1.4e+03;
 Matches 7; Conservative 2; Mismatches 4; Indels 5; Gaps 1;

OY 8 MLLG-----QKYLHN 20
 11:1111
 1 MMDGHRNKKIDIKVRLHN 18

RESULT 7
 ID Q9UAR8 PRELIMINARY; PRT: 11 AA.
 AC Q9UAR8;
 DT 01-MAY-2000 (TREMBLREL. 13, Created)
 DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLREL. 14, Last annotation update)
 DE STALOKININ I PREPROTEIN (FRAGMENT).
 OS Aedes aegypti (yellow fever mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 OC Culicidae; Aedes.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ROCKEFELLER/RED. TISSUE=SALIVARY GLAND;
 RA Beerltsen B.T., Champagne D.E., Coleman J.L., Campos Y.A., James A.A.;
 RT Characterization of the stialokinin I gene encoding the salivary
 RT vasodilator of the yellow fever mosquito, Aedes aegypti."
 RL Insect Mol. Biol. 0:0-0(1999).
 DR EMBL: AF108100; AAD16884.1; -
 DR INTERPRO: IPR002040; -
 FT PROSITE: PS00267; TACHYKININ; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 11 AA: 1203 MW: 8BADC77C6B59C33A CRC64;

Query Match 23.1%; Score 24; DB 5; Length 11;
 Best Local Similarity 50.0%; Pred. No. 9.4e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 TGEKAMMLG 12
 11:1111
 Db 2 TGDKFXGLMG 11

RESULT 8
 ID Q9TQZ5 PRELIMINARY; PRT: 17 AA.
 AC Q9TQZ5;
 DT 01-MAY-2000 (TREMBLREL. 13, Created)
 DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLREL. 14, Last annotation update)
 DE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (FRAGMENT).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 RN [1]
 RP SEQUENCE.
 RA MEDLINE: 96273610.
 RA Nicolas M.G., Fujiki K., Murayama K., Suzuki M.T., Mineki R.,
 RA Hayakawa M., Yoshikawa Y., Cho F., Kanai A.;
 RT "Studies on the mechanism of early onset macular degeneration in
 RT cynomolgus (Macaca fascicularis) monkeys. I. Abnormal concentrations
 RT of two proteins in the retina."
 RL Exp. Eye Res. 62:211-219(1996).
 SQ SEQUENCE 17 AA: 1671 MW: 52CCDD0D1A9B3DAF CRC64;

Query Match 22.1%; Score 23; DB 6; Length 17;
 Best Local Similarity 50.0%; Pred. No. 2.3e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 12 GOVKYGLH 19
 11:111111
 Db 1 GKVKGVN 8

RESULT 9
 ID Q9RAA3 PRELIMINARY; PRT: 19 AA.
 AC Q9RAA3;
 DT 01-MAY-2000 (TREMBLREL. 13, Created)
 DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLREL. 13, Last annotation update)
 DE N-ACETYL-D-NEURAMINIC ACID LYASE (EC 4.1.3.3) (FRAGMENT).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE.
 RA MEDLINE: 96276413.
 RA Ferrero M.A., Reglero A., Fernandez-Lopez M., Ordas R.,
 RA Rodriguez-Aparicio L.B.;
 RT "N-acetyl-D-neuraminic acid lyase generates the stialic acid for
 RT colominic acid biosynthesis in Escherichia coli K1."
 RL Biochem. J. 317:157-165(1996).
 SQ SEQUENCE 19 AA: 2061 MW: 7202247A20EBBE3 CRC64;

Query Match 22.1%; Score 23; DB 2; Length 19;
 Best Local Similarity 45.5%; Pred. No. 2.6e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 NITGEKAMML 11
 11:111111
 Db 3 NLRGVMAALLL 13

RESULT 10
 ID Q9R5L1 PRELIMINARY; PRT: 20 AA.
 AC Q9R5L1;
 DT 01-MAY-2000 (TREMBLREL. 13, Created)
 DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLREL. 14, Last annotation update)
 DE THYMIDINE 5'-DIPHOSPHATE D-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
 DE (FRAGMENT).
 OS Streptomyces peucetius.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
 RN [1]
 RP SEQUENCE.
 RA MEDLINE: 92268857.
 RA Thompson M.W., Strohl W.R., Floss H.G.;
 RT "Purification and characterization of TDP-D-glucose 4,6-dehydratase
 RT from anthracycline-producing streptomycetes."
 RL J. Gen. Microbiol. 138:779-786(1992).
 SQ SEQUENCE 20 AA: 1943 MW: 7958730238C00AC9 CRC64;

Query Match 22.1%; Score 23; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 GOVKYGL 18
 11:111111
 Db 14 GQIGVAL 20

RESULT 11
 Q05403

ID Q05403 PRELIMINARY; PRT; 8 AA.
AC Q05403;
RX MEDLINE: 96085138.
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE DNA FOR ORF'S FROM CHROMOSOME XV (FRAGMENT).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE: 96021609.
RA Zumaeta E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RT "A 29,425 kb segment on the left arm of yeast chromosome XV contains
RL more than twice as many unknown as known open reading frames.";
DR EMBL: X83121; CAA58183.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 21.2%; Score 22; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 17 GLHN 20
I : I I
DB 1 GITH 4

RESULT 12
O9T2S1 PRELIMINARY; PRT; 17 AA.
AC O9T2S1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE CYTOCHROME-C REDUCTASE 55 KDA SUBUNIT (EC 1.10.2.2) (FRAGMENT).
OS Solanum tuberosum (Potato).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
OC Solanaceae; Solanum.
RN [1]
RP SEQUENCE.
RA Braun H.P., Kruft V., Schmitz U.K.;
RL Planta 193:99-106(1994).
SQ SEQUENCE 17 AA; 1870 MW; 207804E213CD4009 CRC64;

Query Match 21.2%; Score 22; DB 8; Length 17;
Best Local Similarity 44.4%; Pred. No. 3.3e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 6 KAMMLGOV 14
I : I I I
DB 1 KAVDILGDI 9

RESULT 13
O9PRM8 PRELIMINARY; PRT; 18 AA.
AC O9PRM8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE AFAACYLIN CHAIN RCM-BETA (FRAGMENT).
OS Cerastes cerastes (Horned desert viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Cerastes.
RN [1]

RP SEQUENCE.
RX MEDLINE: 96085138.
RA Iaraba-tjebari F., Martin-Eauclaire M.F., Mauco G., Marchot P.;
RT "Afaacylin, an alpha beta-fibrinogenase from Cerastes cerastes (horned
RT viper) venom, activates purified factor X and induces serotonin
RL release from human blood platelets.";
RL Eur. J. Biochem. 233:756-765(1995).
SQ SEQUENCE 18 AA; 1937 MW; CF680343FE55327 CRC64;

Query Match 21.2%; Score 22; DB 13; Length 18;
Best Local Similarity 36.4%; Pred. No. 3.5e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 NINGEKAMML 11
I : I I I I I
DB 8 NINEHRSVLV 18

RESULT 14
O36277 PRELIMINARY; PRT; 19 AA.
AC O36277;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE NADH DEHYDROGENASE SUBUNIT I (FRAGMENT).
GN NAD1.
OS Zea mays (maize).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRB73; TISSUE=HYPOCOTYL;
RX MEDLINE: 95140641.
RA Thomson M.C., Macfarlane J.L., Beagley C.T., Wolstenholme D.R.;
RT "RNA editing of mat-r transcripts in maize and soybean increases
RT similarity of the encoded protein to fungal and bryophyte group II
RT intron maturases: evidence that mat-r encodes a functional protein.";
RL Nucleic Acids Res. 22:5745-5752(1994).
DR EMBL: U09986; AAA67712.1; -.
DR INTERPRO: IPR001694; -.
DR PFM: PFM0146; NADHdn. 1.
KM Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 19 AA; 2082 MW; C2DA5548846188D3 CRC64;

Query Match 21.2%; Score 22; DB 8; Length 19;
Best Local Similarity 62.5%; Pred. No. 3.8e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 GEKAMML 11
I : I I I I I
DB 11 GEYANMIL 18

RESULT 15
O9S901 PRELIMINARY; PRT; 19 AA.
AC O9S901;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE C6 PEPTIDE.
OS Vigna sinensis (Cowpea).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Fabales; Fabaceae;
OC Papilionoideae; Vigna.
RN [1]
SQ SEQUENCE.

RA Hirano H., Kagawa H., Okubo K.;
 RL Phytochemistry 31:731-735(1992).
 SQ SEQUENCE 19 AA; 1989 MW; 6281AFF927726D74 CRC64;

Query Match 21.2%; Score 22; DB 10; Length 19;
 Best Local Similarity 50.0%; Pred. No. 3.8e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 9 MLGQVKKYL 18
 I : I I I : I
 Db 1 MTVGVGVGNL 10

Search completed: December 21, 2000, 08:35:40
 Job Time: 603 sec

